

F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS).//0.94:  
 65:29//STREPTOCOCCUS EQUISIMILIS./P30053  
 F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//0.098:79:31//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53074  
 5 F-PLACE1003936  
 F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//  
 4.7e-68:164:78//RATTUS NORVEGICUS (RAT).//P80385  
 F-PLACE1004103//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!/1.9e-14:60:73//HOMO SAPIENS (HUMAN).//  
 P39192  
 10 F-PLACE1004104//EXOCYST COMPLEX COMPONENT SEC5.//0.020:202:20//SACCHAROMYCES CEREVI-  
 SIAE (BAKER'S YEAST).//P89102  
 F-PLACE1004114//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!/2.1e-15:69:60//HOMO SAPIENS (HUMAN).//  
 P39188  
 15 F-PLACE1004118//REGULATORY PROTEIN E2.//0.73:58:36//CANINE ORAL PAPILLOMAVIRUS (COPV).//  
 Q89420  
 F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA  
 CHAIN 4).//7.7e-62:108:100//MUS MUSCULUS (MOUSE).//P29387  
 F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN.//0.0011:73:42//PSEUDORABIES VIRUS (STRAIN KAP-  
 LAN) (PRV).//P33485  
 20 F-PLACE1004156//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.00061:39:48//OWENIA FUSI-  
 FORMIS.//P21260  
 F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMENT).//0.033:108:27//  
 STREPTOCOCCUS PYOGENES.//P49054  
 F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5 INTERGENIC REGION.//4.0e-07:146:  
 25 35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38817  
 F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//5.9e-11:208:27//MUS MUSCULUS (MOUSE).//  
 Q62556  
 F-PLACE1004203//PROTEIN A39.//8.5e-18:139:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062  
 F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//1.0:28:42//PISUM SATIVUM (GAR-  
 30 DEN PEA).//P13555  
 F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D).//0.73:134:25//CAENORHABDITIS ELEGANS.//P02567  
 F-PLACE1004257//HYPOTHETICAL PROTEIN HI0490.//0.13:75:29//HAEMOPHILUS INFLUENZAE.//P44006  
 F-PLACE1004258//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.027:128:  
 35//HOMO SAPIENS (HUMAN).//P25067  
 35 F-PLACE1004270//LARGE TEGUMENT PROTEIN.//1.8e-10:100:44//EPSTEIN-BARR VIRUS (STRAIN B95-8)  
 (HUMAN HERPESVIRUS 4).//P03186  
 F-PLACE1004274//HYPOTHETICAL PROTEIN E-95.//0.44:61:42//HUMAN ADENOVIRUS TYPE 2.//P03286  
 F-PLACE1004277//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:55:38//BOS TAURUS (BOVINE).//  
 P25508  
 40 F-PLACE1004284//7 KD PROTEIN (ORF 4).//1.0:63:23//CHRYSANTHEMUM VIRUS B (CVB).//P37990  
 F-PLACE1004289//SPERM PROTAMINE P3.//0.00057:22:77//MUS MUSCULUS (MOUSE).//Q62100  
 F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-).//0.0065:148:29//STREPTOMY-  
 CES COELICOLOR.//P54741  
 F-PLACE1004316//AUTOPHAGY PROTEIN APG5.//8.8e-06:117:29//SACCHAROMYCES CEREVISIAE (BAK-  
 45 ER'S YEAST).//Q12380  
 F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0027:83:36//HOMO SAPIENS (HU-  
 MAN).//P53420  
 F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.9e-05:200:33//GALLUS GALLUS  
 (CHICKEN).//P02457  
 50 F-PLACE1004376//AXONEME-ASSOCIATED PROTEIN MST101(2).//2.4e-05:179:29//DROSOPHILA HYDEI  
 (FRUIT FLY).//Q08696  
 F-PLACE1004384//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!/1.6e-28:46:76//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//5.7e-34:202:  
 55 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722  
 F-PLACE1004405//NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLAC-  
 TOSE- BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH) (FLAGELLAR  
 SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).//0.93:74:33//HELICOBACTER ACINONYX.//Q47947

F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.81:70:42//HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.9e-31:203:39//RATTUS NORVEGICUS (RAT).//Q63448  
 5 F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD], MITOCHONDRIAL SUBUNIT BETA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) (FRAGMENT).//4.2e-93:140:100//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28479  
 F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00013:40:62//HOMO SAPIENS (HUMAN).//P39188  
 10 F-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0066:218:23//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25823  
 F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//7.8e-10:33:87//HOMO SAPIENS (HUMAN).//P39193  
 15 F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-56:92:58//HOMO SAPIENS (HUMAN).//P51522  
 F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//0.019:136:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844  
 F-PLACE1004491//LYSIS PROTEIN.//0.95:53:30//BACTERIOPHAGE FR.//P19903  
 20 F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LAGE-1).//0.58:66:34//HOMO SAPIENS (HUMAN).//P78358  
 F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150).//3.0e-07:63:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325  
 F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH PROTEINS (FRAGMENT).//0.95:62:29//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14587  
 25 F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III).//0.91:28:42//MYTILUS EDULIS (BLUE MUSSEL).//P80248  
 F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT.//0.94:75:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P19518  
 F-PLACE1004550//CUTICLE COLLAGEN 2.//0.90:155:31//CAENORHABDITIS ELEGANS.//P17656  
 30 F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//3.2e-70:121:100//BOS TAURUS (BOVINE).//Q10568  
 F-PLACE1004629//PROTEIN OS-9 PRECURSOR.//1.7e-10:132:36//HOMO SAPIENS (HUMAN).//Q13438  
 F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB).//0.00036:100:30//PYROCOCCUS FURIOSUS.//Q51731  
 35 F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9).//0.91:58:29//KLEBSIELLA PNEUMONIAE.//Q48481  
 F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D).//0.031:134:32//MUS MUSCULUS (MOUSE).//Q03391  
 40 F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//0.025:125:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781  
 F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7:14C IN CHROMOSOME I.//7.6e-52:158:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704  
 45 F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.4e-88:144:93//MUS MUSCULUS (MOUSE).//P12815  
 F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.0e-34:70:100//MUS MUSCULUS (MOUSE).//Q60809  
 F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.4e-08:48:62//HOMO SAPIENS (HUMAN).//P39192  
 50 F-PLACE1004691//METALLOTHIONEIN (MT).//0.064:24:45//ARIANTA ARBUSTORUM.//P55946  
 F-PLACE1004693  
 F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//PAN PANISCUS (PYGMY CHIMPANZEE) (BONOBO).//Q35587  
 55 F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.//0.95:53:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48565  
 F-PLACE1004736//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.014:163:30//RATTUS NORVEGICUS (RAT).//Q05175  
 F-PLACE1004740//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.9e-09:37:70//HOMO SAPIENS (HUMAN).//

P39194

F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN ALGR3 3'REGION./.0.99:72:33//PSEUDOMONAS AERUGINOSA./.P21484

5 F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANS-FERASE (EC 2.4.99.-)(BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//2.2e-08:90:38//HOMO SAPIENS (HUMAN).//Q11206

F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2)(ERYTHROCYTE ANKYRIN).//3.2e-25:233:32//HOMO

SAPIENS (HUMAN).//P16157

10 F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//8.1e-26:210:30//

RATTUS NORVEGICUS (RAT).//P30337

F-PLACE1004793//ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36].//0.00062:106:25//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10259

F-PLACE1004804

15 F-PLACE1004813//HYPOTHETICAL PROTEIN UL12./.1.0:22:40//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16777

F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II./.2.8e-06:136:25//CAENORHABDITIS ELEGANS./.Q09217

F-PLACE1004815

20 F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION./.2.3e-09:70:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53236

F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3).//0.54:25:56//BACILLUS LICHENIFORMIS./.P22754

F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.0066:12:66//BOS TAURUS (BOVINE).//P20072

F-PLACE1004838

25 F-PLACE1004840

F-PLACE1004868//MALE STERILITY PROTEIN 2./.4.0e-16:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

F-PLACE1004885

30 F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PRECURSOR (MCDP) (MCD) (PEPTIDE 401).//1.0:23:47//APIS MELLIFERA (HONEYBEE).//P01499

F-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C./.7.3e-15:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42643

F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BCSA-DEGR INTERGENIC REGION./.1.0:42:33//BACILLUS SUBTILIS./.P54165

35 F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RPS21B-MRS3 INTERGENIC REGION./.0.98:50:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47012

F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562./.0.82:44:36//METHANOCOCCUS JANNASCHII./.Q57982

F-PLACE1004934

40 F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I./.9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X./.4.0e-14:184:25//CAENORHABDITIS ELEGANS./.Q11073

45 F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-II) (BROMELAIN INHIBITOR VI) (BI-VI).//1.0:35:37//ANANAS COMOSUS (PINEAPPLE).//P27478

F-PLACE1004979//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!./.5.3e-30:55:72//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).//0.00049:124:27//STREPTOCOCCUS PYOGENES./.P19401

50 F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:26:34//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942

F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG./.0.0011:179:27//EUPLOTES CRASSUS./.Q06183

F-PLACE1005027

55 F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.082:44:36//BOS TAURUS (BOVINE).//P20072

F-PLACE1005052//MALE SPECIFIC SPERM PROTEIN MST84DD./.0.38:36:44//DROSOPHILA MELANOGLASTER (FRUIT FLY).//Q01645

F-PLACE1005055

F-PLACE1005066//RING CANAL PROTEIN (KELCH PROTEIN).//2.9e-38:194:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-PLACE1005077  
 F-PLACE1005085//INSECT TOXIN 1 (BOT IT1).//0.85:36:33//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION).//P55902  
 5 F-PLACE1005086!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//8.5e-38:93:76//HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGMENT).//1.6e-11:35:100//HOMO SAPIENS (HUMAN).//P49753  
 10 F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//3.0e-14:110:38//MUS MUSCULUS (MOUSE).//Q60821  
 F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.41:35:34//BOS TAURUS (BOVINE).//P37359  
 15 F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGERIN II).//1.0:29:41//RATTUS NORVEGICUS (RAT).//P11608  
 F-PLACE1005128//RABPHILIN-3A (FRAGMENT).//5.9e-05:95:36//MUS MUSCULUS (MOUSE).//P47708  
 F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN15).//0.17:48:35//MUS MUSCULUS (MOUSE).//Q61075  
 20 F-PLACE1005162!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.0e-31:60:76//HOMO SAPIENS (HUMAN).//P39189  
 F-PLACE1005176  
 F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN.//1.0:31:45//MEASLES VIRUS (STRAIN HALLE) (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).//P06831  
 25 F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHASE) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE).//0.0025:58:34//NEUROSPORA CRASSA.//P38678  
 F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN.//0.34:57:42//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20511  
 F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR.//0.70:60:35//HOMO SAPIENS (HUMAN).//Q99218  
 30 F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//0.0017:114:27//PHYCOMYCETES BLAKESLEEANUS.//Q01577  
 F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II.//1.2e-38:206:41//CAENORHABDITIS ELEGANS.//Q10003  
 F-PLACE1005266  
 35 F-PLACE1005277//PROTEIN GURKEN PRECURSOR.//0.58:95:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P42287  
 F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.0e-12:211:29//GALLUS GALLUS (CHICKEN).//P53352  
 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-78:205:  
 40 78//BOS TAURUS (BOVINE).//P08760  
 F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN.//0.99:40:40//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//Q09020  
 F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEUX-FECE INTERGENIC REGION (O67).//0.15:36:  
 45 41//ESCHERICHIA COLI.//P39355  
 F-PLACE1005327//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:19:52//HOMO SAPIENS (HUMAN).//P30808  
 F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN.//0.00021:98:35//HOMO SAPIENS (HUMAN).//P11274  
 50 F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3.//0.37:98:33//MUS MUSCULUS (MOUSE).//P81067  
 F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINE SYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLASE).//0.010:96:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48567  
 F-PLACE1005374  
 55 F-PLACE1005409  
 F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE).//1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO).//P07979  
 F-PLACE1005467//KERATIN, FEATHER (F-KER).//0.0095:42:35//LARUS NOVAE-HOLLANDIAE (SILVER

GULL).//P02451  
F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.23:49:32//PHYTOPHTHORA INFESTANS (POTATO LATE BLIGHT FUNGUS).//Q37598  
F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137.//9.6e-13:115:38//MUS MUSCULUS (MOUSE).//  
5 P11260  
F-PLACE1005480//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.97:33:30//HORDEUM VULGARE (BARLEY).//P17991  
F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT).//0.30:52:38//APIS MELLIFERA (HONEYBEE).//  
10 P31504  
F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN.//3.9e-05:87:33//DROSOPHILA MELANOASTER (FRUIT FLY).//P19334  
F-PLACE1005502  
F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180.//4.6e-05:132:32//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479  
15 F-PLACE1005528//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.4e-09:31:74//HOMO SAPIENS (HUMAN).//  
P39195  
F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//9.7e-50:148:58//  
CAENORHABDITIS ELEGANS.//Q09251  
F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III.//3.0e-21:127:37//  
20 CAENORHABDITIS ELEGANS.//P34524  
F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.84:38:31//DIPODOMYS CALIFORNICUS (KANGAROO RAT).//P16359  
F-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//4.8e-09:60:48//CRYPTOCOCCUS NEOFORMANS (FILO-BASIDIELLA NEOFORMANS).//P46288  
25 F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.89:44:29//BOS TAURUS (BOVINE).//  
P03929  
F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87F.//0.00030:33:48//DROSOPHILA MELANOASTER (FRUIT FLY).//P08175  
F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180.//0.00048:162:30//PSEUDORABIES VIRUS (STRAIN  
30 INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675  
F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN).//  
0.00034:83:30//TETRAHYMENA PYRIFORMIS.//P40625  
F-PLACE1005611//DNAJ PROTEIN.//8.6e-20:108:48//CLOSTRIDIUM ACETOBUTYLCUM.//P30725  
F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ERK5) (ERK4) (BMK1 KI-  
35 NASE).//0.80:116:31//HOMO SAPIENS (HUMAN).//Q13164  
F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH  
FACTOR) (HMW-BCGF).//0.0024:74:39//HOMO SAPIENS (HUMAN).//P40222  
F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT P85) (FRAGMENT).//  
0.72:18:61//RATTUS NORVEGICUS (RAT).//Q62894  
40 F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10.//4.8e-29:172:45//NICOTIANA SYLVESTRIS (WOOD  
TOBACCO).//P46942  
F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLE-  
OTIDE REDUCTASE).//3.7e-64:133:75//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q60561  
F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28.//0.57:36.41//PORPHYRA PURPUREA.//  
45 P51224  
F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3'REGION (ORFC) (FRAGMENT).//0.50:61:29//BACILLUS SUBTILIS.//P40405  
F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).//0.46:  
27:51//BRASSICA NAPUS (RAPE).//P40603  
50 F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//0.95:21:52//ORYCTOLAGUS CUNICULUS  
(RABBIT).//P02456  
F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11.//3.4e-46:111:53//MUS MUSCULUS  
(MOUSE).//Q60710  
F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION.//2.6e-12:66:  
55 51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951  
F-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)  
(THIOESTERASE II).//1.5e-26:69:57//RATTUS NORVEGICUS (RAT).//P08635  
F-PLACE1005799//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.028:96:32//HOMO

SAPIENS (HUMAN).//P26371  
F-PLACE1005802//PROTEIN PROSPERO.//0.86:64:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//  
P29617  
F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.0:95:25//MUS  
5 MUSCULUS (MOUSE).//P17564  
F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//  
2.8e-73:198:73//MUS MUSCULUS (MOUSE).//P39098  
F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.022:78:38//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057  
10 F-PLACE1005828!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!/1.8e-23:56:76//HOMO SAPIENS (HUMAN).//  
P39195  
F-PLACE1005834//LATE CONTROL GENE B PROTEIN (GPB).//0.97:33:39//BACTERIOPHAGE 186.//P08711  
F-PLACE1005845  
15 F-PLACE1005850!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!/5.5e-28:96:73//HOMO SAPIENS (HUMAN).//  
P39194  
F-PLACE1005851  
F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100  
KD SUBUNIT).//2.2e-99:155:95//BOS TAURUS (BOVINE).//Q10568  
F-PLACE1005884  
20 F-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//1.8e-33:137:49//SCHIZOSACCHAROMYCES POMBE  
(FISSION YEAST).//P54069  
F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3)  
(COMPLEX I-MLRQ) (CI-MLRQ).//0.77:58:34//HOMO SAPIENS (HUMAN).//Q00483  
F-PLACE1005921//AIG1 PROTEIN.//1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//  
25 P54120  
F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16).//0.90:118:28//PARAMECIUM TETRAURE-  
LIA.//P15617  
F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN.//0.94:57:29//HERPESVIRUS SAIMIRI (STRAIN 11).//  
Q01010  
30 F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)(RPB1) (FRAG-  
MENT).//0.40:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414  
F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.50:15:66//HUMAN IMMU-  
35 NODEFICIENCY VIRUS TYPE 1 (CLONE 12) (HIV-1).//P04326  
F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
0.0025:135:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPPIP).//0.64:57:33//RHODOFERAX FER-  
MENTANS.//P80882  
40 F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.0e-32:110:  
50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821  
F-PLACE1005966//TACHYPLESIN II PRECURSOR.//0.97:31:35//TACHYPLEUS TRIDENTATUS (JAPANESE  
HORSESHOE CRAB).//P14214  
F-PLACE1005968//GATA FACTOR SREP.//0.17:52:40//PENICILLIUM CHRYSOGENUM.//Q92259  
45 F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED PROTEIN.//0.36:55:36//EMERICELLA NIDU-  
LANS (ASPERGILLUS NIDULANS).//P36011  
F-PLACE1006002!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!/1.5e-36:102:75//HOMO SAPIENS (HU-  
MAN).//P39192  
50 F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION (ORF 61).//1.0:  
22:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38473  
F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPR) (NAD(+)) ADP- RIBO-  
SYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE).//2.8e-21:163:36//ARABIDOPSIS THALIANA  
(MOUSE-EAR CRESS).//Q11207  
F-PLACE1006017!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!/1.1e-10:43:67//HOMO SAPIENS (HUMAN).//  
55 P39192  
F-PLACE1006037//VITELLOGENIN I PRECURSOR (VTG I) [CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN  
(PV); LIPOVITELLIN 2 (LV2)].//0.00019:123:37//FUNDULUS HETEROCLITUS (KILLIFISH) (MUMMICHOOG).//  
Q90508

F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19 (ARPP-19).//3.2e-40:110:76//HOMO SAPIENS (HUMAN).//P56211  
F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR A-II.//0.99:30:40//ARACHIS HYPOGAEA (PEANUT).//P01066  
5 F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RAN-BINDING PROTEIN 5).//8.8e-94:218:76//HOMO SAPIENS (HUMAN).//O00410  
F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00092:228:26//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P32323  
F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//5.9e-55:  
10 128:50//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P43616  
F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.4e-25:107:63//HOMO SAPIENS (HUMAN).//P39194  
F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//1.3e-21:168:  
15 32//SUS SCROFA (PIG).//P98110  
F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIR1 PRECURSOR (SERINE-RICH PROTEIN 1).//0.46:  
98:29//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P10863  
F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0:70:28:42//ARTEMIA SALINA (BRINE SHRIMP).//P19049  
20 F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.9e-05:167:32//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P08640  
F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.1e-67:157:88//MUS MUSCULUS (MOUSE).//P17427  
25 F-PLACE1006187//G1/S-SPECIFIC CYCLIN E.//5.6e-75:224:62//HOMO SAPIENS (HUMAN).//P24864  
F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENTERON PROTEIN).//0.99:177:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55965  
F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.0e-33:183:46//SCHIZOSAC-  
30 CHAROMYCES POMBE (FISSION YEAST).//Q09747  
F-PLACE1006205  
F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.00015:22:50//MUS MUSCULUS (MOUSE).//P15265  
F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PROTEIN).//1.0:63:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18805  
35 F-PLACE1006236  
F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.48:23:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407  
F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR).//0.012:84:30//MUS MUSCULUS (MOUSE).//Q61420  
40 F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.017:203:22//RATTUS NORVEGICUS (RAT).//P41777  
F-PLACE1006262//L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17).//0.84:25:52//HAEMOPHILUS INFLUENZAE.//P44777  
45 F-PLACE1006288  
F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1).//1.0:29:48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA).//P30231  
F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2).//0.99:97:32//HOMO SAPIENS (HUMAN).//P49918  
50 F-PLACE1006335//PROLINE-RICH PEPTIDE P-B.//0.56:19:52//HOMO SAPIENS (HUMAN).//P02814  
F-PLACE1006357  
F-PLACE1006360  
F-PLACE1006368//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//0.0057:122:31//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P32380  
55 F-PLACE1006371//ARS BINDING PROTEIN 1.//0.00030:142:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P49777  
F-PLACE1006382//NEUROTOXIN V.//0.85:28:39//ANDROCTONUS MAURETANICUS MAURETANICUS (SCORPION).//P01482

F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION./.3.1e-35:165:  
 47//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P47160  
 F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG./.4.3e-08:40:47//HOMO SAPIENS (HUMAN).//P08547  
 5 F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4).//3.8e-05:123:39//HOMO SAPIENS (HUMAN).//Q16676  
 F-PLACE1006438//ZINC FINGER PROTEIN 165./.2.8e-21:76:64//HOMO SAPIENS (HUMAN).//P49910  
 F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN./.0.058:99:29//DROSOPHILA VIRILIS (FRUIT FLY).//Q08876  
 10 F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.8e-64:177:50//ESCHERICHIA COLI//P27550  
 F-PLACE1006470  
 F-PLACE1006482//TRANSCRIPTION FACTOR MAFF./.2.0e-47:120:85//GALLUS GALLUS (CHICKEN).//Q90595  
 15 F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.8e-85:173:95//CANIS FA-MILIARIS (DOG).//Q00004  
 F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN C56F8.13 IN CHROMOSOME I./.0.75:32:56// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261  
 F-PLACE1006506  
 20 F-PLACE1006521  
 F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III./.1.3e-53:167:61// CAENORHABDITIS ELEGANS//P34681  
 F-PLACE1006534  
 F-PLACE1006540  
 25 F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.3e-07:242:23//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922  
 F-PLACE1006598//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!/.0.17:43:51//HOMO SAPIENS (HUMAN).//P39190  
 F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10).//3.6e-05:66:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038  
 30 F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPUCATION).//1.0:74:29// STAPHYLOCOCCUS AUREUS//P03861  
 F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III./.2.9e-10:73:46//CAENORHAB-DITIS ELEGANS//P34529  
 35 F-PLACE1006629//HYPOTHETICAL PROTEIN BB0410./.1.0:23:43//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51371  
 F-PLACE1006640  
 F-PLACE1006673  
 40 F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456  
 F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-Z1) [CONTAINS: BROAD-COMPLEX CORE-Q1-Z1  
 PROTEIN].//0.00062:157:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01295  
 45 F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//1.3e-07:127:36//CORYNEBACTERIUM AMMO-NIAGENES (BREVIBACTERIUM AMMONIAGENES).//Q59263  
 F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CGM1 PRECURSOR (CD66D ANTIGEN).//1.9e-19:78:  
 53//HOMO SAPIENS (HUMAN).//P40198  
 F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.21:107:30//RATTUS NORVEGICUS (RAT).//P13941  
 F-PLACE1006779//CYTOTOXIN 5 (CTX V).//1.0:20:30//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P25517  
 F-PLACE1006782//ZINC FINGER PROTEIN 1//.0.00052:178:28//CANDIDA ALBICANS (YEAST).//P28875  
 F-PLACE1006792  
 55 F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2).//1:0:80:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17972  
 F-PLACE1006800//HYPOTHETICAL 9.4 KD PROTEIN./.0.99:62:33//VACCINIA VIRUS (STRAIN COPENHA-GEN).//P20569  
 F-PLACE1006805

F-PLACE1006815//HYPOTHETICAL PROTEIN UL61//0.038:146:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818  
 F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//7.3e-98:239:76//HOMO SAPIENS (HUMAN).//P08547  
 5 F-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//0.061:34:58//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P50102  
 F-PLACE1006860  
 F-PLACE1006867  
 10 F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOBL 3'REGION (ORF 3).//0.85:27:37//THIOBACILLUS FERROOXIDANS.//P20087  
 F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).//0.78:51:37//MUS MUSCULUS (MOUSE).//P48281  
 15 F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN.//0.99:55:23//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20567  
 F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1 PROTEIN.//0.95:86:26//USTILAGO MAYDIS (SMUT FUNGUS).//P22015  
 F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME II.//6.9e-15:101:45//CAENORHABDITIS ELEGANS.//Q09442  
 20 F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.089:28:39//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251  
 F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//0.93:35:48//CAENORHABDITIS ELEGANS.//Q10000  
 F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)  
 25 (TAFII-130) (TAFII130).//0.00079:122:36//HOMO SAPIENS (HUMAN).//O00268  
 F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1).//8.8e-70:  
 140:98//MUS MUSCULUS (MOUSE).//P48722  
 F-PLACE1006961  
 F-PLACE1006962//APOLIPOPROTEIN C-I PRECURSOR (APO-C1).//1.0:25:40//PAPIO HAMADRYAS (HAMADRYAS BABOON).//P34929  
 30 F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION.//1.6e-47:221:  
 45//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P40160  
 F-PLACE1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN P37 5'REGION.//0.15:46:32//MYCOPLASMA HYORHINIS.//P32083  
 35 F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12)  
 (DER12).//3.4e-09:120:29//HOMO SAPIENS (HUMAN).//Q14542  
 F-PLACE1007021!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00046:42:59//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137.//8.1e-14:115:35//MUS MUSCULUS (MOUSE).//  
 40 P11260  
 F-PLACE1007053//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:48:39//HOMO SAPIENS  
 (HUMAN).//P22531  
 F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE).//0.0040:113:  
 39//GALLUS GALLUS (CHICKEN).//Q05063  
 45 F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//0.97:47:29//  
 AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41663  
 F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A10.10 IN CHROMOSOME L.//2.9e-33:219:37//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13730  
 F-PLACE1007111  
 50 F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN.//0.47:75:28//ESCHERICHIA COLI.//P03853  
 F-PLACE1007132!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.8e-11:56:57//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE1007140//GAR2 PROTEIN.//0.72:185:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//  
 P41891  
 55 F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.97:79:30//MYCOBACTERIUM TUBER-  
 CULOSIS.//Q10826  
 F-PLACE1007226//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378).//1.9e-  
 15:123:32//ESCHERICHIA COLI.//P52062

F-PLACE1007238//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//5.5e-10:98:44//ACANTHAMOEBA CASTELLANII (AMOEBA).//P19706  
 F-PLACE1007239//TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A).//3.9e-19:96:57//HOMO SAPIENS (HUMAN).//P23193  
 5 F-PLACE1007242//GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B (RALGEF).//1.0:132:30//RATTUS NORVEGICUS (RAT).//Q03386  
 F-PLACE1007243//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.//0.041:114:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981  
 10 F-PLACE1007257//DIAPHANOUS PROTEIN.//1.3e-42:205:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608  
 F-PLACE1007274//CADMIUM-METALLOTHIONEIN (CD-MT).//0.054:60:30//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187  
 F-PLACE1007276//BETA-DEFENSIN 1 PRECURSOR (RHBD-1) (DEFENSIN, BETA 1).//1.0:42:28//SUS SCROFA (PIG).//O62697  
 15 F-PLACE1007282//OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].//0.070:126:27//HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3).//P11200  
 F-PLACE1007286  
 20 F-PLACE1007301//HYPOTHETICAL PROTEIN KIAA0168.//0.042:61:39//HOMO SAPIENS (HUMAN).//P50749  
 F-PLACE1007317  
 F-PLACE1007342//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.7e-06:77:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002  
 25 F-PLACE1007346//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1).//0.0026:147:27//MUS MUSCULUS (MOUSE).//Q62318  
 F-PLACE1007367!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.3e-37:110:76//HOMO SAPIENS (HUMAN).//P39189  
 F-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13./4.7e-07:71:39//CAENORHABDITIS ELEGANS//P27715  
 30 F-PLACE1007386//HYPOTHETICAL 7.6 KD PROTEIN IN FLO1-PHO11 INTERGENIC REGION.//0.74:48:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39561  
 F-PLACE1007402//TRANSCRIPTIONAL REGULATORY PROTEIN ENTR (ENTERICIDIN R).//0.99:63:36//CITROBACTER FREUNDII//O69280  
 F-PLACE1007409//WHITE PROTEIN.//7.9e-38:179:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P10090  
 35 F-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//0.031:159:23//HOMO SAPIENS (HUMAN).//P27487  
 F-PLACE1007450//ZINC FINGER PROTEIN 39 (ZINC FINGER PROTEIN KOX27) (FRAGMENT).//0.023:36:50//HOMO SAPIENS (HUMAN).//P17038  
 40 F-PLACE1007452//HYPOTHETICAL 22.1 KD PROTEIN IN CCP1-MET1 INTERGENIC REGION.//2.2e-18:85:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36149  
 F-PLACE1007454//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//0.66:13:53//CHLAMYDOMONAS REINHARDTII//Q06480  
 45 F-PLACE1007460//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:45:33//SUS SCROFA (PIG).//Q35914  
 F-PLACE1007478//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//5.3e-08:50:56//MUS MUSCULUS (MOUSE).//P11369  
 F-PLACE1007484//HYPOTHETICAL 6.8 KD PROTEIN IN REPLICATION ORIGIN REGION.//0.87:43:37//ESCHERICHIA COLI//P03849  
 50 F-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN).//1.2e-25:202:31//HOMO SAPIENS (HUMAN).//P98174  
 F-PLACE1007507//HYPOTHETICAL 16.0 KD PROTEIN IN TAF60-G4P1 INTERGENIC REGION.//0.12:128:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53139  
 55 F-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//2.1e-45:209:48//BOS TAURUS (BOVINE).//P08728  
 F-PLACE1007524//HYPOTHETICAL 9.2 KD PROTEIN.//0.74:80:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20550  
 F-PLACE1007525

F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.045:92:  
 30//MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P80144  
 F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180.//1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN  
 KAPLAN) (PRV).//P33479  
 5 F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.5e-16:188:34//  
 CAENORHABDITIS ELEGANS.//P34537  
 F-PLACE1007557  
 F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.98:  
 72:33//DAUCUS CAROTA (CARROT) .//P06600  
 10 F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT).//1.7e-11:88:  
 43//HOMO SAPIENS (HUMAN).//Q03936  
 F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP).//0.19:  
 109:27//MUS MUSCULUS (MOUSE).//P13808  
 F-PLACE1007621//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.98:34:  
 15 41//PSEUDOMONAS AERUGINOSA.//P23621  
 F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.70:110:34//BOS TAURUS (BOVINE).//  
 P02465  
 F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:20:45//STRUTHIO CAMELUS (OS-  
 TRICH).//O21401  
 20 F-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.1e-06:197:26//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P08640  
 F-PLACE1007677//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.0:47:46//HOMO SAPIENS (HUMAN).//  
 P39192  
 25 F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//  
 2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO).//Q26457  
 F-PLACE1007690//SPERM PROTAMINE P1.//0.12:26:50//TACHYGLOSSUS ACULEATUS ACULEATUS (AUS-  
 TRALIAN ECHIDNA).//P35311  
 F-PLACE1007697//SPERM PROTAMINE P1.//0.19:34:52//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH  
 30 AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305  
 F-PLACE1007705//BIOH PROTEIN.//0.015:97:29//ESCHERICHIA COLI.//P13001  
 F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1).//5.3e-  
 55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32898  
 F-PLACE1007725  
 35 F-PLACE1007729//PROTEASE (EC 3.4.23.-).//1.8e-21:136:42//MOUSE MAMMARY TUMOR VIRUS (STRAIN  
 BR6).//P10271  
 F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.0031:77:40//HOMO SAPIENS  
 (HUMAN).//P81489  
 F-PLACE1007737//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.78:39:56//HOMO SAPIENS (HUMAN).//  
 40 P39195  
 F-PLACE1007743  
 F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT).//0.0066:168:25//HOMO SAPIENS  
 (HUMAN).//Q14690  
 F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT).//0.62:17:41//LITHOBius FORficatus.//Q01872  
 45 F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPOIIIC INTERGENIC REGION.//1.0:40:30//BA-  
 CILLUS SUBTILIS.//P54446  
 F-PLACE1007810//ANTHOPLEURIN A (TOXIN AP-A).//0.79:28:46//ANTHOPLERA XANTHOGRAMMICA (GI-  
 ANT GREEN SEA ANEMONE).//P01530  
 F-PLACE1007829//SPORE COAT PROTEIN G.//1.0:65:38//BACILLUS SUBTILIS.//P39801  
 50 F-PLACE1007843  
 F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-32:37:94//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOH (GTP-BINDING PROTEIN TTF).//8.7e-05:  
 138:30//HOMO SAPIENS (HUMAN).//Q15669  
 55 F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN.//0.0039:127:25//SACCHAROMYCES CER-  
 EVISIAE (BAKER'S YEAST).//P50275  
 F-PLACE1007866  
 F-PLACE1007877

F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EX-TRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HAM1 ANTI-GEN).//0.44:128:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q60522  
 5 F-PLACE1007908!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!/5.5e-28:61:65//HOMO SAPIENS (HUMAN).//P39192  
 F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.84:48:37//PSEUDOMONAS AERUGINOSA./P04139  
 10 F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//0.00070:96:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38226  
 F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.//0.00027:255:23//CAENORHABDITIS ELEGANS./Q09625  
 F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17).//1.7e-09:127:30//MUS MUSCULUS (MOUSE).//P70453  
 15 F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//2.4e-05:104:37//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479  
 F-PLACE1007990//SPERM PROTAMINE P1.//0.78:36:47//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS).//P35307  
 20 F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//1.2e-16:128:39//RATTUS NORVEGICUS (RAT).//Q63622  
 F-PLACE1008002  
 F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//3.9e-106:208:93//RATTUS NORVEGICUS (RAT).//P52590  
 25 F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.9e-09:49:53//BOS TAURUS (BOVINE).//P25508  
 F-PLACE1008080//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//0.00025:100:27//EGGPLANT MOSAIC VIRUS./P20126  
 F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO).//0.90:74:25//MYCOBACTERIUM TUBERCULOSIS./O53230  
 30 F-PLACE1008111//HYPOTHETICAL PROTEIN MJEC512.//0.30:38:42//METHANOCOCCUS JANNASCHII./Q60311  
 F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN).//0.0085:117:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40091  
 F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//1.8e-06:154:36//GALLUS GALLUS (CHICKEN).//P02467  
 35 F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.4e-13:227:36//CAENORHABDITIS ELEGANS./Q09531  
 F-PLACE1008177//TRICHOHYALIN.//2.7e-10:230:26//OVIS ARIES (SHEEP).//P22793  
 F-PLACE1008181  
 F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.00044:121:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
 F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A.//3.0e-05:82:37//MICROPTERUS SALMOIDES (LARGEMOUTH BASS).//P38621  
 40 F-PLACE1008209//METALLOTHIONEIN-I (MT-I).//0.95:39:35//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P02797  
 F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (PROCYCLIN) (PARP).//0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI./P08469  
 F-PLACE1008244//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//2.2e-23:148:38//PODOSPORA ANSERINA./Q00808  
 45 F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.1e-97:222:81//BOS TAURUS (BOVINE).//P53620  
 F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//5.8e-20:161:37//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P12689  
 F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.1e-23:124:42//HOMO SAPIENS (HUMAN).//P08547  
 50 F-PLACE1008309//HYPOTHETICAL 98.3 KD PROTEIN C9G1.06C IN CHROMOSOME I.//0.47:99:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14302  
 F-PLACE1008329//PUTATIVE Z PROTEIN.//0.73:52:28//OVIS ARIES (SHEEP).//P08105

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F-PLACE1008330//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.0e-37:75:81//HOMO SAPIENS (HUMAN).//P39194  
F-PLACE1008331//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.1e-08:70:50//HOMO SAPIENS (HUMAN).//P39188  
5 F-PLACE1008356//FRUIT PROTEIN PKIWI501.//0.0037:148:29//ACTINIDIA CHINENSIS (KIWI) (YANGTAO).//P43393  
F-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:205:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
F-PLACE1008369  
10 F-PLACE1008392  
F-PLACE1008398//GENE 33 POLYPEPTIDE.//1.5e-102:225:84//RATTUS NORVEGICUS (RAT).//P05432  
F-PLACE1008401//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.9e-08:186:34//MUS MUSCULUS (MOUSE).//P05143  
15 F-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//9.4e-105:207:98//BOS TAURUS (BOVINE).//P41541  
F-PLACE1008405  
F-PLACE1008424//PROTEIN UL56.//1.0:65:33//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN HFEM).//P36297  
F-PLACE1008426//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//4.4e-05:185:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q99323  
20 F-PLACE1008429//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.00054:172:25//RATTUS NORVEGICUS (RAT).//Q05175  
F-PLACE1008437//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//1.9e-23:226:34//CAENORHABDITIS ELEGANS.//P34681  
25 F-PLACE1008455//DNA-BINDING PROTEIN (AGNOPROTEIN).//0.97:23:52//BUDGERIGAR FLEDGLING DISEASE VIRUS (BFDV).//P13893  
F-PLACE1008457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.1e-12:89:47//HOMO SAPIENS (HUMAN).//P39188  
F-PLACE1008465//ZINC FINGER PROTEIN 31 (ZINC FINGER PROTEIN KOX29) (FRAGMENT).//0.00017:23:43//HOMO SAPIENS (HUMAN).//P17040  
30 F-PLACE1008488//HYPOTHETICAL PROTEIN UL61.//9.1e-05:204:30//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818  
F-PLACE1008524//HOMEobox PROTEIN HLX1 (HOMEobox PROTEIN HB24).//0.95:74:36//HOMO SAPIENS (HUMAN).//Q14774  
F-PLACE1008531//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.1e-05:86:45//HOMO SAPIENS (HUMAN).//P39192  
35 F-PLACE1008532//HYPOTHETICAL 36.4 KD PROTEIN IN SMP1-MBA1 INTERGENIC REGION.//3.9e-21:62:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38298  
F-PLACE1008533//HYPOTHETICAL 86.2 KD PROTEIN C4G8.04 IN CHROMOSOME I.//3.5e-06:118:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09830  
40 F-PLACE1008568//NEURONATIN.//0.046:34:52//HOMO SAPIENS (HUMAN).//Q16517  
F-PLACE1008584//HUNCHBACK PROTEIN (FRAGMENT).//0.94:30:43//LITHOBIOUS FORFICATUS.//Q02030  
F-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//3.9e-123:224:96//RATTUS NORVEGICUS (RAT).//P37199  
F-PLACE1008621//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//5.0e-05:31:67//HOMO SAPIENS (HUMAN).//P20931  
45 F-PLACE1008625//DISAGREGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//0.87:17:52//ORNITHODOROS MOUBATA (SOFT TICK).//P36235  
F-PLACE1008626//METALLOTHIONEIN-I (MT-I).//0.77:33:36//SCYLLA SERRATA (MUD CRAB).//P02805  
F-PLACE1008627//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).//0.14:44:31//HOMO SAPIENS (HUMAN).//P25713  
F-PLACE1008629  
50 F-PLACE1008630//PROTAMINE Z3 (SCYLIORHININE Z3).//0.78:33:36//SCYLIORHINUS CANICULA (SPOTTED DOGFISH) (SPOTTED CATSHARK).//P30258  
F-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120).//1.7e-30:220:41//HOMO SAPIENS (HUMAN).//Q14624  
55 F-PLACE1008650//PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1.//2.5e-10:106:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42384

F-PLACE1008693//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//1.0:36:38//MEDICAGO SCUTEL-LATA (SNAIL MEDIC).//P80321  
 F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-23KD) (CI-23KD) (TYKY SUBUNIT).//4.8e-14:47:80//HOMO SAPIENS (HUMAN).//O00217  
 5 F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//0.66:105:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834  
 F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.10:178:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214  
 10 F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.60:44:34//ESCHERICHIA COLI.//P33669  
 F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.0e-69:191:80//MUS MUSCULUS (MOUSE).//Q35345  
 15 F-PLACE1008798//BACTERIOCIN LACTOBIN A.//1.0:34:41//LACTOBACILLUS AMYLOVORUS .//P80696  
 F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.91:77:36//HOMO SAPIENS (HUMAN).//P08547  
 F-PLACE1008808//REC1 PROTEIN.//0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS).//P14746  
 F-PLACE1008813  
 20 F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DUR1,2 INTERGENIC REGION.//1.0:62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38309  
 F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//1.0:82:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170  
 F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN).//0.65:61:36//SOLANUM TUBERO-SUM (POTATO).//P15478  
 25 F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-56:180:54//NYCTICEBUS COUCANG (SLOW LORIS).//P08548  
 F-PLACE1008902  
 F-PLACE1008920  
 30 F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//0.90:77:33//ESCHERICHIA COLI.//P76242  
 F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5'REGION (ORF3) (FRAGMENT).//0.14:77:45//GLU CONOBACTER SUBOXYDANS.//O05543  
 F-PLACE1008941//ZINC FINGER PROTEIN 141.//1.1e-17:45:95//HOMO SAPIENS (HUMAN).//Q15928  
 35 F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//4.1e-14:136:39//MUS MUSCULUS (MOUSE).//P27790  
 F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.74:37:48//BOS TAURUS (BOVINE).//P20072  
 F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.39:57:36//BALAENOPTERA MUSCULUS (BLUE WHALE).//P41301  
 F-PLACE1009039  
 40 F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83).//0.48:32:43//ESCHERICHIA COLI.//P46879  
 F-PLACE1009048  
 F-PLACE1009050  
 F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III.//4.9e-23:244:31//CAENORHABDITIS ELEGANS.//P34552  
 45 F-PLACE1009090//50S RIBOSOMAL PROTEIN L35.//1.0:27:51//MYCOPLASMA GENITALIUM.//P47439  
 F-PLACE1009091  
 F-PLACE1009094//NEL-LIKE PROTEIN (FRAGMENT).//3.6e-15:180:30//HOMO SAPIENS (HUMAN).//Q92832  
 F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (MKR4 PROTEIN) (FRAGMENT).//1.4e-94:228:71//MUS MUSCULUS (MOUSE).//P10077  
 50 F-PLACE1009110//HIRUDIN HV1 (BUFRUDIN).//1.0:49:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//P81492  
 F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.4e-05:30:83//HOMO SAPIENS (HUMAN).//P39195  
 55 F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.032:40:52//BOS TAURUS (BOVINE).//P20072  
 F-PLACE1009130//HYPOTHETICAL PROTEIN KIAA0032.//3.3e-37:214:38//HOMO SAPIENS (HUMAN).//Q15034  
 F-PLACE1009150//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.6e-32:56:76//HOMO SAPIENS (HUMAN).//

P39195  
F-PLACE1009155//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!/1.2e-17:101:57//HOMO SAPIENS (HUMAN).//P39194  
F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFX (J1I).//0.0058:73:42//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P09711  
5 F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//0.0086:96:30//HOMO SAPIENS (HUMAN).//P49902  
F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//1.0:19:52//ES-CHERICHIA COLI.//P76246  
10 F-PLACE1009174//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!/3.1e-17:47:82//HOMO SAPIENS (HUMAN).//P39194  
F-PLACE1009183  
F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I.//0.019:62:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09783  
15 F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.2) (LONG-CHAIN FATTY-ACYL-COA HYDROLASE) (FRAGMENT).//0.027:53:28//RATTUS NORVEGICUS (RAT).//P80250  
F-PLACE1009200//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!/5.4e-28:84:71//HOMO SAPIENS (HUMAN).//P39194  
20 F-PLACE1009230//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!/2.8e-12:50:74//HOMO SAPIENS (HUMAN).//P39189  
F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (EC 1.10.2.2) (MITOCHONDRIAL HINGE PROTEIN) (CR7).//1.0:17:52//SOLANUM TUBEROSUM (POTATO).//P48504  
F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//6.6e-41:177:53//SAC-CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110  
25 F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.00034:108:33//HOMO SAPIENS (HUMAN).//P26371  
F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//5.3e-16:84:50//HOMO SAPIENS (HUMAN).//P78352  
F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.9e-82:263:67//HOMO SAPIENS (HUMAN).//P08547  
30 F-PLACE1009335//60S RIBOSOMAL PROTEIN L32.//0.95:71:36//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P02433  
F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY AND ENHANCER OF SPLIT 5).//0.90:42:40//MUS MUSCULUS (MOUSE).//P70120  
35 F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE IB-1.//0.013:33:48//HOMO SAPIENS (HUMAN).//P04281  
F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.//0.0022:135:21//CAENORHABDITIS ELEGANS.//P34492  
F-PLACE1009388//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!/4.8e-22:73:65//HOMO SAPIENS (HUMAN).//P39195  
40 F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.1e-83:223:65//HOMO SAPIENS (HUMAN).//P51523  
F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.//0.047:145:29//TRITICUM AESTIVUM (WHEAT).//P08489  
F-PLACE1009410//TOXIN C13S1C1 PRECURSOR.//0.22:21:47//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329  
45 F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K (EC 1.6.5.3) (FRAGMENT).//0.81:61:29//ANTHOCEROS FORMOSAE.//Q31791  
F-PLACE1009443//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//9.1e-05:93:32//MUS MUSCULUS (MOUSE).//Q62203  
50 F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//6.4e-15:41:97//HOMO SAPIENS (HUMAN).//P42356  
F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.//0.0011:119:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874  
55 F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-34:101:75//RATTUS NORVEGICUS (RAT).//P54319  
F-PLACE1009476//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.086:21:52//HOMO SAPIENS (HUMAN).//P30808  
F-PLACE1009477

F-PLACE1009493//HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X.//1.4e-18:138:39//  
CAENORHABDITIS ELEGANS.//Q11069

F-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//9.4e-80:155:85//HOMO SAPIENS (HUMAN).//Q99418

5 F-PLACE1009539//GTP-BINDING NUCLEAR PROTEIN RAN/TC4.//1.0:76:26//GIARDIA LAMBLIA (GIARDIA INTESTINALIS).//P38543

F-PLACE1009542!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00016:31:77//HOMO SAPIENS (HUMAN).//P39188

10 F-PLACE1009571//ATP SYNTHASE B CHAIN (EC 3.6.1.34) (SUBUNIT I).//0.88:116:29//STREPTOCOCCUS PNEUMONIAE.//Q59952

F-PLACE1009581//50S RIBOSOMAL PROTEIN L32.//0.00023:37:51//RHODOBACTER CAPSULATUS (RHO-DOPSEUDOMONAS CAPSULATA).//P30788

F-PLACE1009595

15 F-PLACE1009596//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//2.1e-36:116:49//CAENORHABDITIS ELEGANS.//Q17963

F-PLACE1009607!!!! ALU SUBFAMILY J WARNING ENTRY !!!//1.8e-43:73:69//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1009613

20 F-PLACE1009621//TRANSCRIPTION FACTOR BTF3 HOMOLOG 2.//0.91:29:44//HOMO SAPIENS (HUMAN).//Q13891

F-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3e-22:132:47//DROSOPHILA MELANOGLASTER (FRUIT FLY).//P25159

F-PLACE1009637//HYPOTHETICAL 18.1 KD PROTEIN IN CFXA 3'REGION.//0.30:28:57//BACTEROIDES VULGATUS.//P30905

25 F-PLACE1009639//LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN).//0.23:79:31//PSEUDOMONAS AERUGINOSA.//Q04591

F-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (BRAIN PROTEIN H19) (MH19) (FRAGMENT).//3.9e-126:227:96//MUS MUSCULUS (MOUSE).//P28660

F-PLACE1009665//IG KAPPA CHAIN V-I REGION (HAU).//0.52:89:35//HOMO SAPIENS (HUMAN).//P01600

30 F-PLACE1009670//CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19) (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).//0.16:114:29//PAENIBACILLUS MACERANS (BACILLUS MACERANS).//P31835

F-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//9.6e-19:156:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876

35 F-PLACE1009721//MSF1 PROTEIN.//7.7e-23:176:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35200

F-PLACE1009731//AIG1 PROTEIN.//1.1e-09:91:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P54120

40 F-PLACE1009763//HYPOTHETICAL 48.9 KD PROTEIN C24H6.12C IN CHROMOSOME I.//8.3e-42:171:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09765

F-PLACE1009794//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.99:36:33//HORDEUM VULGARE (BARLEY).//P17991

F-PLACE1009798//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT).//2.6e-34:191:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779

45 F-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.2e-19:190:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968

F-PLACE1009861//CATHEPSIN B PRECURSOR (EC 3.4.22.1).//4.4e-20:171:33//BOS TAURUS (BOVINE).//P07688

F-PLACE1009879//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.99:30:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779

50 F-PLACE1009886

F-PLACE1009888//NONSTRUCTURAL POLYPROTEIN [CONTAINS: NONSTRUCTURAL PROTEIN NSP4] (FRAGMENT).//1.0:33:42//WESTERN EQUINE ENCEPHALITIS VIRUS.//P13896

F-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME I.//3.1e-42:205:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10190

55 F-PLACE1009921

F-PLACE1009924//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.70:128:29//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.99:111:27//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P30902  
 F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258.//0.063:75:32//METHANOCOCCUS JANNASCHII.//Q57706  
 5 F-PLACE1009947//NEUROGRANIN (NG) (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT).//0.33:51:45//BOS TAURUS (BOVINE).//P35722  
 F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//0.022:84:27//MUS MUSCULUS (MOUSE).//P28575  
 10 F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24-) (BMP-1).//0.00011:35:51//HOMO SAPIENS (HUMAN).//P13497  
 F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTM1.//0.052:185:22//CIONA INTESTINALIS.//Q07068  
 15 F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FACTOR DMS-II) (TFIIS).//0.68:98:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P20232  
 F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//6.6e-06:111:32//CAENORHABDITIS ELEGANS.//Q18262  
 20 F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.0024:72:33//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479  
 F-PLACE1010053//HYPOTHETICAL PROTEIN HI0593.//0.83:24:45//HAEMOPHILUS INFLUENZAE.//P44022  
 25 F-PLACE1010069  
 F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00027:192:28//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//Q92331  
 F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT).//0.80:39:30//SCIARA COPROPHILA (FUNGUS GNAT).//Q01790  
 30 F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//2.7e-48:177:46//HOMO SAPIENS (HUMAN).//P98171  
 F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (KIAA0055).//7.9e-07:55:43//HOMO SAPIENS (HUMAN).//P40818  
 35 F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.0e-107:232:90//RATTUS NORVEGICUS (RAT).//Q62671  
 F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//1.0:33:45//METHANOCOCUS JANNASCHII.//Q57649  
 F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 40 F-PLACE1010106//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.2e-14:94:41//MUS MUSCULUS (MOUSE).//P11369  
 F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC REGION.//4.0e-28:78:76//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P53115  
 F-PLACE1010148//GAR2 PROTEIN.//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891  
 45 F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574  
 F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87F.//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175  
 F-PLACE1010194//SPLICING FACTOR, ARGinine/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//1.4e-07:95:43//GALLUS GALLUS (CHICKEN).//P30352  
 50 F-PLACE1010202//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36).//0.094:109:29//RATTUS NORVEGICUS (RAT).//P47973  
 F-PLACE1010231//LANTIBIOTIC Nisin A PRECURSOR.//0.99:42:35//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P13068  
 F-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//6.0e-71:201:62//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25722  
 F-PLACE1010270  
 55 F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN C4F8.01 IN CHROMOSOME 1.//4.4e-08:100:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14177  
 F-PLACE1010293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!.//3.9e-26:94:64//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1010310//SYNAPSINS IA AND IB//5.7e-09:89:37//RATTUS NORVEGICUS (RAT).//P09951  
F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180//0.033:145:31//PSEUDORABIES VIRUS (STRAIN KA-PLAN) (PRV).//P33479  
F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD).//0.60:25:48//MEGABOMBUS  
5 PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE).//P04567  
F-PLACE1010329//TOXIN S5C10//1.0:39:33//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P01419  
F-PLACE1010341!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.0049:49:55//HOMO SAPIENS (HUMAN).//  
P39189  
10 F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE)  
(GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PLC).//0.0034:89:30//  
TRYPANOSOMA CRUZI.//015886  
F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COM-  
PLEX I-B17) (CI-B17).//1.0:40:35//SUS SCROFA (PIG).//Q29259  
15 F-PLACE1010383  
F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.10:174:22//RATTUS NORVEGI-  
CUS (RAT).//P41777  
F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME III.//1.5e-21:170:35//  
CAENORHABDITIS ELEGANS.//P46555  
20 F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//1.0:31:41//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490  
F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.//0.77:97:30//  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874  
F-PLACE1010522//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.74:45:37//HOMO SAPIENS  
25 (HUMAN).//P22531  
F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE  
5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE  
(GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMAL-  
DEHYDE DEHYDROGENASE)].//0.70:58:39//VIGNA ACONITIFOLIA (MOTHBEAN).//P32296  
30 F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BUD9-RME1 INTERGENIC REGION.//0.17:68:39//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53227  
F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.50:48:29//PORPHYRA PURPUREA.//  
P51255  
F-PLACE1010579//HYPOTHETICAL PROTEIN HI1571.//0.29:37:43//HAEMOPHILUS INFLUENZAE.//P44260  
35 F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//3.3e-38:178:48//SCHIZOSAC-  
CHAROMYCES POMBE (FISSION YEAST).//Q09747  
F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PER10 (PEROXIN-14).//4.6e-17:192:31//PICHIA  
ANGUSTA (YEAST) (HANSENULA POLYMORPHA).//P78723  
F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION.//0.44:32:37//PSEUDOMONAS PUT-  
40 IDA.//P25753  
F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//5.0e-06:102:42//SACCHAROMY-  
CES CEREVISIAE (BAKER'S YEAST).//P32323  
F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-  
MENT).//0.00036:134:321//HOMO SAPIENS (HUMAN).//P10162  
45 F-PLACE1010628  
F-PLACE1010629!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.7e-12:37:81//HOMO SAPIENS (HUMAN).//  
P39194  
F-PLACE1010630  
50 F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT).//0.49:62:30//EUMECES SKILTONIANUS (WESTERN  
SKINK).//P28118  
F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN.//1.0:95:30//DROSOPHILA PSEUDOBOBSURA  
(FRUIT FLY).//Q24617  
F-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
(DUGT).//3.2e-05:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332  
55 F-PLACE1010702//ZINC FINGER PROTEIN 195.//1.4e-62:117:62//HOMO SAPIENS (HUMAN).//O14628  
F-PLACE1010714  
F-PLACE1010720//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//1.1e-64:176:76//XENOPUS LAEVIS (AF-  
RICAN CLAWED FROG).//P50532

F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.97:31:41//  
 HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612  
 F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//3.8e-05:253:30//MUS MUSCULUS  
 (MOUSE).//P05143

5 F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//1.5e-14:175:25//  
 CAENORHABDITIS ELEGANS.//Q09217

F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.3e-120:216:89//MUS MUSCULUS  
 (MOUSE).//Q02614

10 F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN).//0.97:133:24//DROSOPHILA MELANOGASTER  
 (FRUIT FLY).//P54623

F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TRAX-FINO INTERGENIC REGION (ORFC).//  
 0.0060:111:31//ESCHERICHIA COLI.//Q99390

F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI.//0.82:44:29//BACILLUS SP. (STRAIN TB-90).//  
 Q07415

15 F-PLACE1010811//CYTOCHROME C-551 (C551).//0.99:42:38//ECTOTHIORHODOSPIRA HALOCHLORIS.  
 //P38587

F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN).//2.8e-09:90:34//HOMO SAPIENS (HUMAN).//  
 P41208

20 F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP  
 CRAYFISH).//P55848

F-PLACE1010857//IG ALPHA-1 CHAIN C REGION.//0.49:73:34//GORILLA GORILLA GORILLA (LOWLAND GO-  
 RILLA).//P20758

F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.2e-56:173:58//HO-  
 MO SAPIENS (HUMAN).//Q05481

25 F-PLACE1010877//HEAT SHOCK PROTEIN 82.//0.13:130:25//ZEA MAYS (MAIZE).//Q08277

F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN IN BLTR-SPOIIIC INTERGENIC REGION.//0.95:51:27//  
 BACILLUS SUBTILIS.//P54436

F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PTK1/STK1 (EC 2.7.1.).//0.98:71:30//SACCHA-  
 ROMYCES CEREVISIAE (BAKER'S YEAST).//P36002

30 F-PLACE1010900//HYPOTHETICAL PROTEIN HI0840.//1.0:42:30//HAEMOPHILUS INFLUENZAE.//P44897

F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB3.//0.060:59:35//OVIS ARIES (SHEEP).//  
 P02444

F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).//  
 0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9).//P25191

35 F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN.//1.0:17:58//THERMOPROTEUS TENAX VIRUS 1  
 (STRAIN KRA1) (TTV1).//P19285

F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.011:51:45//HOMO SAPIENS (HU-  
 MAN).//Q92558

40 F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 EPS15).//3.1e-09:64:37//MUS MUSCULUS (MOUSE).//P42567

F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//0.17:71:38//BOS TAURUS  
 (BOVINE).//P41987

F-PLACE1010947

F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//0.011:144:26//HOMO SAPIENS  
 (HUMAN).//P09493

45 F-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//1.1 e-60:136:52//DROSOPHILA MELANOGASTER (FRUIT  
 FLY).//P45890

F-PLACE1010965

F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT).//1.0:64:31//DROSOPHILA ANANASAE (FRUIT  
 FLY).//Q03293

50 F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNASE HI) (RIBONUCLEASE H) (RNASE H).//1.0:32:37//  
 SALMONELLA TYPHIMURIUM.//P23329

F-PLACE1011041//HOMEobox PROTEIN VAB-7.//0.36:65:30//CAENORHABDITIS ELEGANS.//Q93899

55 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC  
 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//1.3e-22:58:93//RATTUS NORVEGI-  
 CUS (RAT).//P10687

F-PLACE1011054//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!.//1.6e-07:38:73//HOMO SAPIENS (HUMAN).//  
 P39195

F-PLACE1011056//HISTONE H1.//2.2e-10:109:41//PISUM SATIVUM (GARDEN PEA).//P08283  
F-PLACE1011057  
F-PLACE1011090//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION.//1.8e-07:133:  
32//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P38892  
5 F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.4e-25:63:88//RAT-  
TUS NORVEGICUS (RAT).//Q07803  
F-PLACE1011114//PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C.//8.4e-31:157:45//SCHIZOSAC-  
CHAROMYCES POMBE (FISSION YEAST).//Q09916  
10 F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-GLYCOPRO-  
TEIN).//0.92:58:31//HOMO SAPIENS (HUMAN).//P02743  
F-PLACE1011143//PROBABLE E5 PROTEIN.//0.24:42:35//HUMAN PAPILLOMAVIRUS TYPE31.//P17385  
F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.88:98:27//GLYCINE MAX  
(SOYBEAN).//Q02917  
15 F-PLACE1011165//HISTIDINE-RICH PROTEIN.//0.013:13:76//PLASMODIUM FALCIPARUM (ISOLATE FCM17 /  
SENEGAL).//P14586  
F-PLACE1011185//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.4e-13:98:50//HOMO SAPIENS (HUMAN).//  
P39188  
F-PLACE1011203  
20 F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:48:27//EQUUS ASINUS (DONKEY).//  
P92479  
F-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.----).//1.9e-15:162:31//STREPTOMYCES ANTI-  
OTICUS.//Q03326  
F-PLACE1011221//ANTITHROMBIN-III HOMOLOG.//0.84:74:33//FOWLPOX VIRUS (ISOLATE HP-438[MU-  
NICH]).//P14369  
25 F-PLACE1011229//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-  
RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-  
TOUS NUCLEAR PROTEIN HOMOLOG).//3.5e-86:218:68//HOMO SAPIENS (HUMAN).//Q13107  
F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//  
3.0e-07:99:36//HOMO SAPIENS (HUMAN).//Q01485  
30 F-PLACE1011273  
F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0.011:36:50//RATTUS  
NORVEGICUS (RAT).//P20468  
F-PLACE1011296//HOMEobox PROTEIN DLX-6.//0.76:55:32//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA  
DANIO).//Q98877  
35 F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN).//  
0.46:43:44//PETUNIA SP. (PETUNIA).//Q07060  
F-PLACE1011325//HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C IN CHROMOSOME I.//0.00021:171:27//  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10411  
40 F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR.//7.3e-27:113:52//  
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q05211  
F-PLACE1011340//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-07:40:62//HOMO SAPIENS (HUMAN).//  
P39188  
F-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN  
H2).//2.2e-54:227:44//MUS MUSCULUS (MOUSE).//Q61703  
45 F-PLACE1011375//PROBABLE E5 PROTEIN.//0.93:28:57//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553  
F-PLACE1011399//HISTONE H2B-IV.//0.19:129:27//VOLVOX CARTERI.//P16868  
F-PLACE1011419  
F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT).//3.4e-05:133:24//GALLUS GALLUS (CHICK-  
EN).//P55879  
50 F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-25:76:63//HOMO SAPIENS (HU-  
MAN).//P08547  
F-PLACE1011465//ECTODERMAL DYSPLASIA PROTEIN (EDA PROTEIN).//0.97:36:41//HOMO SAPIENS (HU-  
MAN).//Q92838  
55 F-PLACE1011472//METALLOTHIONEIN-1 (CUMT-1).//0.084:55:30//HOMARUS AMERICANUS (AMERICAN  
LOBSTER).//P29499  
F-PLACE1011477//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER  
PROTEIN 1).//0.028:129:34//CLOSTRIDIUM THERMOCELLUM.//Q06852  
F-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

2.9e-13:147:31//BRASSICA OLERACEA (CAULIFLOWER).//P52178  
 F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC REGION (086).//0.66:  
 32:40//ESCHERICHIA COLI//P52102  
 F-PLACE1011520  
 5 F-PLACE1011563//LORICRIN.//0.00023:112:39//HOMO SAPIENS (HUMAN).//P23490  
 F-PLACE1011567!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!/9.2e-31:78:76//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5e-32:45:86//HO-  
 MO SAPIENS (HUMAN).//Q05481  
 10 F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-  
 TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT).//0.26:81:37//HOMO SAPIENS (HUMAN).//Q00975  
 F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE180.//0.00045:170:30//PSEUDORABIES VIRUS (STRAIN  
 INDIANA-FUNKHAUSER /BECKER) (PRV).//P11675  
 F-PLACE1011641  
 15 F-PLACE1011643//CUTICLE COLLAGEN 40.//1.0:128:32//CAENORHABDITIS ELEGANS//P34804  
 F-PLACE1011646!!!! ALU SUBFAMILY J WARNING ENTRY !!!!/1.1e-15:44:63//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE1011649//HYPOTHETICAL PROTEIN F-215.//0.48:106:34//HUMAN ADENOVIRUS TYPE 2//P03291  
 F-PLACE1011650  
 20 F-PLACE1011664//CROOKED NECK PROTEIN.//1.2e-79:201:68//DROSOPHILA MELANOGASTER (FRUIT  
 FLY).//P17886  
 F-PLACE1011675//FERREDOXIN.//1.0:44:29//METHANOCOCCUS THERMOLITHOTROPHICUS//P21305  
 F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS26A-COX4 INTERGENIC REGION.//1.0:40:22//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53098  
 25 F-PLACE1011719//NEUROTOXIN TX2-6.//0.90:31:35//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPI-  
 DER).//P29425  
 F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//  
 0.0065:125:25//RATTUS NORVEGICUS (RAT).//Q63083  
 F-PLACE1011729//SRY-RELATED PROTEIN LG27 (FRAGMENT).//0.97:48:39//EUBLEPHARIS MACULAR-  
 30 IUS//P40654  
 F-PLACE1011749  
 F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).//0.028:91:39//MUS  
 MUSCULUS (MOUSE).//Q60925  
 F-PLACE1011778  
 35 F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).//0.97:48:  
 43//MUS MUSCULUS (MOUSE).//P20863  
 F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0027:154:33//BOS TAURUS (BOVINE).//P23206  
 F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCHL A PROTEIN) (BCP).//1.0:60:26//PROSTHE-  
 COCHLORIS AESTUARII..//P11741  
 40 F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP54-ALT INTERGENIC REGION.//0.99:34:35//AC-  
 TERIOPHAGE T4..//P39495  
 F-PLACE1011891//SMOOTHELIN.//0.018:122:31//HOMO SAPIENS (HUMAN).//P53814  
 F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//6.3e-09:203:35//  
 XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
 45 F-PLACE1011922//CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).//0.067:37:48//MUS MUSCU-  
 LUS (MOUSE).//P50715  
 F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE).//  
 1.5e-83:175:89//MUS MUSCULUS (MOUSE).//P53351  
 F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.50:46:41//SCHIZOPHYLLUM  
 50 COMMUNE (BRACKET FUNGUS).//Q02593  
 F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-05:47:51//NYCTICEBUS COU-  
 CANG (SLOW LORIS).//P08548  
 F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).//0.98:  
 83:31//PLASMODIUM FRAGILE..//P22622  
 55 F-PLACE1011995  
 F-PLACE1012031//HYPOTHETICAL PROTEIN KIAA0254.//0.032:62:33//HOMO SAPIENS (HUMAN).//Q92543  
 F-PLACE2000003!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!/5.4e-18:63:73//HOMO SAPIENS (HUMAN).//  
 P39193

F-PLACE2000006//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.14:20:50//BOS TAURUS (BOVINE).//P20072  
 F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0045:176:30//MUS MUSCULUS (MOUSE).//P05143  
 F-PLACE200011//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.6e-25:57:78//HOMO SAPIENS (HUMAN).//  
 5 P39194  
 F-PLACE200014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.00013:237:27//  
 CAENORHABDITIS ELEGANS.//Q09475  
 F-PLACE200015//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.4e-33:60:80//HOMO SAPIENS (HUMAN).//  
 P39193  
 10 F-PLACE200017//FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP).//1.0:83:31//HOMO SAPIENS (HUMAN).//P14207  
 F-PLACE200021//EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8).//0.99:103:26//GALLUS GALLUS (CHICKEN).//Q07496  
 15 F-PLACE200030//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.69:29:44//DROSOPHILA MELANOGLASTER (FRUIT FLY).//Q01642  
 F-PLACE200033//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//1.1e-05:74:41//STREPTOMYCES ANTIBIOTICUS.//Q03326  
 20 F-PLACE200034//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCO-OPROTEIN 1).//6.7e-18:191:35//HOMO SAPIENS (HUMAN).//Q02246  
 F-PLACE200039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//4.7e-80:163:96//RATTUS NOR-VEGICUS (RAT).//P38650  
 F-PLACE200047//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//6.4e-06:63:49//HOMO SAPIENS (HUMAN).//P39191  
 25 F-PLACE200050//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.2e-22:74:64//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-PLACE200061  
 F-PLACE200062//GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL STRESS PROTEIN B).//1.9e-06:108:37//BACILLUS SUBTILIS.//P26907  
 30 F-PLACE200072//ZINC FINGER PROTEIN 165.//3.5e-34:175:49//HOMO SAPIENS (HUMAN).//P49910  
 F-PLACE200097//RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).//0.36:39:38//ONDATRA ZIBETHICUS (MUSKRAT).//P00681  
 F-PLACE2000100  
 35 F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS).//0.18:32:37//ZEA MAYS (MAIZE).//P33626  
 F-PLACE2000111//CMRF35 ANTIGEN PRECURSOR.//0.056:107:27//HOMO SAPIENS (HUMAN).//Q08708  
 F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP EPIMERASE) (FRAGMENT).//1.0:21:  
 52//CLOSTRIDIUM PERFRINGENS.//Q46185  
 F-PLACE2000124//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.4e-37:108:68//HOMO SAPIENS (HUMAN).//P39194  
 40 F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85.//0.99:133:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03224  
 F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR) (PACAP TYPE III RECEPTOR) (PACAP-R-3).//0.83:65:32//MUS MUSCULUS (MOUSE).//P41588  
 45 F-PLACE2000140  
 F-PLACE2000164//TIPD PROTEIN.//5.7e-12:190:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//  
 O15736  
 F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BM1 PRECURSOR (CARNOBACTERIOCIN B1).//  
 1.0:30:26//CARNOBACTERIUM PISCICOLA.//P38579  
 50 F-PLACE2000172  
 F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526.//0.76:44:43//ARCHAEOGLOBUS FULgidus.//O29724  
 F-PLACE2000187//EM-LIKE PROTEIN GEA6.//0.84:42:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//  
 Q02973  
 F-PLACE2000216  
 55 F-PLACE2000223//NEUROTOXIN III (LQQ III).//0.99:38:34//LEIURUS QUINQUESTRIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01487  
 F-PLACE2000235  
 F-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//5.1e-37:121:42//DROSOPHILA MELA-

NOGASTER (FRUIT FLY).//Q04652  
F-PLACE2000264!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//2.4e-05:77:42//HOMO SAPIENS (HUMAN).//P39191

5 F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//5.3e-46:232:45//TRIPNEUSTES GRATILLA (HAWAIIAN SEA URCHIN).//P23098  
F-PLACE2000302//TRICHOHYALIN.//1.5e-06:215:29//ORYCTOLAGUS CUNICULUS (RABBIT).//P37709  
F-PLACE2000305!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.3e-06:33:66//HOMO SAPIENS (HUMAN).//P39188

10 F-PLACE2000317//TOXIN C13S1C1 PRECURSOR.//0.44:45:33//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329  
F-PLACE2000335!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//7.9e-08:35:71//HOMO SAPIENS (HUMAN).//P39195  
F-PLACE2000341//SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.014:141:24//ORYCTOLAGUS CUNICULUS (RABBIT).//P11170

15 F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//5.7e-09:96:38//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479  
F-PLACE2000347//ZINC FINGER PROTEIN 177.//5.9e-05:49:53//HOMO SAPIENS (HUMAN).//Q13360  
F-PLACE2000359!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.5e-10:69:52//HOMO SAPIENS (HUMAN).//P39194

20 F-PLACE2000366  
F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.5e-05:216:29//HOMO SAPIENS (HUMAN).//P54259  
F-PLACE2000373//MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT).//0.27:63:33//HOMO SAPIENS (HUMAN).//Q99583

25 F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN.//0.72:120:31//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28978  
F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.95:40:42//HOMO SAPIENS (HUMAN).//P02811

30 F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.-).//0.88:88:31//AEROMONAS HYDROPHILA.//Q07465  
F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//7.6e-16:180:39//HOMO SAPIENS (HUMAN).//P14209

35 F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS).//1.7e-94:243:64//CAENORHABDITIS ELEGANS.//Q09996  
F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.2e-09:78:39//MUS MUSCULUS (MOUSE).//Q60676  
F-PLACE2000419!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-20:61:62//HOMO SAPIENS (HUMAN).//P39188

40 F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MSB2-UGA1 INTERGENIC REGION.//0.98:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53211  
F-PLACE2000427//INSULIN PRECURSOR.//0.98:55:34//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P30407  
F-PLACE2000433!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.5e-07:65:50//HOMO SAPIENS (HUMAN).//P39188

45 F-PLACE2000435  
F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III.//4.7e-66:178:47//CAENORHABDITIS ELEGANS.//P34678  
F-PLACE2000450!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.1e-23:88:62//HOMO SAPIENS (HUMAN).//P39195

50 F-PLACE2000455//TOXIN II (TOXIN II.10.9.2) (FRAGMENT).//0.093:18:44//CENTRUROIDES LIMPIDUS LIMPIDUS (MEXICAN SCORPION).//P45630  
F-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.1e-23:165:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450  
F-PLACE2000465!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.6e-23:73:63//HOMO SAPIENS (HUMAN).//P39188  
F-PLACE2000477!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-37:90:78//HOMO SAPIENS (HUMAN).//P39194

F-PLACE3000004//EYES ABSENT HOMOLOG 3//1.1e-09:27:100//MUS MUSCULUS (MOUSE).//P97480  
 F-PLACE3000009//PUTATIVE CUTICLE COLLAGEN C09G5.6//0.0061:148:34//CAENORHABDITIS ELEGANS.//Q09457  
 5 F-PLACE3000020//ADENYLATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (TYPE III) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//8.8e-93:193:92//RATTUS NORVEGICUS (RAT).//P21932  
 F-PLACE3000029//50S RIBOSOMAL PROTEIN L31E.//0.15:50:38//METHANOCOCCUS JANNASCHII.//P54009  
 F-PLACE3000059//TCP1-CHAPERONIN COFACTOR A.//0.96:50:34//BOS TAURUS (BOVINE).//P48427  
 F-PLACE3000070//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.29:22:59//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898  
 10 F-PLACE3000103//LYSIS PROTEIN (E PROTEIN) (GPE).//0.99:53:32//BACTERIOPHAGE ALPHA-3.//P31280  
 F-PLACE3000119//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//5.4e-41:87:78//HOMO SAPIENS (HUMAN).//P39189  
 F-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC151/1.0e-07:269:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22224  
 15 F-PLACE3000124//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.2e-29:97:73//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE3000136//PARS INTERCEREBRALIS MAJOR PEPTIDE D1 (PMP-D1).//0.77:26:42//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P80059  
 20 F-PLACE3000142//HYPOTHETICAL 7.1 KD PROTEIN IN NAD2 3'REGION (ORF 63).//0.82:34:41//MARCHANTIA POLYMORPHA (LIVERWORT).//P38468  
 F-PLACE3000145//TENSIN.//3.5e-91:238:74//GALLUS GALLUS (CHICKEN).//Q04205  
 F-PLACE3000147//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-30:61:65//HOMO SAPIENS (HUMAN).//P39194  
 25 F-PLACE3000148//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.4e-18:226:34//GIBBON APE LEUKEMIA VIRUS.//P21414  
 F-PLACE3000155//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.00014:107:33//ZEA MAYS (MAIZE).//P14918  
 F-PLACE3000156//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//2.7e-19:169:30//BABOON ENDOGENOUS VIRUS (STRAIN M7).//P10272  
 30 F-PLACE3000157//PROBABLE SERINE/THREONINE-PROTEIN KINASE CY50.16 (EC 2.7.1.-).//0.0061:92:30//MYCOBACTERIUM TUBERCULOSIS.//Q11053  
 F-PLACE3000158//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//5.7e-49:56:80//HOMO SAPIENS (HUMAN).//P39189  
 F-PLACE3000160//DNA TRANSFORMATION PROTEIN TFOX (COMPETENCE ACTIVATOR) (PROTEIN SXY).//  
 35 0.39:94:34//HAEMOPHILUS INFLUENZAE.//P43779  
 F-PLACE3000169//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.6e-28:99:59//HOMO SAPIENS (HUMAN).//P39193  
 F-PLACE3000194//PROLINE-RICH PROTEIN LAS17.//0.91:80:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12446  
 40 F-PLACE3000197//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//0.24:119:32//GALLUS GALLUS (CHICKEN).//P16053  
 F-PLACE3000199//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.76:87:37//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-PLACE3000207//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.5e-09:32:78//HOMO SAPIENS (HUMAN).//  
 45 P39188  
 F-PLACE3000208  
 F-PLACE3000218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.2e-34:96:70//HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE3000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC ACID-CONTAINING PROTEIN) (BONE GLA- PROTEIN) (BGP).//0.46:13:53//CANIS FAMILIARIS (DOG).//P81455  
 50 F-PLACE3000221//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.8e-24:178:45//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE3000226//30S RIBOSOMAL PROTEIN S18.//0.98:38:34//NEISSERIA GONORRHOEAE.//O07815  
 F-PLACE3000230//METALLOTHIONEIN (MT).//0.97:25:48//OREOCHROMIS MOSSAMBICUS (MOZAMBIQUE TILAPIA) (TILAPIA MOSSAMBICA).//P52726  
 55 F-PLACE3000242//MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).//8.0e-21:121:39//HOMO SAPIENS (HUMAN).//P43361  
 F-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//2.3e-125:264:87//MUS MUS-

CULUS (MOUSE).//P53995  
 F-PLACE3000254//RTOA PROTEIN (RATIO-A).//0.99:142:23//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681  
 F-PLACE3000271//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.2e-12:63:53//HOMO SAPIENS (HUMAN).//  
 5 P39188  
 F-PLACE3000276//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//1.0:55:38//  
 HOMO SAPIENS (HUMAN).//P27658  
 F-PLACE3000304//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.0028:31:54//HO-  
 MO SAPIENS (HUMAN).//P30808  
 10 F-PLACE3000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//0.98:82:34//  
 RATTUS NORVEGICUS (RAT).//P54258  
 F-PLACE3000320  
 F-PLACE3000322//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//2.2e-22:61:52//  
 ORYZA SATIVA (RICE).//P25074  
 15 F-PLACE3000331//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.32:15:53//HOMO SAPIENS  
 (HUMAN).//P22532  
 F-PLACE3000339//CHORION PROTEIN S19.//0.34:89:37//DROSOPHILA VIRILIS (FRUIT FLY).//P24516  
 F-PLACE3000341//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//1.0:47:38//  
 COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P24968  
 20 F-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//3.9e-50:168:60//  
 CAENORHABDITIS ELEGANS //P46549  
 F-PLACE3000352//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.8e-29:76:71//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE3000353//POLYPEPTTOE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-  
 25 UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-  
 AMINYLTRANSFERASE) (GALNAC-T1).//3.0e-09:100:41//HOMO SAPIENS (HUMAN).//Q10472  
 F-PLACE3000362//HYPOTHETICAL PROTEIN TP0064.//1.0:75:26//TREPONEMA PALLIDUM.//O83103  
 F-PLACE3000363//METALLOTHIONEIN (MT).//0.067:42:33//ASTACUS FLUVIATILIS (BROAD-FINGERED  
 CRAYFISH) (ASTACUS ASTACUS).//P55951  
 30 F-PLACE3000365//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:65:27//BACTERIOPHAGE PHI-K.//Q38040  
 F-PLACE3000373//RETROVIRUS-RELATED ENV POLYPOLYPROTEIN.//1.5e-18:90:47//HOMO SAPIENS (HU-  
 MAN).//P10267  
 F-PLACE3000388  
 F-PLACE3000399//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//6.3e-45:60:75//HOMO SAPIENS (HUMAN).//  
 35 P39193  
 F-PLACE3000400  
 F-PLACE3000401//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.6e-09:46:73//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE3000402//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.036:43:44//HOMO SAPIENS (HUMAN).//  
 40 P39188  
 F-PLACE3000405//POSTERIOR PITUITARY PEPTIDE.//0.70:25:40//BOS TAURUS (BOVINE).//P01154  
 F-PLACE3000406//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.3e-09:49:67//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-PLACE3000413//MALE SPECIFIC SPERM PROTEIN MST87F.//0.12:42:40//DROSOPHILA MELANOGASTER  
 45 (FRUIT FLY).//P08175  
 F-PLACE3000416//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.67:236:21//BOS TAURUS (BOVINE).//  
 P35662  
 F-PLACE3000425//PROLINE-RICH PEPTIDE P-B.//0.45:19:42//HOMO SAPIENS (HUMAN).//P02814  
 F-PLACE3000455//AMELOGENIN, CLASS I PRECURSOR.//0.0073:81:43//BOS TAURUS (BOVINE).//P02817  
 50 F-PLACE3000475//8.6 KD TRANSGLUTAMINASE SUBSTRATE.//1.0:53:32//TACHYPLEUS TRIDENTATUS  
 (JAPANESE HORSESHOE CRAB).//P81281  
 F-PLACE3000477//MUSCARINIC TOXIN 7 (MT-7).//0.13:55:32//DENDROASPIS ANGUSTICEPS (EASTERN  
 GREEN MAMBA).//P80970  
 F-PLACE4000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//7.0e-19:  
 55 180:27//HOMO SAPIENS (HUMAN).//P35749  
 F-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.2e-15:193:30//HOMO  
 SAPIENS (HUMAN).//P46100  
 F-PLACE4000034//BRIDE OF SEVENLESS PROTEIN PRECURSOR.//0.0024:97:29//DROSOPHILA MELA-

NOGASTER (FRUIT FLY).//P22815  
 F-PLACE4000049//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.8e-32:79:75//HOMO SAPIENS (HUMAN).//  
 P39194

5 F-PLACE4000052//ATP-BINDING CASSETTE TRANSPORTER 1.//2.2e-99:178:97//MUS MUSCULUS  
 (MOUSE).//P41233

F-PLACE4000063//IMMEDIATE-EARLY PROTEIN.//0.0017:159:25//HERPESVIRUS SAIMIRI (STRAIN 11).//  
 Q01042

F-PLACE4000089  
 F-PLACE4000093

10 F-PLACE4000100//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-14:68:60//HOMO SAPIENS (HUMAN).//  
 P39188

F-PLACE4000106//1A PROTEIN [CONTAINS: HELICASE; METHYLTRANSFERASE].//1.0:46:41//BROAD BEAN  
 MOTTLE VIRUS.//Q00020

15 F-PLACE4000128//HYPOTHETICAL PROTEIN E-115.//0.00020:101:30//HUMAN ADENOVIRUS TYPE 2.//  
 P03290

F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN).//  
 0.15:57:31//HOMO SAPIENS (HUMAN).//P22528

F-PLACE4000131  
 F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR.//1.0:45:24//BACILLUS SUBTILIS.//P45453

20 F-PLACE4000156//ZINC FINGER PROTEIN 136.//2.1e-88:194:59//HOMO SAPIENS (HUMAN).//P52737

F-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.083:148:26//HOMO SAPIENS (HU-  
 MAN).//P52746

F-PLACE4000211//CALPHOTIN.//0.20:43:39//DROSOPHILA MELANOGLASTER (FRUIT FLY).//Q02910

F-PLACE4000222//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-05:20:85//HOMO SAPIENS (HUMAN).//  
 25 P39188

F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE SYNTHASE (EC 2.1.1.45)  
 (DHFR-TS).//1.0:96:28//TRYpanosoma brucei brucei.//Q27783

F-PLACE4000233  
 F-PLACE4000247//METALLOTHIONEIN (MT).//1.0e-05:34:41//PLEURONECTES PLATESSA (PLAICE).//  
 30 P07216

F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//0.99:33:42//CAPRINE ARTHRITIS EN-  
 CEPHALITIS VIRUS (CAEV).//P31834

F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.42:24:45//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q01643

35 F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//3.5e-09:189:32//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P32639

F-PLACE4000261//PEREGRIN (BR140 PROTEIN).//5.0e-11:103:37//HOMO SAPIENS (HUMAN).//P55201

F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.037:181:25//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//P25386

40 F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//1.0:46:39//MUS MUSCULUS  
 (MOUSE).//P70375

F-PLACE4000300//50S RIBOSOMAL PROTEIN L32.//0.81:28:46//THERMUS AQUATICUS (SUBSP. THER-  
 MOPHILUS).//P80339

F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN).//  
 45 1.6e-29:44:93//HOMO SAPIENS (HUMAN).//P42345

F-PLACE4000323  
 F-PLACE4000326//PARATHYMOSEN.//0.0018:54:48//HOMO SAPIENS (HUMAN).//P20962

F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT).//0.97:28:42//SUS SCROFA (PIG).//  
 Q00968

50 F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-I) (SHNA) (NEUROTOXIN SHI).//1.0:33:36//STOICHACTIS  
 HELIANTHUS (CARIBBEAN SEA ANEMONE) (STICHODACTyla HELIANTHUS).//P19651

F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.071:42:42//SORGHUM  
 VULGARE (SORGHUM).//P24152

F-PLACE4000379//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.4e-16:54:77//HOMO SAPIENS (HUMAN).//  
 55 P39193

F-PLACE4000387//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//0.25:21:52//HOR-  
 DEUM VULGARE (BARLEY), AND SECALE CEREALE (RYE).//P25877

F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE)

(FRAGMENT).//0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS//Q05338  
 F-PLACE4000401!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-29:96:67//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE4000411!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-18:41:73//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//5.4e-21:237:33//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P32639  
 F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SDL1 5'REGION PRECURSOR.//0.00081:210:26//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40442  
 F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION FACTOR  
 HBP1).//0.020:87:33//TRITICUM AESTIVUM (WHEAT).//P23922  
 F-PLACE4000465//METALLOTHIONEIN-IL (MT-1L) (MT1X).//0.20:18:38//HOMO SAPIENS (HUMAN).//P80297  
 F-PLACE4000487!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-19:73:52//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE4000489  
 F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//0.17:130:30//MUS MUSCULUS  
 (MOUSE).//Q03173  
 F-PLACE4000521//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE] (FRAGMENT).//3.0e-05:50:36//MUS MUSCULUS (MOUSE).//P10400  
 F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.//1.8e-45:231:47//  
 RATTUS NORVEGICUS (RAT).//Q07008  
 F-PLACE4000548//CYTOCHROME C-551 (C551).//0.96:50:34//ECTOTHIORHODOSPIRA HALOPHILA.//  
 P00122  
 F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN  
 THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME  
 FAF) (FAT FACETS PROTEIN).//1.6e-28:223:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55824  
 F-PLACE000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)  
 (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//9.7e-11:166:281//HOMO  
 SAPIENS (HUMAN).//P16109  
 F-PLACE4000590//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE].//1.6e-17:134:35//GIBBON APE LEUKEMIA VIRUS.//P21414  
 F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).//1.0:54:29//RATTUS  
 NORVEGICUS (RAT).//P30969  
 F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12;  
 CORE SHELL PROTEIN P30].//2.6e-14:221:32//MOLONEY MURINE SARCOMA VIRUS (STRAIN TS110).//  
 P32594  
 F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NRDB-INAA INTERGENIC REGION.//0.65:37:40//ES-  
 CHERICIA COLI.//P37910  
 F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN KOX9) (FRAGMENT).//1.0:33:33//HO-  
 MO SAPIENS (HUMAN).//P17020  
 F-PLACE4000654  
 F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION.//1.6e-07:161:  
 25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33313  
 F-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//7.4e-15:223:  
 31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q60100  
 F-SKNMC1000013//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//0.0013:128:  
 35//GALLUS GALLUS (CHICKEN).//Q98937  
 F-SKNMC1000046//CUTICLE COLLAGEN 1.//0.0010:154:33//CAENORHABDITIS ELEGANS.//P08124  
 F-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-  
 TRAL PROTEINASE) (CANP) (M-TYPE).//3.2e-41:87:98//HOMO SAPIENS (HUMAN).//P17655  
 F-SKNMC1000091//NTAK PROTEIN (NEURAL- AND THYMUS- DERIVED ACTIVATOR FOR ERBB KINASES).//  
 0.0032:154:35//HOMO SAPIENS (HUMAN).//Q14511  
 F-THYRO1000017//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXI-  
 DASE).//1.6e-23:124:37//CAENORHABDITIS ELEGANS.//Q20939  
 F-THYRO1000026!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.0e-13:54:66//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-THYRO1000034//HYPOTHETICAL 10.4 KD PROTEIN.//0.16:44:34//HEPATITIS B VIRUS (SUBTYPE AYW).//  
 P03163

F-THYRO1000035//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CDW52) (CAMBRIDGE PATHOLOGY 1 ANTIGEN).//0.83:59:37//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P32763  
 5 F-THYRO1000040//60S RIBOSOMAL PROTEIN L37 (FRAGMENT).//0.25:23:39//BOS TAURUS (BOVINE).//P79244  
 F-THYRO1000070//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//2.3e-11:133:36//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341  
 10 F-THYRO1000072//C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM.//1.5e-14:205:29//HOMO SAPIENS (HUMAN).//Q00872  
 F-THYRO1000085  
 15 F-THYRO1000092//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.063:59:33//HOMO SAPIENS (HUMAN).//P49901  
 F-THYRO1000107  
 F-THYRO1000111//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-58:110:67//NYCTICEBUS CUCANG (SLOW LORIS).//P08548  
 20 F-THYRO1000121//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//2.6e-06:134:35//MUS MUSCULUS (MOUSE).//Q62203  
 F-THYRO1000124//TENECIN 3 PRECURSOR.//0.047:76:35//TENEBCRIO MOLITOR (YELLOW MEALWORM).//Q27270  
 25 F-THYRO1000129//FBROSIN (FRAGMENT).//0.35:43:34//MUS MUSCULUS (MOUSE).//Q60791  
 F-THYRO1000132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.7e-14:104:42//HOMO SAPIENS (HUMAN).//P39188  
 F-THYRO1000156  
 30 F-THYRO1000163//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//3.7e-20:71:71//HOMO SAPIENS (HUMAN).//P39189  
 F-THYRO1000173//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//6.7e-88:216:76//MUS MUSCULUS (MOUSE).//P35585  
 F-THYRO1000186//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.9e-24:72:77//HOMO SAPIENS (HUMAN).//P39192  
 F-THYRO1000187  
 35 F-THYRO1000190//PROTEIN TRANSPORT PROTEIN SEC61 BETA 2 SUBUNIT.//0.060:50:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52871  
 F-THYRO1000197  
 F-THYRO1000199//HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN CHROMOSOME III.//2.0e-06:88:35//CAENORHABDITIS ELEGANS.//34379  
 40 F-THYRO1000206  
 F-THYRO1000221  
 F-THYRO1000241//HYPOTHETICAL 11.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//1.0:51:35//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41661  
 F-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.4e-37:137:36//HOMO SAPIENS (HUMAN).//P51523  
 F-THYRO1000253//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.11:21:52//HOMO SAPIENS (HUMAN).//P30808  
 45 F-THYRO1000270//WDNM1 PROTEIN PRECURSOR.//0.40:52:32//MUS MUSCULUS (MOUSE).//Q62477  
 F-THYRO1000279//BETA CRYSTALLIN A4.//0.97:64:26//BOS TAURUS (BOVINE).//P11842  
 F-THYRO1000288//POTENTIAL CAAX PRENLY PROTEASE 1 (EC 3.4.24.-) (PRENLY PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).//3.4e-48:142:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10071  
 50 F-THYRO1000320//ZINC FINGER PROTEIN 14 (ZFP-14) (KROX-9 PROTEIN) (FRAGMENT).//0.87:35:45//MUS MUSCULUS (MOUSE).//P10755  
 F-THYRO1000327//HYPOTHETICAL 64.7 KD PROTEIN F26E4.11 IN CHROMOSOME I.//0.00010:75:26//CAENORHABDITIS ELEGANS.//P90859  
 55 F-THYRO1000343//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14].//0.88:107:26//MUS MUSCULUS (MOUSE).//P26339  
 F-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//4.6e-25:49:81//MUS MUSCULUS (MOUSE).//P17563  
 F-THYRO1000368//LOCOMOTION-RELATED PROTEIN HIKARU GENKI PRECURSOR.//1.0:136:26//DRO-

SOPHILA MELANOGASTER (FRUIT FLY).//Q09101  
 F-THYRO1000381//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12;  
 CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].//0.032:99:35//SIMIAN SARCOMA VIRUS.//P03330  
 F-THYRO1000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.90:46:30//HALICHOERUS GRYPUS  
 (GRAY SEAL).//P38592  
 5 F-THYRO1000394//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.00019:48:37//HOMO SAPIENS (HUMAN).//P22531  
 F-THYRO1000395//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-33:186:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 10 F-THYRO1000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT).//0.57:67:31//STAPHYLOCOCCUS AUREUS.//P48860  
 F-THYRO1000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:38//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997  
 15 F-THYRO1000452//BACTERIOCIN CARNOBACTERIOCIN A PRECURSOR (PISCICOLIN 61).//0.31:34:44//CARNOBACTERIUM PISCICOLA.//P38578  
 F-THYRO1000471!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2,1e-31:94:72//HOMO SAPIENS (HUMAN).//P39194  
 F-THYRO1000484!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.9e-08:30:86//HOMO SAPIENS (HUMAN).//P39195  
 20 F-THYRO1000488//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.93:98:27//GLYCINE MAX (SOYBEAN).//Q02917  
 F-THYRO1000501//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//2.4e-51:198:50//MUS MUSCULUS (MOUSE).//P15533  
 25 F-THYRO1000502//HUNCHBACK PROTEIN (FRAGMENT).//0.84:41:43//APIS MELLIFERA (HONEYBEE).//P31504  
 F-THYRO1000505//HYPOTHETICAL BHLF1 PROTEIN.//0.99:231:33//EPSTEIN-BARR VIRUS (STRAIN B95-8)  
 (HUMAN HERPESVIRUS 4).//P03181  
 F-THYRO1000558//ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).//0.47:58:37//GALLUS GALLUS  
 (CHICKEN).//Q03352  
 30 F-THYRO1000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00048:64:42//RATTUS NORVEGICUS  
 (RAT).//P02454  
 F-THYRO1000570//HYPOTHETICAL 11.6 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//0.94:61:32//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39725  
 35 F-THYRO1000585//SPLICING FACTOR, ARGinine/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55).//0.050:104:36//HOMO SAPIENS (HUMAN).//Q13247  
 F-THYRO1000596//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.99:37:40//  
 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37319  
 F-THYRO1000602//EAMZP30-47 PROTEIN (FRAGMENT).//0.88:61:34//EIMERIA ACERVULINA.//P21959  
 40 F-THYRO1000605//SUPPRESSOR PROTEIN SRP40.//0.0016:116:26//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P32583  
 F-THYRO1000625!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.4e-33:88:78//HOMO SAPIENS (HUMAN).//P39194  
 F-THYRO1000637//METALLOTHIONEIN A (MT A).//1.0:23:43//SPARUS AURATA (GILTHEAD SEA BREAM).//  
 P52727  
 45 F-THYRO1000641//PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN.//0.99:26:46//CYANIDIUM CALDARIUM  
 (GALDIERIA SULPHURARIA).//O19925  
 F-THYRO1000658!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.5e-49:116:69//HOMO SAPIENS (HUMAN).//P39189  
 50 F-THYRO1000662//DNA-DAMAGE-INDUCIBLE PROTEIN P.//3.7e-15:119:43//ESCHERICHIA COLI.//Q47155  
 F-THYRO1000666//KINESIN-LIKE PROTEIN KLP1.//1.0e-44:232:41//CHLAMYDOMONAS REINHARDTII.//  
 P46870  
 F-THYRO1000676!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.1e-15:144:39//HOMO SAPIENS (HUMAN).//P39193  
 55 F-THYRO1000684//HYPOTHETICAL 73.5 KD PROTEIN IN SCS3-RPS2 INTERGENIC REGION.//0.00033:84:  
 30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53129  
 F-THYRO1000699!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//0.97:20:85//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-THYRO1000712!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.2e-10:69:59//HOMO SAPIENS (HUMAN).//

P39188  
F-THYRO1000715//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.6e-10:204:32//HOMO SAPIENS (HUMAN).//P04280  
F-THYRO1000734  
5 F-THYRO1000748//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-46:130:70//HOMO SAPIENS (HUMAN).//O43295  
F-THYRO1000756//ALPHA-N-ACETYLGLUCOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY).//1.1e-06:95:31//RATTUS NORVEGICUS (RAT).//Q64686  
F-THYRO1000777//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0031:119:34//HAEMONCHUS CONTORTUS.//  
10 P16252  
F-THYRO1000783//MYOSIN IC HEAVY CHAIN.//0.0014:121:37//ACANTHAMOEBA CASTELLANII (AMOEBA).//  
P10569  
F-THYRO1000787//HUNCHBACK PROTEIN (FRAGMENT).//0.54:25:52//PHOLCUS PHALANGOIDES.//  
Q02031  
15 F-THYRO1000793//PRE-MRNA SPLICING FACTOR PRP9.//0.91:3 0:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19736  
F-THYRO1000796  
F-THYRO1000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.081:31:38//HUMAN ADENOVIRUS TYPE 41.//P23691  
20 F-THYRO1000815!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//6.0e-30:81:70//HOMO SAPIENS (HUMAN).//  
P39195  
F-THYRO1000829//NEUROTOXIN III (BOM III).//0.022:32:34//BUTHUS OCCITANUS MARDOCHEI (MOROC-  
CAN SCORPION).//P13488  
F-THYRO1000843//HYPOTHETICAL 7.7 KD PROTEIN IN GENES 5-4 INTERGENIC REGION (ORF 109).//0.98:  
25 25:44//BACTERIOPHAGE P22.//P26750  
F-THYRO1000852//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//7.3e-09:83:42//VOLVOX CART-  
ERI.//P21997  
F-THYRO1000855//ANTIFREEZE PEPTIDE 4 PRECURSOR.//1.0:54:35//PSEUDOPLEURONECTA AMERICA-  
NUS (WINTER FLOUNDER).//P02734  
30 F-THYRO1000865!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//5.2e-17:66:57//HOMO SAPIENS (HUMAN).//  
P39188  
F-THYRO1000895!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.0e-12:58:62//HOMO SAPIENS (HUMAN).//  
P39189  
F-THYRO1000916!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.0e-32:101:69//HOMO SAPIENS (HU-  
35 MAN).//P39189  
F-THYRO1000926//NITROGEN FIXATION REGULATORY PROTEIN.//5.5e-05:108:27//KLEBSIELLA OXYTO-  
CA.//P56267  
F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//  
3.9e-50:147:40//HOMO SAPIENS (HUMAN).//P32322  
40 F-THYRO1000951//DIHYDROXYACETONE KINASE (EC 2.7.1.29) (GLYCERONE KINASE).//1.8e-31:136:56//  
CITROBACTER FREUNDII.//P45510  
F-THYRO1000952//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//2.4e-05:91:  
34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170  
F-THYRO1000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR.//1.0:35:40//  
45 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32580  
F-THYRO1000975  
F-THYRO1000983//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//1.3e-20:96:51//  
CAENORHABDITIS ELEGANS.//Q11076  
F-THYRO1000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROTEIN.//0.011:76:34//DRO-  
50 SOPHILA MELANOGASTER (FRUIT FLY).//P25160  
F-THYRO1000988  
F-THYRO1001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSCL-RPLQ INTERGENIC REGION.//0.97:60:31//  
ESCHERICHIA COLI.//P36675  
F-THYRO1001031!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//9.5e-18:56:66//HOMO SAPIENS (HUMAN).//  
55 P39195  
F-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//5.0e-13:126:35//HOMO SAPI-  
ENS (HUMAN).//P31948  
F-THYRO1001062!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.1e-35:97:79//HOMO SAPIENS (HUMAN).//

P39194  
F-THYRO1001093!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!/6.4e-13:70:57//HOMO SAPIENS (HUMAN).//  
P39194  
F-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//4.2e-63:219:63//HOMO SAPIENS  
(HUMAN).//P98168  
F-THYRO1001120//SPLICEROSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.00068:160:31//HOMO  
SAPIENS (HUMAN).//Q15427  
F-THYRO1001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I.//0.37:158:28//  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263  
F-THYRO1001133!!!! ALU SUBFAMILY J WARNING ENTRY !!!!/7.3e-15:59:66//HOMO SAPIENS (HUMAN).//  
P39188  
F-THYRO1001134//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAG-  
MENT).//0.00088:159:29//HOMO SAPIENS (HUMAN).//P10161  
F-THYRO1001142!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!/3.0e-29:81:71//HOMO SAPIENS (HUMAN).//  
P39194  
F-THYRO1001173//CYTOCHROME C OXIDASE POLYPEPTIDE VII (EC 1.9.3.1).//0.88:51:35//DICTYOSTEL-  
IUM DISCOIDEUM (SLIME MOLD).//P20610  
F-THYRO1001177!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!/3.0e-24:91:68//HOMO SAPIENS (HUMAN).//  
P39192  
F-THYRO1001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2).//7.3e-27:165:39//MUS MUSCULUS  
(MOUSE).//P08043  
F-THYRO1001204//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.67:42:42//HOMO SAPIENS (HUMAN).//  
P02811  
F-THYRO1001213!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!/2.9e-16:61:68//HOMO SAPIENS (HUMM).//  
P39194  
F-THYRO1001262!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!/1.4e-36:50:84//HOMO SAPIENS (HUMAN).//  
P39193  
F-THYRO1001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.62: 126:30//STREPTO-  
MYCES FRADIAE.//P20186  
F-THYRO1001287//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION.//1.9e-26:208:  
37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888  
F-THYRO1001290//GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT).//1.0:31:38//LAMELLIBRACHIA SP.  
(DEEP-SEA GIANT TUBE WORM).//P20413  
F-THYRO1001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00042:105:31//SAC-  
CHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331  
F-THYRO1001320//COLLAGEN ALPHA 1(III) CHAIN.//0.27:57:38//BOS TAURUS (BOVINE).//P04258  
F-THYRO1001321!!!! ALU SUBFAMILY J WARNING ENTRY !!!!/5.5e-20:74:64//HOMO SAPIENS (HUMAN).//  
P39188  
F-THYRO1001322//HYPOTHETICAL 7.2 KD PROTEIN.//0.66:49:30//VACCINIA VIRUS (STRAIN COPENHA-  
GEN).//P21123  
F-THYRO1001347//TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAF8).//0.94:61:36//DENDROASPIS AN-  
GUSTICEPS (EASTERN GREEN MAMBA).//P01404  
F-THYRO1001363!!!! ALU SUBFAMILY J WARNING ENTRY !!!!/0.0025:23:73//HOMO SAPIENS (HUMAN).//  
P39188  
F-THYRO1001365//MERSACIDIN PRECURSOR.//0.35:38:42//BACILLUS SP. (STRAIN HIL-Y85/54728).//  
P43683  
F-THYRO1001374//PROTEIN VDLD.//1.6e- 3:140:31//HELICOBACTER PYLORI (CAMPYLOBACTER PY-  
LORI).//O05729  
F-THYRO1001401!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!/0.047:43:48//HOMO SAPIENS (HUMAN).//  
P39192  
F-THYRO1001403  
F-THYRO1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0068:26:42//HOMO SAPIENS  
(HUMAN).//P22531  
F-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.1e-81:97:83//MUS MUSCU-  
LUS (MOUSE).//O70503  
F-THYRO1001411!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!/1.9e-26:89:74//HOMO SAPIENS (HUMAN).//  
P39193  
F-THYRO1001426!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!/1.4e-09:55:61//HOMO SAPIENS (HUMAN).//

P39193  
F-THYRO1001434//BETA-DEFENSIN 4 PRECURSOR (BNDB-4).//0.68:44:34//BOS TAURUS (BOVINE).//  
P46162  
F-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE  
5 B) (NMMHC-B).//3.8e-64:216:62//HOMO SAPIENS (HUMAN).//P35580  
F-THYRO1001480//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.3e-29:88:75//HOMO SAPIENS (HUMAN).//  
P39194  
F-THYRO1001487//HOMEobox PROTEIN HOX-B4 (HOX-2.6).//0.99:59:37//MUS MUSCULUS (MOUSE).//  
P10284  
10 F-THYRO1001534//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.4e-14:40:82//HOMO SAPIENS (HUMAN).//  
P39194  
F-THYRO1001537//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION.//2.4e-07:142:  
32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892  
F-THYRO1001541//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.98:26:61//HOMO SAPIENS (HUMAN).//  
15 P39195  
F-THYRO1001559//PROTEIN Q300.//2.6e-05:20:75//MUS MUSCULUS (MOUSE).//Q02722  
F-THYRO1001570  
F-THYRO1001573//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.033:71:36//MUS MUS-  
CULUS (MOUSE).//P15265  
20 F-THYRO1001584//SUPPRESSOR PROTEIN SRP40.//2.1e-05:188:27//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST).//P32583  
F-THYRO1001595//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.1e-21:35:91//HO-  
MO SAPIENS (HUMAN).//Q15404  
F-THYRO1001602//TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH.//1.0:57:42//HAEMOPHILUS INFLU-  
25 ENZAE.//P44843  
F-THYRO1001605//VENOM BASIC PROTEASE INHIBITORS IX AND VIIIB.//1.0:34:38//BUNGARUS FASCIA-  
TUS (BANDED KRAIT).//P25660  
F-THYRO1001617//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.0e-18:55:81//HOMO SAPIENS (HUMAN).//  
P39194  
30 F-THYRO1001637//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.00020:25:80//HOMO SAPIENS (HU-  
MAN).//P39195  
F-THYRO1001656//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0091:54:42//MUS MUSCULUS  
(MOUSE).//P05142  
F-THYRO1001661//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182).//0.033:  
35 77:35//ESCHERICHIA COLI.//P09160  
F-THYRO1001671//(2'-5')OLIGOADENYLATE SYNTHETASE 1 (EC 2.7.7.-) ((2'-5')OLIGO(A) SYNTHETASE 1)  
(2'-5A SYNTHETASE 1) (P46/P41) (E18/E16).//4.3e-34:207:34//HOMO SAPIENS (HUMAN).//P00973  
F-THYRO1001673//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.9e-08:49:65//HOMO SAPIENS (HUMAN).//  
P39194  
40 F-THYRO1001703//HYPOTHETICAL 69.8 KD PROTEIN IN BDF1-SFP1 INTERGENIC REGION.//6.4e-16:134:  
35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06053  
F-THYRO1001706  
F-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-27:191:36//DROSOPHILA MELA-  
NOGASTER (FRUIT FLY).//Q04652  
45 F-THYRO1001738//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE  
A INTERFERENCE PROTEIN).//0.0032:105:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027  
F-THYRO1001745  
F-THYRO1001746//GENE 10 PROTEIN.//1.0:55:30//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15901  
F-THYRO1001772//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.2e-05:41:63//HOMO SAPIENS (HUMAN).//  
50 P39188  
F-THYRO1001793//HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III.//1.5e-26:161:42//  
CAENORHABDITIS ELEGANS.//P41880  
F-THYRO1001809//LATENCY-RELATED PROTEIN 2.//0.49:74:27//HERPES SIMPLEX VIRUS (TYPE 1 /  
STRAIN F).//P17589  
55 F-THYRO1001828//PROTEINASE INHIBITOR.//0.11:34:50//SOLANUM MELOGENA (EGGPLANT) (AUBER-  
GINE).//P01078  
F-THYRO1001854//ACYL-COA-BINDING PROTEIN HOMOLOG (ACBP) (DIAZEPAM BINDING INHIBITOR HO-  
MOLOG) (DBI).//0.63:50:38//RANA RIDIBUNDA (LAUGHING FROG) (MARSH FROG).//P45883

F-THYRO1001895!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//6.1e-09:72:47//HOMO SAPIENS (HUMAN).//P39188  
 F-THYRO1001907//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT).//0.79:36:  
 44//TRYPANOSOMA CRUZI//Q26327  
 5 F-VESEN1000122//HOMEobox PROTEIN HB9.//0.57:64:32//HOMO SAPIENS (HUMAN).//P50219  
 F-Y79AA1000013//METALLOTHIONEIN B (MT-B).//0.034:35:48//SALMO SALAR (ATLANTIC SALMON).//  
 P52720  
 F-Y79AA1000033//CHOLECYSTOKININ.//0.97:49:30//PSEUDEMYS SCRIPTA (SLIDER TURTLE).//P80345  
 F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//1.4e-23:80:60//HOMO SAPIENS (HUMAN).//P35226  
 10 F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.0075:127:36//STREPTO-  
 MYCES FRADIAE.//P20186  
 F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-  
 MENT).//0.022:135:29//HOMO SAPIENS (HUMAN).//P10162  
 F-Y79AA1000131//REGULATORY PROTEIN E2.//1.1e-05:175:26//HUMAN PAPILLOMAVIRUS TYPE 24.//  
 15 P50770  
 F-Y79AA1000181//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.4e-06:187:29//MUS MUSCULUS  
 (MOUSE).//P05143  
 F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//6.2e-09:47:53//OWENIA FUSI-  
 FORMIS.//P21260  
 20 F-Y79AA1000214//HISTONE H2A VARIANT.//1.7e-50:107:100//GALLUS GALLUS (CHICKEN).//P02272  
 F-Y79AA1000230//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I)  
 (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I).//0.27:64:34//HOMO SAPIENS  
 (HUMAN).//P01148  
 25 F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN M021B04.12.//2.5e-72:277:53//ARABIDOPSIS THAL-  
 IANA (MOUSE-EAR CRESS).//Q04658  
 F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.8e-08:174:35//MUS MUSCULUS  
 (MOUSE).//P05142  
 F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.00020:176:33//RATTUS NORVEGICUS  
 (RAT).//P13941  
 30 F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A3.1 IN CHROMOSOME III.//0.092:127:21//  
 CAENORHABDITIS ELEGANS.//Q09260  
 F-Y79AA1000328//SEL-10 PROTEIN.//5.3e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794  
 F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//1.0:73:30//OVIS AR-  
 IES (SHEEP).//P26372  
 35 F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.8e-95:205:  
 83//BOS TAURUS (BOVINE).//P53620  
 F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.036:37:54//PSEUDOPLEURONECTA AMERI-  
 CANUS (WINTER FLOUNDER).//P02734  
 40 F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME III.//0.0031:106:28//  
 CAENORHABDITIS ELEGANS.//Q10120  
 F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.4e-16:208:28//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//P25343  
 F-Y79AA1000405//LIGHT-HARVESTING PROTEIN B-800-850, ALPHA CHAIN C (ANTENNA PIGMENT PRO-  
 TEIN, ALPHA CHAIN C) (LH II-C ALPHA).//0.98:50:30//RHODOPSEUDOMONAS PALUSTRIS.//P35103  
 45 F-Y79AA1000410!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.9e-20:62:79//HOMO SAPIENS (HUMAN).//  
 P39 194  
 F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UME3-HDA1 INTERGENIC REGION.//1.4e-06:86:38//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53970  
 F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F44B9.5 IN CHROMOSOME III.//2.8e-34:211:40//  
 50 CAENORHABDITIS ELEGANS.//P34426  
 F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//3.9e-15:90:32//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414  
 F-Y79AA1000538!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.37:41:48//HOMO SAPIENS (HUMAN).//  
 P39195  
 55 F-Y79AA1000539//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//  
 1.8e-21:190:37//HOMO SAPIENS (HUMAN).//Q08170  
 F-Y79AA1000540//SPERM PROTAMINE P1.//0.00045:66:45//DASYURUS VIVERRINUS (SOUTHEASTERN  
 QUOLL), AND DASYURUS HALLUCATUS.//P42135

F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.6e-79:186:87//MUS MUSCULUS (MOUSE).//P17427  
 5 F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.---) (FRAGMENT).//0.010:35:60//STREPTOMYCES PEUCETIUS./P32009  
 F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:197:36//SACCHARO-MYCES CEREVIAE (BAKER'S YEAST).//P28320  
 F-Y79AA1000627//ZINC FINGER PROTEIN 134.//1.6e-34:191:35//HOMO SAPIENS (HUMAN).//P52741  
 F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION.//8.7e-36:250:  
 10 40//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P31380  
 F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A).//0.00037:108:  
 27//CANDIDA BOIDINII (YEAST).//Q00316  
 F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III.//1.0e-23:210:34//  
 CAENORHABDITIS ELEGANS./Q09316  
 15 F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//  
 1.4e-53:156:68//MUS MUSCULUS (MOUSE).//Q61990  
 F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC REGION.//1.2e-11:231:  
 26//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P38205  
 F-Y79AA1000782//CUTICLE COLLAGEN 2.//0.012:56:35//CAENORHABDITIS ELEGANS./P17656  
 20 F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.3e-08:82:39//PLASMODIUM LOPHURAE./P04929  
 F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.043:13:53//HO-  
 MO SAPIENS (HUMAN).//P30808  
 F-Y79AA1000800//PRIA PROTEIN PRECURSOR.//0.031:94:34//LENTINULA EDODES (SHIITAKE MUSH-  
 25 ROOM) (LENTINUS EDODES).//Q01200  
 F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION.//0.26:186:23//  
 SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P53882  
 F-Y79AA1000805//AMP DEAMINASE (EC 3.5.4.6) (MYOADENYLATE DEAMINASE).//0.99:78:35//SCHIZOSAC-  
 CHAROMYCES POMBE (FISSION YEAST).//P50998  
 30 F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION.//3.4e-44:111:  
 49//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P48234  
 F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN.//0.0046:187:33//EPSTEIN-BARR VIRUS (STRAIN  
 B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//1.0e-75:239:66//CRICETULUS GRISEUS (CHINESE HAM-  
 35 STER).//P05209  
 F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.0078:57:31//HOMO SAPI-  
 ENS (HUMAN).//P22532  
 F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//8.5e-11:241:26//GALLUS GALLUS  
 (CHICKEN).//P10587  
 40 F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.69:122:31//TRYPANOSOMA BRU-  
 CEI BRUCEI./P24499  
 F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EX-  
 CHANGE FACTOR).//3.3e-102:211:93//RATTUS NORVEGICUS (RAT).//P70541  
 F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:67:38//GALLUS GALLUS (CHICK-  
 45 EN).//P02457  
 F-Y79AA1000976//INVOLUCRIN.//0.99:66:31//CEBUS ALBIFRONS (WHITE-FRONTED CAPUCHIN).//P24709  
 F-Y79AA1000985//PERICENTRIN.//1.1e-24:116:59//MUS MUSCULUS (MOUSE).//P48725  
 F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.37:79:27//  
 50 SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P38250  
 F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE SP1].//0.93:43:39//  
 SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80001  
 F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC  
 1.3.99.-) (VLCAD).//1.5e-51:211:52//BOS TAURUS (BOVINE).//P48818  
 F-Y79AA1001061!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!.//3.8e-25:85:69//HOMO SAPIENS (HUMAN).//  
 55 P39194  
 F-Y79AA1001068//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//  
 0.0015:207:33//MUS MUSCULUS (MOUSE).//P28481  
 F-Y79AA1001077//ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9).//0.99:36:41//ARANEUS DI-

ADEMATUS (SPIDER).//P80515  
 F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.//1.0e-06:197:23//  
 CAENORHABDITIS ELEGANS .//P34492  
 F-Y79AA1001105//HOMEobox PROTEIN OTX2.//2.9e-62:163:79//MUS MUSCULUS (MOUSE).//P80206  
 5 F-Y79AA1001145!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.024:42:59//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP2-VLF1 INTERGENIC REGION.//0.96:20:50//  
 AUTOGRAPHHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMVNPV).//P41471  
 10 F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN.//3.9e-05:135:34//EPSTEIN-BARR VIRUS (STRAIN  
 B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.00017:93:38//CAENORHABDITIS ELE-  
 GANS.//Q09456  
 F-Y79AA1001211  
 F-Y79AA1001216//TENSIN.//0.012:134:32//GALLUS GALLUS (CHICKEN).//Q04205  
 15 F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.088:75:34//HOMO SAPIENS (HUMAN).//  
 Q02817  
 F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-  
 DROXYSTEROID DEHYDROGENASE 1).//1.1e-40:139:51//RATTUS NORVEGICUS (RAT).//P51657  
 20 F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//2.0e-22:108:53//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38238  
 F-Y79AA1001281  
 F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0022:49:44//MUS MUSCULUS  
 (MOUSE).//P05143  
 25 F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR.//0.98:117:25//ARABIDOP-  
 SIS THALIANA (MOUSE-EAR CRESS).//P92959  
 F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUA-  
 MOUS CELL MARKER) (SPRP).//0.082:44:40//SUS SCROFA (PIG).//P35323  
 F-Y79AA1001384//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.99:47:40//MUS MUSCULUS  
 (MOUSE).//P33622  
 30 F-Y79AA1001391//HOMEobox PROTEIN HOX-A13 (HOX-1J).//9.8e-58:157:62//HOMO SAPIENS (HUMAN).//  
 P31271  
 F-Y79AA1001394//TRICHOHYALIN.//4.7e-08:121:36//HOMO SAPIENS (HUMAN).//Q07283  
 F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ERF.//0.0087:81:33//MUS MUSCULUS  
 (MOUSE).//P70459  
 35 F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//4.5e-21:125:44//  
 CAENORHABDITIS ELEGANS.//Q11076  
 F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.3e-17:249:  
 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313  
 40 F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE I49 KD POLYPEPTIDE (EC 2.7.7.6) (A49).//0.0099:  
 155:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q01080  
 F-Y79AA1001541  
 F-Y79AA1001548!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.1e-17:53:83//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-Y79AA1001555//MAJOR SURFACE ANTIGEN.//0.046:62:29//HEPATITIS B VIRUS.//P31873  
 45 F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//8.6e-11:144:31//ESCHERICHIA COLI.//P27550  
 F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.012:64:40//MUS MUS-  
 CULUS (MOUSE).//P15265  
 50 F-Y79AA1001594//CORNIFIN BETA.//0.61:88:31//MUS MUSCULUS (MOUSE).//O09116  
 F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)  
 (TAFII-130) (TAFII130).//0.024:170:30//HOMO SAPIENS (HUMAN).//O00268  
 F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//4.5e-09:136:27//HOMO  
 SAPIENS (HUMAN).//P28698  
 55 F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.093:94:26//MYCOBACTERIUM TUBER-  
 CULOSIS.//P71779  
 F-Y79AA1001665//HOMEobox PROTEIN DLX-2 (HOMEobox PROTEIN TES-1).//0.79:90:26//MUS MUSCU-  
 LUS (MOUSE).//P40764  
 F-Y79AA1001679//LAMBDA-CRYSTALLIN.//1.6e-95:224:81//ORYCTOLAGUS CUNICULUS (RABBIT).//P14755

F-Y79AA1001692//GERM CELL-LESS PROTEIN//3.5e-08:78:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820  
 F-Y79AA1001696//INSULIN//1.0:33:27//ANGUILLA ROSTRATA (AMERICAN EEL).//P42633  
 F-Y79AA1001705//HYPOTHETICAL BHLF1 PROTEIN//0.0013:192:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 5 F-Y79AA1001711//PARATHYMOSEN (ZINC-BINDING 11.5 KD PROTEIN).//0.032:38:34//RATTUS NORVEGICUS (RAT).//P04550  
 F-Y79AA1001781  
 10 F-Y79AA1001805//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0063:128:30//HOMO SAPIENS (HUMAN).//P50552  
 F-Y79AA1001827//SPERM PROTAMINE P1//0.015:45:40//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305  
 F-Y79AA1001846!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//2.4e-09:42:73//HOMO SAPIENS (HUMAN).//  
 P39188  
 15 F-Y79AA1001848//KRUEPPEL PROTEIN (FRAGMENT).//1.8e-10:63:44//PSYCHODA CINEREA.//Q02035  
 F-Y79AA1001866//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//0.00036:108:37//  
 MUS MUSCULUS (MOUSE).//Q61967  
 F-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN-1 RECEPTOR) (CD134 ANTIGEN).//3.2e-07:100:35//HOMO SAPIENS (HUMAN).//  
 20 P43489  
 F-Y79AA1001875//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.020:25:64//HOMO SAPIENS (HUMAN).//P20931  
 F-Y79AA1001923//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.016:83:36//HOMO SAPIENS (HUMAN).//P10162  
 25 F-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//8.1e-13:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42643  
 F-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.8e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743  
 30 F-Y79AA1002083//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.036:53:45//HOMO SAPIENS (HUMAN).//P30808  
 F-Y79AA1002089//HYPOTHETICAL 49.1 KD PROTEIN F02A9.4 IN CHROMOSOME III.//0.12:171:22//  
 CAENORHABDITIS ELEGANS.//P34384  
 35 F-Y79AA1002093//MAX PROTEIN.//3.1e-07:111:29//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//  
 P52161  
 F-Y79AA1002103//SHORT NEUROTOXIN C.//0.040:21:47//AIPYSURUS LAEVIS (OLIVE SEA SNAKE).//  
 P19958  
 F-Y79AA1002115//HYPOTHETICAL PROTEIN MJ0827.//0.84:68:30//METHANOCOCCUS JANNASCHII.//  
 Q58237  
 40 F-Y79AA1002125//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION.//3.4e-29:  
 197:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40206  
 F-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//1.9e-19:120:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24133  
 45 F-Y79AA1002204//TBX6 PROTEIN (T-BOX PROTEIN 6).//0.0011:162:32//MUS MUSCULUS (MOUSE).//P70327  
 F-Y79AA1002208//ANKYRIN.//2.9e-08:231:29//MUS MUSCULUS (MOUSE).//Q02357  
 F-Y79AA1002209//TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.1) (TYROSINE-TRNA LIGASE) (TYRRS).//3.7e-23:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P48527  
 50 F-Y79AA1002210//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK).//0.0061:69:31//HOMO SAPIENS (HUMAN).//P35321  
 F-Y79AA1002211!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//9.2e-10:43:62//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-Y79AA1002220  
 55 F-Y79AA1002229//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//1.9e-21:147:40//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264  
 F-Y79AA1002234  
 F-Y79AA1002246//MYOSIN IC HEAVY CHAIN.//0.00066:131:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III./.4.3e-45:164:48//  
 CAENORHABDITIS ELEGANS./Q02328  
 F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAG-  
 MENT).//0.0063:99:31//HOMO SAPIENS (HUMAN).//P10161  
 5 F-Y79AA1002307  
 F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III./.0.75:198:24//  
 CAENORHABDITIS ELEGANS./P46012  
 F-Y79AA1002351//CUTICLE COLLAGEN 34./.0.74:128:35//CAENORHABDITIS ELEGANS./P34687  
 10 F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2./.0.050:71:29//SACCHAROMYCES CEREVIAE (BAK-  
 ER'S YEAST).//P40036  
 F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1)  
 (CALMODULIN-BINDING PROTEIN P-57).//1.0:89:30//CARASSIUS AURATUS (GOLDFISH).//P17691  
 F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION./.3.7e-16:232:  
 15 28//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P53899  
 F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//6.7e-72:  
 162:84//HOMO SAPIENS (HUMAN).//P17812  
 F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.81:34:41//HOMO SAPIENS  
 20 (HUMAN).//P22531  
 F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68./.0.00024:85:27//SACCHAROMYCES CEREVIAE  
 (BAKER'S YEAST).//P32558  
 F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35).//2.3e-60:217:44//MUS MUSCULUS (MOUSE).//  
 P15620  
 F-Y79AA1002482//ZINC FINGER PROTEIN 141./.2.Oe-31:90:55//HOMO SAPIENS (HUMAN).//Q15928  
 25 F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN  
 CHROMOSOME I./.0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

## Homology Search Result Data 2.

[0300] The result of the homology search of the GenBank using the clone sequence of 5'-end except EST and STS.

30 [0301] Data include

the name of clone,  
 definition of the top hit data,  
 35 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

[0302] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds./.3.4e-106:695:86//L16953  
 F-HEMBA1000012//Caenorhabditis-elegans cosmid C16C10, complete sequence./.1.5e-24:374:66//Z46787  
 40 F-HEMBA1000020//Homo sapiens beta 2 gene./.3.5e-112:529:90//X02344  
 F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GT-  
 Pase-activating protein (GIT1) mRNA, complete cds./.5.6e-124:743:88//AF085693  
 F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3  
 45 unordered pieces./.1.1e-25:529:65//AC004581  
 F-HEMBA1000046//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING  
 DRAFT SEQUENCE./.3.2e-11:330:63//AL033528  
 F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS  
 and chromosome 6 fragment, complete sequence./.0.32:407:59//AL022477  
 50 F-HEMBA1000076//Homo sapiens full-length insert cDNA clone ZB97G06./.6.2e-135:594:98//AF086182  
 F-HEMBA1000111//CIT-HSP-2291M18.TF CIT-HSP Homo sapiens genomic clone 2291M18 genomic survey se-  
 quence./.2.8e-16:132:79//AQ004134  
 F-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence./.8.6e-98:230:93//  
 AC003104  
 F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds./.2.1e-167:791:98//AB018340  
 55 F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds./.2.2e-44:242:96//AB018331  
 F-HEMBA1000156//Rattus norvegicus scaffold attachment factor B mRNA, complete cds./.1.1e-10:409:60//  
 AF056324  
 F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial cds./.1.6e-35:365:73//U80741

F-HEMBA1000168//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE //0.99:290:61//AL031033  
F-HEMBA1000180//rat u2 small nuclear rna gene and flanks //3.7e-18:112:98//K00034  
F-HEMBA1000185  
5 F-HEMBA1000193//Human FMR1 gene, 5' end //0.0012:191:67//L19476  
F-HEMBA1000201//Human In1 mRNA, complete cds //2.0e-73:440:92//U04847  
F-HEMBA1000213//Plasmodium falciparum MAL3P7, complete sequence //0.90:332:59//AL034559  
F-HEMBA1000216//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds //4.8e-117:585:83//AF060194  
10 F-HEMBA1000227//H.sapiens CpG island DNA genomic Mse1 fragment, clone 179h6, reverse read cpg179h6.rt1a//1.9e-14:95:98//Z64921  
F-HEMBA1000231//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.rt1a//5.1e-34:186:97//Z56144  
F-HEMBA1000243//Human DNA sequence from PAC 440O21 on chromosome X contains ESTs and STS //4.1e-15:291:82//Z84481  
F-HEMBA1000244//M.musculus Ank-1 mRNA for erythroid ankyd //0.029:316:59//X69065  
F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence //0.35:467:60//AC004454  
F-HEMBA1000264  
20 F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces //8.9e-20:218:78//AC004825  
F-HEMBA1000282//Homo sapiens chromosome Y, clone 264,M,20, complete sequence //4.2e-08:134:77//AC004617  
F-HEMBA1000288//345L5.TPB CIT978SKA1 Homo sapiens genomic clone A-345L05, genomic survey se-25 quence //1.1e-06:152:73//B17459  
F-HEMBA1000290//Human ornithine decarboxylase gene, complete cds //3.2e-11:507:62//M33764  
F-HEMBA1000302//CIT-HSP-2169N13.TF CIT-HSP Homo sapiens genomic clone 2169N13, genomic survey se-quence //5.4e-06:86:88//B90730  
F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds //7.9e-111:701:86//AF030131  
30 F-HEMBA1000304//HS\_3006\_A1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-nomic clone Plate=3006 Col=17 Row=A, genomic survey sequence //5.2e-40:240:92//AQ118226  
F-HEMBA1000307//Mus musculus mRNA for CDV-1R protein //7.9e-127:815:84//Y10495  
F-HEMBA1000327//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-nomic clone Plate=3124 Col=16 Row=P, genomic survey sequence //1.4e-11:87:96//AQ187492  
35 F-HEMBA1000333  
F-HEMBA1000338//Homo sapiens chromosome X, PAC 671D9, complete sequence //4.0e-66:271:84//AF031078  
F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence //0.64:334:60//AC004848  
F-HEMBA1000355//Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease 40 (AN) gene, complete cds //0.017:313:63//U25056  
F-HEMBA1000356//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds //0.87:198:61//L40178  
F-HEMBA1000357//HS\_3194\_A1\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-nomic clone Plate=3194 Col=9 Row=G, genomic survey sequence //6.5e-90:436:98//AQ173748  
F-HEMBA1000366//HS\_3027\_B2\_G06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-45 nomic clone Plate=3027 Col=12 Row=N, genomic survey sequence //0.0074:192:64//AQ128843  
F-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene simi-lar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence //4.2e-106:133:99//AL031587  
F-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence //1.6e-50:22:659:63//AC006116  
F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPCI11-264F23, WORKING DRAFT SE-  
QUENCE, 90 unordered pieces //3.2e-06:136:75//AC006122  
F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15, complete sequence //3.5e-111:284:95//AC004520  
55 F-HEMBA1000392//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE //1.8e-39:332:80//AL031984  
F-HEMBA1000396//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, com-plete sequence //9.5e-35:364:73//U80460

F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//8.1e-18:424:64//U96409  
 F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region.//0.0026:564:59//U11584  
 F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112  
 F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554  
 F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393  
 F-HEMBA1000442  
 5 F-HEMBA1000456//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//6.3e-06:62:96//B85188  
 F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808  
 F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//2.8e-154:746:98//  
 10 AC004839  
 F-HEMBA1000464//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.8e-25:397:72//AC006213  
 F-HEMBA1000469//CIT-HSP-2167P21.TF CIT-HSP Homo sapiens genomic clone 2167P21, genomic survey sequence.//4.0e-83:406:99//B94160  
 F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2-GGT Region, complete  
 15 sequence.//4.2e-53:312:93//AC004033  
 F-HEMBA1000490//Campylobacter jejuni groES, groEL genes.//0.59:451:62//Y13334  
 F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transforming p21 gene.//8.6e-06:338:58//X00740  
 F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence.//9.4e-41:591:  
 20 69//AC005884  
 F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:57:100//D13666  
 F-HEMBA1000505  
 F-HEMBA1000508//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0135005;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.035:329:61//AC004661  
 F-HEMBA1000518//Caenorhabditis elegans cosmid C17H12.//0.96:425:58//AF045642  
 25 F-HEMBA1000519//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//1.6e-53:300:89//AC004616  
 F-HEMBA1000520//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.7e-10:117:86//AC006006  
 F-HEMBA1000523  
 30 F-HEMBA1000531//Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.//3.9e-35:290:80//U08215  
 F-HEMBA1000534//Homo sapiens chromosome 17, clone hRPK.177\_H\_5, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973  
 F-HEMBA1000540//Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project).//0.057:265:63//  
 AL033545  
 35 F-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//1.2e-110:572:88//D89340  
 F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z49237  
 F-HEMBA1000555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134O19, WORKING  
 40 DRAFT SEQUENCE.//3.2e-175:838:98//AL034555  
 F-HEMBA1000557//CIT-HSP-2369F15.TF CIT-HSP Homo sapiens genomic clone 2369F15, genomic survey sequence.//2.8e-32:315:78//AQ074611  
 F-HEMBA1000561//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//3.4e-69:665:72//U92564  
 45 F-HEMBA1000563//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.59:261:61//AC005504  
 F-HEMBA1000568//HS\_3243\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=24 Row=B, genomic survey sequence.//3.1e-54:323:91//AQ219628  
 F-HEMBA1000569//M.musculus mRNA for GPI-anchored protein.//1.4e-19:440:61//X89571  
 50 F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0016:557:57//AC005506  
 F-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//1.7e-11:132:79//  
 AF045573  
 F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.3e-43:228:97//AJ007509

- F-HEMBA1000592//*Mus musculus* clone OST7314, genomic survey sequence.//7.3e-07:68:94//AF046733  
 F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//8.7e-71:553:79//Z83822  
 5 F-HEMBA1000604//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 237J2, WORKING DRAFT SEQUENCE.//2.9e-21:158:75//AL021394  
 F-HEMBA1000608//*Homo sapiens* mRNA for KIAA0456 protein, partial cds.//1.1e-118:561:99//AB007925  
 F-HEMBA1000622//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//2.2e-28:426:70//AC004382  
 F-HEMBA1000636//Human CpG island sequence, clone Q28B8.//1.0e-15:274:68//D85773  
 10 F-HEMBA1000637//*Homo sapiens* mRNA for KIAA0690 protein, partial cds.//6.7e-137:639:99//AB014590  
 F-HEMBA1000655//, complete sequence.//5.1e-83:685:80//AC005815  
 F-HEMBA1000657//*Rattus norvegicus* ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.1e-91:597:84//U35776  
 15 F-HEMBA1000662//*Homo sapiens* clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.019:695:57//AC004907  
 F-HEMBA1000673//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//1.5e-48:325:85//Z86090  
 F-HEMBA1000682//*Homo sapiens* (subclone 5\_g5 from P1 H25) DNA sequence.//7.7e-61:615:74//L43411  
 20 F-HEMBA1000686  
 F-HEMBA1000702  
 F-HEMBA1000705//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0037:569:57//AC005507  
 F-HEMBA1000719//*Streptomyces coelicolor* cosmid 1C2.//2.0e-09:483:62//AL031124  
 25 F-HEMBA1000722//*Toxoplasma gondii* chloroplast, complete genome.//0.00058:762:57//U87145  
 F-HEMBA1000726//*H.sapiens* HLA-DRB1\*15 gene.//9.8e-49:189:89//X88791  
 F-HEMBA1000727//CIT-HSP-387P22.TRB CIT-HSP *Homo sapiens* genomic clone 387P22, genomic survey sequence.//0.0054:206:67//B60158  
 F-HEMBA1000747  
 30 F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.3e-05:124:75//AL024509  
 F-HEMBA1000752//Human Chromosome X, complete sequence.//5.9e-48:502:75//AC004073  
 F-HEMBA1000769//*Homo sapiens* clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.011:179:67//AC005043  
 35 F-HEMBA1000773//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y59A8, WORKING DRAFT SEQUENCE.//0.070:231:63//Z98870  
 F-HEMBA1000774//*Homo sapiens* PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//6.2e-40:385:75//AC004953  
 F-HEMBA1000791  
 40 F-HEMBA1000817//*Myrmecia pilosula* HI87-135 mitochondrion cytochrome b gene, partial cds.//0.99:244:58//U15678  
 F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//0.033:294:62//Z81370  
 45 F-HEMBA1000827//*Borrelia burgdorferi* (section 50 of 70) of the complete genome.//9.7e-05:463:58//AE001164  
 F-HEMBA1000843//*Homo sapiens* DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//3.0e-153:732:98//AL022394  
 50 F-HEMBA1000851//*Rattus norvegicus* glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//1.6e-31:386:72//AF059273  
 F-HEMBA1000852//*Homo sapiens* Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.5e-115:455:98//AC005295  
 F-HEMBA1000867  
 55 F-HEMBA1000869//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//6.6e-41:424:75//Z72519  
 F-HEMBA1000870//*Gnampetodon pumilio* cytochrome oxidase II gene, partial cds; and tRNA-Asp, tRNA-His, and tRNA-Lys genes, complete sequence, mitochondrial genes for mitochondrial products.//0.0049:211:66//AF034598

F-HEMBA1000872//CIT-HSP-2355D20.TF CIT-HSP Homo sapiens genomic clone 2355D20, genomic survey sequence./.3.7e-33:180:98//AQ059583  
 F-HEMBA1000876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE./.5.6e-37:262:72//Z83826  
 5 F-HEMBA1000908//Triticum aestivum low-affinity cation transporter (LCT1) mRNA, complete cds./.1.0:304:59//AF015523  
 F-HEMBA1000910//M.musculus necdin mRNA, complete cds./.6.1e-08:256:61//M80840  
 F-HEMBA1000918//Tetrahymena thermophila micronuclear developmentally eliminated sequence region./.0.13:232:63//U88158  
 10 F-HEMBA1000919//Gallus domesticus filamin mRNA, complete cds./.1.0:213:65//U00147  
 F-HEMBA1000934//CIT-HSP-2053H24.TR CIT-HSP Homo sapiens genomic clone 2053H24, genomic survey sequence./.5.5e-11:275:64//B69224  
 F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORKING DRAFT SEQUENCE, 15 unordered pieces./.9.7e-05:78:83//AC004878  
 15 F-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence./.5.8e-140:661:99//AC005324  
 F-HEMBA1000946  
 F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORKING DRAFT SEQUENCE, 12 unordered pieces./.8.3e-16:181:75//AC004967  
 20 F-HEMBA1000968//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 69M21, WORKING DRAFT SEQUENCE./.4.4e-117:398:86//AL031735  
 F-HEMBA1000971//H.sapiens CpG island DNA genomic Mse1 fragment, clone 182f4, forward read cpg182f4 ft1a./.1.5e-20:126:96//Z57528  
 25 F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11./.0.34:642:59//AB020858  
 F-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence./.5.1e-183:865:98//AC004817  
 F-HEMBA1000975//Orf virus homologue of retroviral pseudoprotease gene, complete cds./.0.00065:391:62//M30023  
 30 F-HEMBA10009851//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains à pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence./.3.4e-05:243:65//Z93929  
 F-HEMBA1000986//Homo sapiens DNA from chromosome 19-cosmid R31491, genomic sequence./.6.6e-06:508:61//AD000813  
 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds./.1.2e-22:193:84//D84064 F-HEMBA1001007  
 35 F-HEMBA1001008//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence./.7.8e-46:532:73//AL031577  
 F-HEMBA1001009//Human mRNA for IgM heavy chain complete sequence./.0.97:369:59//X17115  
 F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds./.4.4e-139:661:98//AB007937  
 F-HEMBA1001019//Homo sapiens, clone hRPK.15\_A\_1, complete sequence./.1.6e-16:521:64//AC006213  
 40 F-HEMBA1001020//Homo sapiens chromosome 17, clone hRPK.178\_C\_3, complete sequence./.3.8e-50:367:72//AC005702  
 F-HEMBA1001022  
 F-HEMBA1001024//Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence./.5.0e-23:378:69//AE000658  
 45 F-HEMBA1001026//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS./.7.6e-19:867:60//Z86064  
 F-HEMBA1001043//HS\_2219\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=19 Row=B, genomic survey sequence./.3.0e-15:124:88//AQ301521  
 F-HEMBA1001051//Human Chromosome X clone bWxD342, complete sequence./.4.8e-79:308:84//AC004072  
 50 F-HEMBA1001052//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces./.0.53:384:61//AC005341  
 F-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 10./.2.8e-26:397:71//U06084  
 F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855\_D\_21 complete sequence./.0.98:280:62//AC006079  
 55 F-HEMBA1001071//Human mRNA for pro alpha 1 (III) collagen C-terminal propeptide./.1.1e-31:181:96//X01742  
 F-HEMBA1001077//nuclear protein TIF1 [mice, mRNA, 3951 nt]./.3.6e-13:338:65//S78219  
 F-HEMBA1001080//Streptomyces coelicolor cosmid 1A9./.0.00012:364:63//AL034446

F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alphamannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces./.8.5e-134:476:96//AC004586  
 F-HEMBA1001088//Sequence 1 from patent US 5552529./.2.2e-71:303:78//I25863  
 F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence./.8.9e-119:609:96//AC005105  
 5 F-HEMBA1001099  
 F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete sequence./.2.4e-58:347:  
 87//AC005250  
 F-HEMBA1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90G24, WORKING  
 10 DRAFT SEQUENCE./.3.4e-21:226:65//AL008723  
 F-HEMBA1001122//Plasmodium falciparum chromosome 2, section 20 of 73 of the complete sequence./.9.2e-07:  
 732:57//AE001383  
 F-HEMBA1001123//Homo sapiens full-length insert cDNA clone ZD38E12./.1.1e-11:231:68//AF086247  
 11 F-HEMBA1001133//Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces./.  
 0.011:163:69//AC004909  
 15 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds./.6.9e-72:527:77//AB018341  
 F-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces./.2.3e-  
 120:578:98//AC005077  
 F-HEMBA1001172//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 20 DRAFT SEQUENCE, 9 unordered pieces./.0.010:520:59//AC005507  
 F-HEMBA1001174//R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5./.1.0e-59:565:73//X78604  
 F-HEMBA1001197//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces./.0.0037:  
 151:70//AC004815  
 F-HEMBA1001208//Human BAC clone RG264L19 from 7p15-p21, complete sequence./.7.4e-35:195:81//  
 AC002410  
 25 F-HEMBA1001213//Homo sapiens clone DJ0892G19, complete sequence./.1.9e-171:826:98//AC004917  
 F-HEMBA1001226//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces./.  
 0.00010:557:57//AC006009  
 F-HEMBA1001235//Homo sapiens chromosome 17, clone hRPK.601\_N\_13, complete sequence./.0.0086:372:  
 58//AC005389  
 30 F-HEMBA1001247//H.sapiens CpG island DNA genomic Mse1 fragment, clone 11b11, reverse read  
 cpg11b11.rt1a./.2.0e-24:154:93//Z64441  
 F-HEMBA1001257//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds./.1.9e-88:659:81//  
 AF047020  
 F-HEMBA1001265//Human 18S ribosomal RNA./.1.0e-32:180:97//X03205  
 35 F-HEMBA1001281  
 F-HEMBA1001286//B.taurus mRNA for RF-36-DNA-binding protein./.7.7e-26:236:81//X15543  
 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence./.5.5e-  
 28:530:64//AC004131  
 F-HEMBA1001294//Yeast mitochondrial aapl gene for ATPase subunit 8./.2.8e-15:722:60//X00960  
 40 F-HEMBA1001299//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS,  
 CpG island, complete sequence./.4.2e-24:288:76//AL031003  
 F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell./.  
 7.2e-121:439:96//E12260  
 F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
 45 DRAFT SEQUENCE, 8 unordered pieces./.0.011:637:56//AC005505  
 F-HEMBA1001310//HS\_3252\_B2\_B12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3252 Col=24 Row=D, genomic survey sequence./.1.2e-16:166:82//AQ217054  
 F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 2034J6, genomic survey se-  
 quence./.0.33:256:59//B79408  
 50 F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds./.7.8e-30:165:99//L20861  
 F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Mus-  
 cular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a mem-  
 brane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five pre-  
 dicted tRNA genes. Contains ESTs, GSSs(BAC end sequences) and a CA repeat polymorphism, complete se-  
 quence./.5.4e-19:347:68//AL021368  
 55 F-HEMBA1001327//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey se-  
 quence./.0.012:152:65//AQ075713  
 F-HEMBA1001330//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-103, com-

plete sequence./0.0037:254:62//AL010208  
F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds./1.1e-103:  
5 516:97//AF057358  
F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence./1.7e-150:706:99//  
AC006241  
F-HEMBA1001375//Streptomyces coelicolor cosmid 1E6./1.0:375:59//AL033505  
F-HEMBA1001377//HS\_3020\_B1\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3020 Col=23 Row=H, genomic survey sequence./0.00022:63:77//AQ105297  
F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 of the complete sequence./0.00035:  
10 317:60//AE001431  
F-HEMBA1001387//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3039 Col=1 Row=H, genomic survey sequence./5.0e-90:437:98//AQ155035  
F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces./  
4.2e-47:159:89//AC005073  
15 F-HEMBA1001391//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS,  
STS, complete sequence./2.0e-06:495:60//AL031256  
F-HEMBA1001398//H.sapiens CpG island DNA genomic Mse1 fragment, clone 70d11, forward read  
cpg70d11.ft1b./0.018:46:97//Z62591  
F-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING  
20 DRAFT SEQUENCE./2.3e-74:623:71//AL034380  
F-HEMBA1001407//Mus musculus domesticus (Sry) gene, complete cds./0.36:363:57//U03645  
F-HEMBA1001411//Homo sapiens genomic DNA, 21q region, clone: S39BG29, genomic survey sequence./8.4e-  
12:516:60//AG001050  
F-HEMBA1001413  
25 F-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING  
DRAFT SEQUENCE./0.98:177:64//AL031732  
F-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces./  
8.0e-177:859:97//AC006146  
F-HEMBA1001433//Homo sapiens clone DJ0892G19, complete sequence./2.0e-35:376:64//AC004917  
30 F-HEMBA1001435//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence./1.2e-74:284:84//  
AC005670  
F-HEMBA1001442//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-66, com-  
plete sequence./0.056:194:63//AL010138  
F-HEMBA1001446//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence./0.96:328:61//  
35 AC004047  
F-HEMBA1001450  
F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.1-11.23 Contains zinc finger  
X-linked proteins ZXDA, ZXDB, ESTs and STS, complete sequence./2.0e-47:468:73//AL031115  
F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK Homo sapiens genomic clone 32J2, genomic survey se-  
40 quence./1.5e-05:223:65//B78859  
F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone  
cSRL-69d1, genomic survey sequence./5.1e-66:564:77//B05652  
F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds./1.9e-102:489:99//AB011144  
F-HEMBA1001478//HS\_2228\_A2\_B03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
45 nomic clone Plate=2228 Col=6 Row=C, genomic survey sequence./4.5e-40:275:88//AQ032041  
F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four  
novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene  
SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic  
marker D6S1553, complete sequence./7.7e-47:311:85//AL031133  
50 F-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein  
(CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence./2.0e-130:699:93//U89337  
F-HEMBA1001515//Homo sapiens chromosome 19, cosmid F24866, complete sequence./4.1e-114:711:85//  
AC005794  
F-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence./5.7e-162:769:98//  
55 AC004549  
F-HEMBA1001522//Caenorhabditis elegans cosmid ZK328./8.6e-17:498:61//U50193  
F-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of  
chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands./0.31:120:69//Z98258

F-HEMBA1001533  
F-HEMBA1001557//*Chionoecetes opilio* (clone COP41) DNA microsatellite repeat regions.//7.0e-25:303:72//L49136  
5 F-HEMBA1001566//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethyl-aniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//7.2e-18:805:60//AL021026  
10 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2).//1.1e-64:338:95//AJ225044  
F-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.1e-148:698:99//AC004453  
F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:99//AJ012449  
15 F-HEMBA1001581//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.30:484:59//AC004980  
F-HEMBA1001585  
F-HEMBA1001589//Human BAC clone RG317G18 from 7q31, complete sequence.//0.98:197:63//AC002432  
F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918  
20 F-HEMBA1001608//RPCI11-72E2.TJ RPCI11 Homo sapiens genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131  
F-HEMBA1001620//*Oryza sativa* RINO1 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107  
F-HEMBA1001635//HS\_3208\_A1\_D07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944  
25 25 F-HEMBA1001636//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//AC004216  
F-HEMBA1001640//HS\_3253\_B2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058  
F-HEMBA1001647//*H.sapiens* gene for plectin.//0.00052:629:61//Z54367  
30 30 F-HEMBA1001651//*Salmo salar* DNA for a cryptic repeat.//7.9e-08:270:64//AJ012206  
F-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//5.9e-164:802:97//AC005368  
F-HEMBA1001658//*M.musculus* COL3A1 gene for collagen alpha-I.//2.4e-30:742:62//X52046  
35 35 F-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.2e-144:682:99//AC005740  
F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//6.1e-152:725:98//AF072247  
F-HEMBA1001675//RPCI11-54F8.TV RPCI11 Homo sapiens genomic clone R-54F8, genomic survey sequence.//5.3e-75:341:85//AQ082126  
40 40 F-HEMBA1001678//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//8.4e-54:551:74//AC002349  
F-HEMBA1001681  
F-HEMBA1001702//*Plasmodium falciparum* chromosome 2, section 35 of 73 of the complete sequence.//0.94:676:54//AE001398  
45 45 F-HEMBA1001709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//0.74:659:58//AL033531  
F-HEMBA1001711//*Lysiphlebus melandriicola* NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//3.0e-07:413:60//AF069178  
50 50 F-HEMBA1001712//Homo sapiens BAC clone RG041H04 from 7q21-q22, complete sequence.//0.091:315:61//AC004519  
F-HEMBA1001714//*Rattus norvegicus* mitochondrial ATPase inhibitor gene, complete cds.//1.6e-28:218:75//U12250  
F-HEMBA1001718//HS\_3056\_A2\_H08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=16 Row=O, genomic survey sequence.//2.0e-79:383:99//AQ106367  
55 55 F-HEMBA1001723//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//3.8e-28:174:94//AQ116793  
F-HEMBA1001731//HS\_3021\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=21 Row=A, genomic survey sequence.//2.5e-11:420:62//AQ154658

F-HEMBA1001734//Homo sapiens chromosome Y, clone 264,M,20, complete sequence./.0.00060:392:60//AC004617

F-HEMBA1001744//HS\_3194\_A1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence./.5.8e-29:163:97//AQ252295

5 F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence./.0.66:627:59//AC002102

F-HEMBA1001746//HS\_2163\_B1\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence./.1.4e-16:238:70//AQ085995

10 F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence./.3.5e-52:198:86//AC002109

F-HEMBA1001781

F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered-pieces./.5.5e-13:296:65//AC002099

F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence./.0.18:534:59//AF038458

15 F-HEMBA1001800//CrT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence./.2.2e-40:335:80//AQ009222

F-HEMBA1001803//M.musculus (Ba1b/C) P/L01 mRNA./.1.7e-25:286:74//Z31360

F-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end./.1.9e-58:358:89//M21977

20 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500./.7.8e-174:809:98//AB007969

F-HEMBA1001809//Bovine herpesvirus 1 complete genome./.9.0e-09:639:57//AJ004801

F-HEMBA1001815

F-HEMBA1001819//HS\_3079\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence./.1.4e-79:396:97//AQ186616

25 F-HEMBA1001820//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence./.0.00026:436:60//AC005013

F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds./.1.2e-40:510:65//AF064243

F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat./.6.1e-20:344:68//AF020275

30 F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence./.0.0094:553:58//AC005161

F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces./.1.2e-22:316:70//AC005867

F-HEMBA1001847//M.musculus Zfp-29 gene for zinc finger protein./.5.3e-27:397:69//X55126

F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds./.8.8e-184:865:98//AB014517

35 F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence./.0.38:337:62//AC005395

F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3./.1.4e-10:224:63//U28735

F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence./.6.7e-98:288:91//AC005065

40 F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence./.4.9e-114:476:84//AC003693

F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds./.2.2e-137:839:86//AF026954

F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence./.0.90:221:63//AC003065

45 F-HEMBA1001912//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence./.9.7e-76:364:100//AQ033732

F-HEMBA1001913//Leishmania major chromosome 3 clone L4625 strain Friedlin, WORKING DRAFT SEQUENCE, 6 unordered pieces./.0.00063:219:65//AC005766

50 F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer , segment 5/10./.0.00011:366:63//AB020873

F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds./.0.00024:562:58//D82031

55 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds./.2.1e-184:855:99//AF000145

F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Ami-notransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)

pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310  
 F-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-175:861:97//AC005629  
 F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//0.097:107:71//AC006057  
 F-HEMBA1001945//Drosophila F family transposable element F12 3' region.//0.94:140:65//X01934  
 F-HEMBA1001950//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, forward read cpg15b5.ft1q.//1.4e-27:168:95//Z54728  
 F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha1 subunit.//0.010:108:71//AJ000390  
 F-HEMBA1001962//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507  
 F-HEMBA1001964  
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178  
 F-HEMBA1001979//HS\_3067\_B1\_A06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506  
 F-HEMBA1001987//Plasmodium falciparum MAL3P6, complete sequence.//1.0:428:56//Z98551  
 F-HEMBA1001991//HS\_2237\_A2\_G09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283  
 F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950 nt].//2.7e-33:364:74//S90449  
 F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214:68//AC005948  
 F-HEMBA1002018  
 F-HEMBA10020227//Human p37NB mRNA, complete cds.//0.014:58:96//U32907  
 F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:200:69//M17284  
 F-HEMBA1002039//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//0.31:497:58//AL031053  
 F-HEMBA1002049//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//4.5e-42:532:63//AC005216  
 F-HEMBA1002084//Homo sapiens chromosome 19 cosmid F15386, genomic sequence, complete sequence.//0.81:435:59//AF025422  
 F-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//7.2e-130:769:87//U92703  
 F-HEMBA1002100//Homo sapiens PAC clone DJ0991G20, complete sequence.//1.3e-47:124:96//AC004943  
 F-HEMBA1002102//Xenopus laevis mRNA for xSox7 protein, complete cds.//2.7e-13:132:71//D83649  
 F-HEMBA1002113//F.rubripes GSS sequence, clone 063K10bB4, genomic survey sequence.//0.029:142:66//Z88840  
 F-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.3e-14:515:62//AC000378  
 F-HEMBA1002125//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds.//0.98:222:61//AF031815  
 F-HEMBA1002139//Caenorhabditis elegans cosmid F55C9, complete sequence.//0.0081:371:60//Z81549  
 F-HEMBA1002144//Saccharomyces cerevisiae mitochondrion transfer RNA-Met (tRNA-Met) gene, oxil gene, and ORF1.//4.9e-06:341:61//L36888  
 F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds.//0.00017:353:62//AB018263  
 F-HEMBA1002151  
 F-HEMBA1002153//CITBI-E1-2519120.TR CITBI-E1 Homo sapiens genomic clone 2519I20, genomic survey sequence.//8.5e-61:334:94//AQ277613  
 F-HEMBA1002160//Homo sapiens clone DJ1189D06, complete sequence.//8.5e-44:385:77//AC005232  
 F-HEMBA1002161//Coturnix coturnix slow myosin heavy chain 2 (qmyhc2) mRNA, partial cds.//2.1e-59:571:74//AF006829  
 F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//5.3e-53:698:67//AC006210  
 F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glycan-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712  
 F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from 7q21-7q22, complete sequence.//2.5e-18:150:88//AC000066  
 F-HEMBA1002185//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00066:466:59//AC004825

F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-23:176:77//AC005015  
 F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds.//1.0:382:59//AB014589  
 F-HEMBA1002199//Homo sapiens chromosome 4 clone B55B24 map 4q25, complete sequence.//1.8e-20:368:  
 5 66//AC005150  
 F-HEMBA1002204//HS\_2055\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2055 Col=17 Row=O, genomic survey sequence.//1.2e-06:178:65//AQ235350  
 F-HEMBA1002212//S.cerevisiae chromosome IV reading frame ORF YDL101c.//0.035:345:60//Z74149  
 F-HEMBA1002215//M.musculus mRNA for testin.//4.6e-80:504:87//X78989  
 10 F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human  
 PAC Library) complete sequence.//5.7e-63:336:74//AC003035  
 F-HEMBA1002229//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//2.6e-39:311:  
 81//AC006044  
 F-HEMBA1002237//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//1.6e-12:397:64//  
 15 AC004861  
 F-HEMBA1002241  
 F-HEMBA1002253  
 F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds.//3.5e-151:731:97//  
 AF061936  
 20 F-HEMBA1002265//Human DNA sequence from cosmid N28H9 on chromosome 22q11.2-qter contains ESTs,  
 STS and endogenous retrovirus.//1.3e-09:313:62//Z771183  
 F-HEMBA1002267  
 F-HEMBA1002270//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-  
 plete sequence.//0.069:495:58//AC006210  
 25 F-HEMBA1002321//Homo sapiens PAC clone DJ0991O23, complete sequence.//0.019:564:58//AC004944  
 F-HEMBA1002328//CIT-HSP-2387N15.TF.1 CIT-HSP Homo sapiens genomic clone 2387N15, genomic survey  
 sequence.//1.8e-71:346:99//AQ240836  
 F-HEMBA1002337//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//  
 0.84:547:57//AB020754  
 30 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-185:872:98//AB018314  
 F-HEMBA1002348//CIT-HSP-2372K24.TR CIT-HSP Homo sapiens genomic clone 2372K24, genomic survey se-  
 quence.//9.1e-33:230:75//AQ110676  
 F-HEMBA1002349//Plasmodium falciparum histidine-rich protein II (HRP II) gene, complete cds.//9.4e-06:504:  
 57//U69551  
 35 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//7.3e-188:  
 872:99//AF092563  
 F-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
 non-small cell lung cancer , segment 11/11.//2.1e-20:262:72//AB020868  
 F-HEMBA1002389//D.discoideum spore coat 60 (sp60) gene, 5' flank.//0.010:95:73//M34546  
 40 F-HEMBA1002417//Canis familiaris ZO-3 (zo-3) mRNA, complete cds.//6.2e-120:767:85//AF023617  
 F-HEMBA1002419//HS-1047-A1-F01-MFab1 CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 Plate=CT 830 Col=1 Row=K, genomic survey sequence.//7.6e-06:111:76//B38165  
 F-HEMBA1002430//HS\_3137\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3137 Col=20 Row=L, genomic survey sequence.//1.6e-56:367:88//AQ148697  
 45 F-HEMBA1002439//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.67:129:64//M25216  
 F-HEMBA1002458//Mus musculus REX-3 mRNA, complete cds.//1.1e-30:274:72//AF051347  
 F-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-173:822:98//AC005378  
 F-HEMBA1002462//Sequence 41 from patent US 5708157.//9.8e-51:519:73//I80067  
 F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds.//4.0e-108:603:92//D50912  
 50 F-HEMBA1002475//Streptomyces coelicolor cosmid 2H4.//0.0068:626:57//AL031514  
 F-HEMBA1002477//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//1.5e-40:349:78//  
 AC005034  
 F-HEMBA1002486  
 F-HEMBA1002495//HS\_3218\_B1\_A12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3218 Col=23 Row=B, genomic survey sequence.//1.0:179:67//AQ181410  
 55 F-HEMBA1002498//Homo sapiens full-length insert cDNA clone ZD76B01.//1.4e-129:619:98//AF086404  
 F-HEMBA1002503//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 1.9e-24:306:68//AC004873

F-HEMBA1002508//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.9e-76:464:83//AC004799  
 F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//2.8e-157:738:98//AJ011972  
 5 F-HEMBA1002515//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//2.6e-07:307:64//AL022329  
 F-HEMBA1002538//HS\_2185\_B2\_B04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2185 Col=8 Row=D, genomic survey sequence.//4.7e-37:339:78//AQ298315  
 10 F-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//3.2e-70:372:95//AQ188792  
 F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//3.5e-137:655:98//AF016903  
 F-HEMBA1002552//Human Hep27 protein mRNA, complete cds.//8.8e-07:173:68//U31875  
 F-HEMBA1002555//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.2e-15:628:60//AC004670  
 15 F-HEMBA1002558//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-41:353:76//AC002366  
 F-HEMBA1002561//Homo sapiens chromosome 17, clone HRPC29G21, complete sequence.//1.1e-39:538:66//AC003687  
 20 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//1.3e-140:457:99//AF075587  
 F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//5.1e-79:385:99//AQ038102  
 F-HEMBA1002590//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.9e-35:430:  
 25 70//AC005940  
 F-HEMBA1002592//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//4Ae-19:303:71//Z93403  
 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//4.4e-175:820:99//AB011169  
 F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 from 7q21, complete sequence.//0.14:353:58//  
 30 AC004413  
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//2.9e-187:632:97//AB018351  
 F-HEMBA1002628//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-05:792:58//AC004153  
 F-HEMBA1002629//Streptomyces coelicolor cosmid 1A9.//8.4e-08:576:58//AL034446  
 35 F-HEMBA1002645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//5.6e-47:222:86//AL031118  
 F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//3.8e-182:859:99//AC004839  
 F-HEMBA1002659//Z.mobilis alcohol dehydrogenase I (adhA) gene, complete cds.//0.97:144:66//M32100  
 40 F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 from 7p21-p22, complete sequence.//1.3e-116:774:84//AC004535  
 F-HEMBA1002666  
 F-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//5.7e-156:750:98//AL034421  
 45 F-HEMBA1002679//nxb0002cc12r CUGI Rice BAC Library Oryza sativa genomic clone nxb0002F23r, genomic survey sequence.//4.3e-09:517:58//AQ051621  
 F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complete genome.//8.3e-20:651:61//Z86099  
 F-HEMBA1002696//Mus musculus proteasome regulator PA28 beta subunit gene, complete cds.//7.6e-62:306:  
 50 81//AF060195  
 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds.//1.9e-10:327:62//AB007924  
 F-HEMBA1002712  
 F-HEMBA1002716//HS\_3064\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, genomic survey sequence.//8.4e-97:491:96//AQ142980  
 55 F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//6.1e-21:217:77//AC004782  
 F-HEMBA1002730//Human platelet glycoprotein IIIa (GPIIIa) gene, exon 1.//0.57:125:67//M57481  
 F-HEMBA1002742//RPCI11-39J10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-39J10, genomic survey sequence.//1.1e-86:414:99//AQ029102

F-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence././/7.1e-70:303:82//AC003694  
F-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 41018, WORKING DRAFT SEQUENCE././/0.096:212:62//AL031732  
5 F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89), complete sequence././/6.7e-40:232:70//AC004622  
F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds././/9.0e-177:834:98//AB011126  
F-HEMBA1002770//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein)././/1.3e-140:840:88//E12829  
10 F-HEMBA1002777//F.rubripes GSS sequence, clone 189C06dB12, genomic survey sequence././/1.1e-28:263:77//AL007965  
F-HEMBA1002779//CIT-HSP-2333I1.TF CIT-HSP Homo sapiens genomic clone 2333I1, genomic survey sequence././/1.8e-32:180:98//AQ036891  
F-HEMBA1002780//Homo sapiens PAC clone DJ0244J05 from 5q31, complete sequence././/7.0e-06:199:67//AC004592  
15 F-HEMBA1002794//H.sapiens mRNA for protein kinase C mu././/0.00015:244:67//X75756  
F-HEMBA1002801//Plasmodium falciparum MAL3P2, complete sequence././/0.0010:534:57//AL034558  
F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds././/1.1e-167:820:97//AF071185  
F-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces././/  
20 3.1e-113:254:90//AC005043  
F-HEMBA1002818//Cricetulus griseus H411 precursor (H411) mRNA, complete cds././/1.2e-122:760:86//AF046870  
F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence././/0.0055:235:65//AL022153  
F-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence././/1.4e-170:744:  
25 99//AC004707  
F-HEMBA1002850//Ephedrus persicae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds././/1.3e-05:334:59//AF069186  
F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP Homo sapiens genomic clone 2323A16, genomic survey sequence././/2.9e-140:750:93//AQ028419  
30 F-HEMBA1002876//HS\_2270\_B1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=5 Row=P, genomic survey sequence././/0.44:163:64//AQ164031  
F-HEMBA1002886  
F-HEMBA1002896//Homo sapiens chromosome 5, P1 clone 793C5 (LBNL H58), complete sequence././/0.00015:  
35 277:61//AC005195  
F-HEMBA1002921  
F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP Homo sapiens genomic clone 2171H4, genomic survey sequence././/0.0016:175:66//B89715  
F-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE././/1.2e-169:797:98//AL031681  
40 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds././/4.9e-173:803:99//AB011148  
F-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE././/1.2e-163:411:99//AL033531  
F-HEMBA1002939//RPCI11-74O14.TJ RPCI11 Homo sapiens genomic clone R-74O14, genomic survey sequence././/1.7e-41:215:99//AQ266676  
45 F-HEMBA1002944//RPCI11-55C2.TV RPCI11 Homo sapiens genomic clone R-55C2, genomic survey sequence././/1.7e-37:375:74//AQ082240  
F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complete sequence././/0.00074:683:58//AC005578  
F-HEMBA1002954//RPCI11-79F7.TV RPCI11 Homo sapiens genomic clone R-79F7, genomic survey sequence././/  
50 6.1e-24:250:78//AQ284146  
F-HEMBA1002968//HS\_2262\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, genomic survey sequence././/0.99:270:60//AQ217059  
F-HEMBA1002970//RPCI11-5L24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5L24, genomic survey sequence././/1.4e-10:189:71//B49289  
55 F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic clone 2363L16, genomic survey sequence././/4.3e-21:181:80//AQ080538  
F-HEMBA1002973//Rattus norvegicus Wistar 3',5'-cyclic AMP phosphodiesterase (PDE4-10) gene, exon 10././/  
2.5e-40:257:89//U01290

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F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic clone 2387H15, genomic survey sequence.//9.5e-17:128:92//AQ240797  
F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.1e-62:713:73//U20286  
5 F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.5e-50:331:85//AC005484  
F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A10-62B5, P1 clones DS02777, DS03222, DS02345, and DS04808, complete sequence.//2.6e-20:357:66//AC005557  
10 F-HEMBA1003034//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//4.5e-60:415:73//Z95704  
F-HEMBA1003035//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//2.3e-05:591:57//AC004617  
F-HEMBA1003037//RPCI11-88F2.TJ RPCI11 Homo sapiens genomic clone R-88F2, genomic survey sequence.//0.68:230:60//AQ286677  
15 F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//8.1e-128:550:94//AC004983  
F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//1.0e-164:777:98//AF054182  
20 F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744:59//AC005505  
F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140:63//M32783  
F-HEMBA1003071//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//1.5e-20:595:65//U72648  
F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.//4.4e-33:176:99//AQ080257  
25 F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//9.4e-43:478:70//Z99297  
F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.96:57:85//AC004673  
30 F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//8.0e-74:359:81//AC004548  
F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//3.6e-11:734:58//AF001550  
35 F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594:71//I13750  
F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome region 11p13. Contains EST and STS.//1.9e-09:230:69//Z83308  
F-HEMBA1003117//Mouse TIS11 primary response gene, complete cds.//0.00054:480:60//M58564  
40 F-HEMBA1003129//HS\_3139\_B2\_F05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey sequence.//2.3e-100:510:97//AQ187635  
F-HEMBA1003133//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//1.3e-78:370:90//AC005259  
F-HEMBA1003136  
F-HEMBA1003142//Homo sapiens full-length insert cDNA clone ZC39B06.//6.9e-121:563:100//AF086197  
45 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850:99//AJ005670  
F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//3.8e-27:229:76//AC002302  
F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837:58//AB000882  
50 F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one with homology to a worm protein. Contains ESTs, complete sequence.//5.4e-115:174:98//AL022325  
F-HEMBA1003197//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//1.1e-05:473:59//AC005824  
55 F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene, exon 1.//1.6e-05:367:61//U09302  
F-HEMBA1003202//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//9.0e-23:247:73//AC004003

F-HEMBA1003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE./.4.7e-26:141:83//Z83824  
 F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence./.1.9e-31:158:86//AC002037  
 5 F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces./.3.4e-24:284:75//AC004150  
 F-HEMBA1003222//RPCI11-47P17.TJ RPCI11 Homo sapiens genomic clone R-47P17, genomic survey sequence./.8.7e-39:202:99//AQ202885  
 F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence./.10 0.86:227:62//AB019230  
 F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence./.8.6e-05:372:61//AE001373  
 F-HEMBA1003250//HS-1063-A1-H02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=3 Row=O, genomic survey sequence./.0.00032:57:96//B46142  
 15 F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein./.2.2e-08:531:59//X64624  
 F-HEMBA1003273//H.sapiens flow-sorted chromosome 6 HindIII·fragment, SC6pA19H4./.0.070:267:64//Z78949  
 F-HEMBA1003276//CIT-HSP-2301B4.TF CIT-HSP Homo sapiens genomic clone 2301B4, genomic survey sequence./.5.2e-08:295:63//AQ015073  
 F-HEMBA1003278//HS\_3075\_A1\_G09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey sequence./.0.98:399:58//AQ120599  
 20 F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces./.4.8e-101:277:97//AC005840  
 F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds./.9.0e-145:539:97//AF038662  
 25 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds./.5.0e-166:799:98//AB011109  
 F-HEMBA1003296//CITBI-E1-2507M8.TR CITBI-E1 Homo sapiens genomic clone 2507M8, genomic survey sequence./.1.9e-05:388:63//AQ262551  
 F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene./.8.0e-05:388:62//L17343  
 30 F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence./.0.0017:210:64//AF051177  
 F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds./.4.6e-188:865:99//AB001872  
 F-HEMBA1003322//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE./.2.4e-54:316:87//Z93015  
 35 F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2024C24, genomic survey sequence./.8.4e-12:166:76//B67147  
 F-HEMBA1003328//HS\_2230\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence./.0.026:128:71//AQ153313  
 F-HEMBA1003330//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete 40 cds./.4.0e-160:745:99//AF045555  
 F-HEMBA1003348//HS\_3194\_A1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence./.5.0e-79:381:99//AQ173779  
 F-HEMBA1003369//H.vulgare GAA-satellite DNA./.0.12:89:71//Z50100  
 F-HEMBA1003370//Homo sapiens cosmid 123E15, complete sequence./.3.5e-32:199:80//AF024533  
 45 F-HEMBA1003373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE./.0.019:117:71//AL034405  
 F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence./.4.2e-30:196:85//U67229  
 F-HEMBA1003380//Homo sapiens DNA sequence from clone 394P21 on chromosome 1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSs, complete sequence./.4.6e-22:206:81//AL021528  
 50 F-HEMBA1003384//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces./.0.00094:72:90//AC006026  
 F-HEMBA1003395//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE./.0.00041:826:57//AL031744  
 F-HEMBA1003402//CIT-HSP-2339K16.TR CIT-HSP Homo sapiens genomic clone 2339K16, genomic survey sequence./.2.4e-05:265:64//AQ056234  
 55 F-HEMBA1003403//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence./.4.3e-135:780:90//AC004066  
 F-HEMBA1003408

F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//1.9e-41:239:95//AL031321  
 F-HEMBA1003418//Rattus norvegicus Wistar polymeric immunoglobulin receptor (PIGR) gene, 3'UTR and trinucleotide repeat microsatellites.//2.2e-06:247:64//U08273  
 5 F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds.//1.4e-149:697:99//AF051334  
 F-HEMBA1003447//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//1.7e-77:461:90//AC004066  
 F-HEMBA1003461//Rhodobacter sphaeroides FliH (fliH) gene, partial cds, F1il (fliI) and FliJ (fliJ) genes, complete cds.//8.6e-08:752:58//U31090  
 10 F-HEMBA1003463//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//0.089:172:68//AC004098  
 F-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//4.5e-150:562:97//AC005041  
 F-HEMBA1003528//Streptomyces fradiae gene for trypsinogen precursor, complete cds.//4.7e-09:433:60//D16687  
 15 F-HEMBA1003531//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//2.3e-48:297:90//AC004990  
 F-HEMBA1003538//Human complement C1r mRNA, complete cds.//4.3e-22:474:63//M14058  
 F-HEMBA1003545//Rattus norvegicus (clone 1.6kB) islet-2 mRNA, complete cds.//3.5e-143:805:91//L35571  
 F-HEMBA1003548  
 20 F-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447E6, WORKING DRAFT SEQUENCE.//3.4e-58:331:83//AL031724  
 F-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSGB-484017 (Genome Systems Human BAC Library) complete sequence.//6.0e-99:703:84//AC005913  
 F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mRNA, complete cds.//1.3e-99:587:89//J05071  
 25 F-HEMBA1003568//HS\_3149\_A1\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3149 Col=7 Row=E, genomic survey sequence.//4.1e-05:389:57//AQ166810  
 F-HEMBA1003569//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.6e-102:669:85//AC005539  
 F-HEMBA1003571//Dictyostelium discoideum RegA (regA) gene, complete cds.//0.00033:649:58//U60170  
 30 F-HEMBA1003579//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00034:623:56//AL031744  
 F-HEMBA1003581//Mouse mRNA for talin.//3.3e-41:181:86//X56123  
 F-HEMBA1003591//Homo sapiens chromosome 16, BAC clone RPCI-11\_192K18, complete sequence.//4.4e-70:273:94//AC006075  
 35 F-HEMBA1003595//Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence.//6.0e-17:768:58//AE001395  
 F-HEMBA1003597//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-09:777:56//AE001398  
 F-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.3e-146:692:  
 40 98//AC005153  
 F-HEMBA1003615//HS\_2010\_A2\_A07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence.//1.1e-22:137:97//AQ226592  
 F-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//2.4e-169:501:97//AB015344  
 F-HEMBA1003621//Mus musculus PIAS3 mRNA, complete cds.//4.7e-37:165:92//AF034080  
 45 F-HEMBA1003622//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0024:514:58//AC005139  
 F-HEMBA1003630//CIT-HSP-2168N15.TR CIT-HSP Homo sapiens genomic clone 2168N15, genomic survey sequence.//6.5e-15:358:63//B92984  
 F-HEMBA1003637//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-  
 50 21:238:76//AC005077  
 F-HEMBA1003640//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 112K5, WORKING DRAFT SEQUENCE.//2.3e-15:371:63//Z85987  
 F-HEMBA1003645//A.thaliana 81kb genomic sequence.//1.0:529:57//X98130  
 F-HEMBA1003646  
 55 F-HEMBA1003656  
 F-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//1.6e-175:824:98//AC005746  
 F-HEMBA1003667//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered piec-

es.//1.1e-24:190:87//AC004765  
 F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.7e-162:579:99//  
 AC005065  
 F-HEMBA1003680//H.sapiens DNA sequence.//7.3e-22:172:87//Z22322  
 5 F-HEMBA1003684//H.sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723  
 F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//2.9e-72:606:77//AF039691  
 F-HEMBA1003692  
 F-HEMBA1003711//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//0.55:450:60//  
 AC003101  
 10 F-HEMBA1003714  
 F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and  
 genomic marker DXS8098, complete sequence.//3.0e-16:316:68//AL023575  
 F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//1.3e-41:483:  
 73//AC004056  
 15 F-HEMBA1003725//CIT-HSP-2351H9.TF CIT-HSP Homo sapiens genomic clone 2351H9, genomic survey se-  
 quence.//1.1e-112:532:99//AQ079348  
 F-HEMBA1003729//HS\_3043\_A1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3043 Col=13 Row=I, genomic survey sequence.//1.6e-12:87:98//AQ129345  
 F-HEMBA1003733//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.7e-104:761:82//AC006213  
 20 F-HEMBA1003742//HS\_3027\_A2\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3027 Col=4 Row=C, genomic survey sequence.//3.4e-08:67:97//AQ154731  
 F-HEMBA1003758//CIT-HSP-2379D18.TR CIT-HSP Homo sapiens genomic clone 2379D18, genomic survey se-  
 quence.//2.9e-10:310:63//AQ113513  
 F-HEMBA1003760//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//  
 25 AF060194  
 F-HEMBA1003773//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139  
 F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3  
 like pseudogene, EST, STS.//9.0e-135:804:89//Z99496  
 30 F-HEMBA1003784//Caenorhabditis elegans cosmid C55B6.//0.054:463:58//U88181  
 F-HEMBA1003799//Homo sapiens Chromosome 22q11.2 Cosmid Clone 105a In DGCR Region, complete se-  
 quence.//1.9e-44:425:76//AC000070  
 F-HEMBA1003803//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178  
 F-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-138:275:99//  
 35 AC004596  
 F-HEMBA1003805//Mus musculus quaking type I (QKI) mRNA, complete cds.//6.6e-148:753:95//U44940  
 F-HEMBA1003807//HS-1068-B1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic  
 clone Plate=CT 278 Col=11 Row=N, genomic survey sequence.//6.7e-07:241:67//B47212  
 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516  
 40 F-HEMBA1003836//S.cerevisiae chromosome IX cosmid 9150.//5.1e-16:368:63//Z38125  
 F-HEMBA1003838//CIT-HSP-384J15.TR CIT-HSP Homo sapiens genomic clone 384J15, genomic survey se-  
 quence.//1.4e-45:180:90//B54810  
 F-HEMBA1003856//Homo sapiens chromosome 10 clone CIT9875K-1188B12 map 10p12.1, complete se-  
 quence.//0.0014:574:58//AC005875  
 45 F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300  
 F-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//5.9e-81:853:71//AF030430  
 F-HEMBA1003879//H.sapiens CBP80 mRNA.//2.0e-08:87:95//X80030  
 F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SE-  
 QUENCE.//1.7e-180:853:98//AP000036  
 50 F-HEMBA1003885//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.5e-39:376:67//  
 AC004079  
 F-HEMBA1003893//H.sapiens CpG island DNA genomic Mse1 fragment, clone 11b6, forward read cpg11b6.ft1a.//  
 3.6e-32:173:99//Z59012  
 F-HEMBA1003902//RPCI11-26M20.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-26M20, genomic survey  
 55 sequence.//8.2e-12:422:61//AQ003455  
 F-HEMBA1003908//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.0063:  
 468:58//AE001401  
 F-HEMBA1003926//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING

DRAFT SEQUENCE./.3.6e-27:278:76//AL031658  
 F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region./.1.4e-55:315:81//AF109718  
 F-HEMBA1003939//HS-1047-A1-G04-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 Plate=CT 830 Col=7 Row=M, genomic survey sequence./.6.1e-09:413:63//B38195  
 5 F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 DRAFT SEQUENCE, 14 unordered pieces./.0.42:205:65//AC005140  
 F-HEMBA1003950//M.capricolum DNA for CONTIG MC072./.0.029:458:58//Z33058  
 F-HEMBA1003953//HS\_2268\_A1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2268 Col=7 Row=C, genomic survey sequence./.9.0e-07:239:64//AQ085098  
 10 F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence./.2.8e-57:424:  
 74//AC004894  
 F-HEMBA1003959//RPCI11-78E8.TV RPCI11 Homo sapiens genomic clone R-78E8, genomic survey sequence./.  
 4.3e-86:441:9611AQ285498  
 15 F-HEMBA1003976//HS\_3146\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3146 Col=17 Row=O, genomic survey sequence./.6.3e-10:129:80//AQ141146  
 F-HEMBA1003978  
 F-HEMBA1003985//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105C5,  
 WORKING DRAFT SEQUENCE./.1.0:258:60//Z98855  
 20 F-HEMBA1003987  
 F-HEMBA1003989//Streptomyces coelicolor cosmid 1A9./.0.40:238:61//AL034446  
 F-HEMBA1004000//Rattus norvegicus satellite sequence d0Mco2./.2.0e-07:116:70//U19354  
 F-HEMBA1004011//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING  
 DRAFT SEQUENCE, 2 unordered pieces./.0.098:286:60//AC004710  
 25 F-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence./.2.8e-185:896:97//  
 AC005670  
 F-HEMBA1004015//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete sequence./.6.3e-68:417:80//  
 AC005411  
 F-HEMBA1004024//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete  
 sequence./.2.0e-47:418:77//AC005859  
 30 F-HEMBA1004038//Homo sapiens genomic DNA, chromosome 21q11.1, segment 23/28, WORKING DRAFT SE-  
 QUENCE./.1.6e-51:564:74//AP000052  
 F-HEMBA1004042//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence./.1.2e-05:  
 636:55//AE001398  
 35 F-HEMBA1004045//Homo sapiens (subclone 1\_g7 from BAC H76) DNA sequence, complete sequence./.1.9e-31:  
 373:76//AC002252  
 F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2./.0.039:234:63//D63393  
 F-HEMBA1004049//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence./.  
 4.8e-135:780:89//AC003106  
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence./.4.7e-09:457:58//L13435  
 40 F-HEMBA1004056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING  
 DRAFT SEQUENCE./.3.3e-25:246 :77//AL021977  
 F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 2053J5, genomic survey se-  
 quence./.7.8e-24:233:76//B68555  
 45 F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence,  
 and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds./.4.5e-08:614:59//  
 U49822  
 F-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds./.5.9e-121:502:85//  
 AF091234  
 F-HEMBA1004111///\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14;  
 50 HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces./.2.0e-36:317:80//AC006160  
 F-HEMBA1004131//Mus musculus clone OST2067, genomic survey sequence./.8.7e-24:320:71//AF046393  
 F-HEMBA1004132//HS\_3226\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3226 Col=19 Row=H, genomic survey sequence./.9.7e-13:232:71//AQ182017  
 F-HEMBA1004133  
 55 F-HEMBA1004138//HS\_3036\_B1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3036 Col=21 Row=N, genomic survey sequence./.0.0035:165:64//AQ294763  
 F-HEMBA1004143  
 F-HEMBA1004146

F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.00011:618:60//Z96811  
 F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.9e-30:454:68//AC005913  
 5 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855  
 F-HEMBA1004199  
 F-HEMBA1004200//HS\_2015\_A1\_B05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957  
 10 F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268\_P\_23, complete sequence.//7.8e-59:216:83//AC004807  
 F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//6.3e-98:173:98//AC005488  
 F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//U50748  
 15 F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:584:60//AE001424  
 F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//AF095927  
 F-HEMBA1004238  
 20 F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708  
 F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77//AL031010  
 25 F-HEMBA1004248//Rattus rattus insulin-induced growth-respons protein (CL-6) mRNA, complete cds.//1.7e-30:315:74//L13619  
 F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60//AC004693  
 F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//3.1e-78:335:87//AC004707  
 30 F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-176:856:97//AC005831  
 F-HEMBA1004274//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993  
 35 F-HEMBA1004275//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING DRAFT SEQUENCE.//5.2e-17:109:99//Z98051  
 F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6, genomic survey sequence.//5.0e-07:63:98//AQ240477  
 F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868:99//AF022795  
 40 F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence.//1.0:387:59//AB013395  
 F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A.//7.8e-06:92:89//AB012254  
 F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:59//AC004897  
 45 F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4.//0.28:522:57//AJ235271  
 F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-136:548:92//AC006130  
 F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3e-32:320:65//Z84720  
 50 F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.93:222:62//AB011094  
 F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4 unordered pieces.//7.0e-168:895:93//AC004995  
 F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//4.6e-73:713:75//AC002980  
 55 F-HEMBA1004335//Human DNA-sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE.//1.3e-25:121:85//AL024498  
 F-HEMBA1004341  
 F-HEMBA1004353//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//6.4e-38:278:85//U14571  
 F-HEMBA1004354//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.1e-45:

190:92//U75968  
 F-HEMBA1004356  
 F-HEMBA1004366//*P.falciparum* complete gene map of plastid-like DNA (IR-A).//2.2e-07:736:57//X95275  
 F-HEMBA1004372//*H.sapiens* dystrophin gene intron 44.//1.0:129:62//X77644  
 5 F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//4.7e-42:237:94//M21977  
 F-HEMBA1004394//*Plasmodium falciparum* chromosome 2, section 39 of 73 of the complete sequence.//5.2e-05:  
 519:59//AE001402  
 F-HEMBA1004396//Human BAC clone RG302F04 from 7q31, complete sequence.//4.0e-32:261:76//AC002463  
 F-HEMBA1004405//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 10 DRAFT SEQUENCE, 9 unordered pieces.//1.4e-07:693:58//AC005507  
 F-HEMBA1004408//*Homo sapiens* clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//  
 1.2e-69:195:100//AC005037  
 F-HEMBA1004429//HS\_3193\_A1\_B06\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* ge-  
 15 nomic clone Plate=3193 Col=11 Row=C, genomic survey sequence.//5.1e-67:386:91//AQ172942  
 F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//3.2e-27:242:82//  
 AC002554  
 F-HEMBA1004460//*Homo sapiens* clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//  
 1.7e-75:590:81//AC004846  
 F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS, com-  
 20 plete sequence.//0.045:215:66//AL034407  
 F-HEMBA1004479//*Mus musculus* hypoxia inducible factor three alpha mRNA, complete cds.//5.2e-43:364:79//  
 AF060194  
 F-HEMBA1004482//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//6.8e-17:791:59//AC005505  
 25 F-HEMBA1004499//*Homo sapiens* chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//4.4e-125:251:  
 94//AC004686  
 F-HEMBA1004502//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces.//0.012:635:57//AC004709  
 F-HEMBA1004506//*Homo sapiens* PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.8e-127:766:  
 30 88//AC004453  
 F-HEMBA1004507  
 F-HEMBA1004509//*Arabidopsis thaliana* DNA chromosome 4, BAC clone T10I14 (ESSAll project).//1.0e-13:244:  
 67//AL021712  
 F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (ABP-280).//1.6e-72:678:74//X53416  
 35 F-HEMBA1004538//Sequence 1 from patent US 5612190.//0.00015:416:59//I36871  
 F-HEMBA1004542//*Homo sapiens* clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.95:  
 202:64//AC005038  
 F-HEMBA1004554//*Arabidopsis thaliana* BAC T26D22.//0.45:624:56//AFO58826  
 F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//9.1e-10:173:70//D87457  
 40 F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence.//6.1e-23:134:73//AC002542  
 F-HEMBA1004577//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-582J2, complete sequence.//1.6e-15:  
 190:77//AC004525  
 F-HEMBA1004586//*Homo sapiens* clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//  
 3.1e-31:388:76//AC004895  
 45 F-HEMBA1004596//RPCI11-81O21.TJ RPCI11 *Homo sapiens* genomic clone R-81O21, genomic survey se-  
 quence.//2.2e-90:458:90//AQ285136  
 F-HEMBA1004604//*Mus musculus* COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//8.6e-105:699:  
 84//AF071316  
 F-HEMBA1004610//*Homo sapiens* PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//5.4e-20:267:  
 50 72//AC004983  
 F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP *Homo sapiens* genomic clone 2319H15, genomic survey se-  
 quence.//6.2e-26:147:99//AQ034944  
 F-HEMBA1004629//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces.//5.6e-06:766:56//AC005504  
 55 F-HEMBA1004631//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NU-  
 CLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//4.7e-73:412:92//Z83843  
 F-HEMBA1004632//Canine herpesvirus DNA for gene homolog of HSV1 UL16, EHV1 ORF 46, VZV ORF 44.//  
 0.92:181:61//X90418

- F-HEMBA1004637//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor./.7.8e-47:784:65//X74904  
 F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds./.6.4e-06:458:  
 61//AF004431
- 5 F-HEMBA1004666//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3,  
 WORKING DRAFT SEQUENCE./.0.30:733:55//Z98865
- F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel  
 genes, ESTs, GSSs and CpG islands, complete sequence./.7.5e-136:521:98//AL031432
- 10 F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence./.0.43:365 :  
 59//AC000045
- F-HEMBA1004672  
 F-HEMBA1004693//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces./.0.096:651:54//AC005308
- 15 F-HEMBA1004697//CIT-HSP-2326C13.TR CIT-HSP Homo sapiens genomic clone 2326C13, genomic survey se-  
 quence./.0.23:238:65//AQ040642
- F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC  
 RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence./.2.1e-27:375:72//AC002357
- 20 F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-  
 plete sequence./.1.6e-36:191:91//AC006210
- F-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence./.1.1e-133:639:  
 99//AC005562
- F-HEMBA1004725//RPCI11-75013.TJ RPCI11 Homo sapiens genomic clone R-75O13, genomic survey se-  
 quence./.6.2e-32:169:100//AQ266512
- 25 F-HEMBA1004730//Human BAC clone RG035E18 from 7q31, complete sequence./.8.0e-68:732:72//AC004029
- F-HEMBA1004733//CIT-HSP-2305M23.TF CIT-HSP Homo sapiens genomic clone 2305M23, genomic survey se-  
 quence./.4.9e-18:209:69//AQ017556
- 30 F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds./.1.8e-  
 13:451:62//AF028340
- F-HEMBA1004736//Human DNA Sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine  
 threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked,  
 juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence./.5.0e-87:646:78//Z94056
- 35 F-HEMBA1004748//Human BAC clone RG204I16 from 7q31, complete sequence./.0.24:526:57//AC002461
- F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces./.1.  
 4e-25:268:76//AC004913
- F-HEMBA1004752//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp)./.1.1e-07:503:  
 61//X83546
- 40 F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete sequence./.4.5e-38:314:81//  
 AC000028
- F-HEMBA1004756//Homo sapiens, complete sequence./.1.4e-111:326:84//AC005854
- F-HEMBA1004758//Sequence 29 from patent US 5534410./.3.9e-135:769:91//I23472
- 45 F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete cds./.3.6e-47:404:79//U75285
- F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence./.6.7e-107:890:  
 78//AC004941
- F-HEMBA1004770//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces./.7.9e-09:806:59//AC004709
- 50 F-HEMBA1004771//G.muris ribosomal RNA operon DNA encoding 16S, 23S and 5.8S ribosomal RNA./.0.69:239:  
 61//X65063
- F-HEMBA1004776
- F-HEMBA1004778
- 55 F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DAKAP550 mRNA, partial cds./.3.4e-46:  
 778:64//AF003622
- F-HEMBA1004803//Homo sapiens chromosome Y, clone 264,M,20, complete sequence./.4.3e-82:580:82//  
 AC004617
- F-HEMBA1004806//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence./.5.4e-07:642:59//  
 AC005083
- F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3./.1.4e-46:  
 171:92//L01042
- F-HEMBA1004816//Homo sapiens calpastatin (CAST) gene, exons 10-14./.3.5e-31:546:66//M86257
- F-HEMBA1004820//C.botulinum progenitor toxin complex genes./.0.0014:343:62//X87972

F-HEMBA1004847//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//1.5e-85:512:88//X53744  
 F-HEMBA1004850//Homo sapiens TGF-beta type I receptor (TGFBR1) gene, exon 1.//0.0065:284:61//AF054590  
 F-HEMBA1004863//Genomic sequence from Mouse 11, complete sequence.//0.92:250:59//AC000400  
 5 F-HEMBA1004864  
 F-HEMBA1004865//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//3.6e-12:214:72//AL031120  
 F-HEMBA1004880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.1e-08:255:69//AC004020  
 10 F-HEMBA1004889//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.062:155:69//U32943  
 F-HEMBA1004900//Plasmodium falciparum unidentified mRNA sequence.//0.00055:323:60//L12043  
 F-HEMBA1004909//Homo sapiens chromosome 17, clone 289A8, complete sequence.//9.6e-16:166:80//AC003051  
 15 F-HEMBA1004918//Turritella communis mitochondrial 16S ribosomal RNA gene, partial.//0.81:146:65//M94003  
 F-HEMBA1004923//Human DNA from overlapping chromosome 19-specific cosmids R32543., and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//1.4e-36:338:78//AC003006  
 F-HEMBA1004929//CIT-HSP-2373I16.TR CIT-HSP Homo sapiens genomic clone 2373I16, genomic survey sequence.//2.4e-86:443:96//AQ108676  
 20 F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete sequence.//4.6e-20:219:73//AC004109  
 F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 497 Col=19 Row=I, genomic survey sequence.//1.4e-28:216:85//B30726  
 25 F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267O10, complete sequence.//0.53:222:61//AF042091  
 F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-58:509:78//AC005482  
 F-HEMBA1004954//HS\_2033\_A2\_A08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey sequence.//3.7e-47:243:99//AQ229758  
 30 F-HEMBA1004956//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.048:421:58//X95276  
 F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8.//0.89:333:58//Z97343  
 F-HEMBA1004972  
 35 F-HEMBA1004973//RPCI11-66P8.TK RPCI11 Homo sapiens genomic clone R-66P8, genomic survey sequence.//3.5e-22:245:77//AQ238471  
 F-HEMBA1004977//Homo sapiens full-length insert cDNA clone YZ83B08.//9.0e-11:84:98//AF086080  
 F-HEMBA1004978//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence.//0.0021:152:66//AQ075713  
 40 F-HEMBA1004980//HS\_3018\_A2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=8 Row=I, genomic survey sequence.//1.9e-77:392:97//AQ071873  
 F-HEMBA1004983//Albinaria corrugata isolate cor. Prm1.1 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.0030:276:61//AF031680  
 F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 306E6 (LANL), complete sequence.//4.2e-138:640:99//AC005590  
 45 F-HEMBA1005008//Human mariner1 transposase gene, complete consensus sequence.//6.8e-20:160:88//U52077  
 F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//2.0e-144:668:99//AF041474  
 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//1.4e-146:693:98//AB014548  
 50 F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//2.2e-115:668:90//AL009179  
 F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//4.6e-138:591:98//AC004596  
 55 F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 2338L5, genomic survey sequence.//3.7e-61:271:88//AQ055486  
 F-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//3.8e-17:218:73//Z22819  
 F-HEMBA1005050//Human Tis11d gene, complete cds.//0.079:251:63//U07802

F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces./.0.018:560:56//AC004688  
F-HEMBA1005066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE./.3.4e-97:432:84//AL034410  
5 F-HEMBA1005075//H.sapiens DNA 3' flanking simple sequence region clone wg2c3./.6.9e-07:176:68//X76589  
F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2325M21, genomic survey sequence./.2.1e-48:274:93//AQ038720  
F-HEMBA1005083//HS\_2248\_B1\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey sequence./.3.4e-06:230:64//AQ129575  
10 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds./.1.3e-161:762:98//AF080561  
F-HEMBA1005113//L.esculentum microsatellite repeat DNA region./.0.0038:742:57//X90770  
F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces./.9.6e-83:479:78//AC004854  
15 F-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE./.3.9e-24:576:64//AL023808  
F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence./.4.7e-36:283:80//AC004542  
20 F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces./.5.0e-10:332:64//AC004469  
F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE./.4.0e-10:734:58//AP000023  
F-HEMBA1005185//H.sapiens CpG island DNA genomic Mse1 fragment, clone 91b2, forward read cpg91b2.ft1a./.12.2e-14:93:100//Z63847  
25 F-HEMBA1005201//Drosophila melanogaster cosmid 152A3./.4.7e-35:679:64//AL009194  
F-HEMBA1005202//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//.6.7e-138:778:90//X53744  
F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and partial o25 gene and Pros26 gene./.7.1e-12:376:62//AJ011320  
30 F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds./.7.1e-05:411:60//AB007914  
F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence./.3.5e-06:212:66//AC004542  
F-HEMBA1005232//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces./.3.7e-07:625:57//AC005308  
35 F-HEMBA1005241//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence./.8.7e-45:567:72//AC005154  
F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence./.0.96:298:62//AC002365  
F-HEMBA1005251  
40 F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence./.4.5e-160:392:99//AC005837  
F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence./.2.3e-05:496:60//AF069291  
F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence./.5.7e-05:220:64//AL033521  
45 F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds./.2.4e-20:338:65//U97018  
F-HEMBA1005296  
F-HEMBA1005304//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence./.1.6e-51:381:78//AL031012  
50 F-HEMBA1005311  
F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE./.0.94:226:63//AP000031  
F-HEMBA1005315//Homo sapiens BAC810, complete sequence./.9.5e-15:684:62//U85198  
55 F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST, STS, CpG island clone./.2.6e-05:472:59//Z83823  
F-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence./.3.3e-90:300:90//AC005803

F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//1.4e-151:740:97//AJ007581  
 F-HEMBA1005353//CIT-HSP-2310N10.TR CIT-HSP Homo sapiens genomic clone 2310N10, genomic survey sequence.//2.1e-86:438:97//AQ016145  
 F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds.//1.8e-98:500:88//U09414  
 5 F-HEMBA1005367//Mus musculus melanatin mRNA, complete cds.//8.3e-72:577:73//AF047714  
 F-HEMBA1005372//Human DNA sequence from PAC 293E14 contains ESTs, STS.//1.3e-07:274:66//Z82900  
 F-HEMBA1005374//Homo sapiens clone 277F10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.9e-48:  
 611:69//AC004813  
 F-HEMBA1005382//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 10 nomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//1.6e-27:154:98//AQ103204  
 F-HEMBA1005389//Plasmodium falciparum telomere nucleotide sequence.//4.0e-07:443:61//M23175  
 F-HEMBA1005394//CIT-HSP-2368B11.TR CIT-HSP Homo sapiens genomic clone 2368B11, genomic survey se-  
 quence.//7.6e-17:225:71//AQ076749  
 F-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
 15 DRAFT SEQUENCE.//4.5e-131:278:98//AL034379  
 F-HEMBA1005408//HS\_3007\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3007 Col=8 Row=N, genomic survey sequence.//8.0e-06:218:66//AQ294366  
 F-HEMBA1005410//Human DNA sequence from cosmid cU120E2, on chromosome X contains Lowe oculocere-  
 20 brorenal syndrome (OCRL) ESTs and STS.//1.5e-41:432:76//Z73496  
 F-HEMBA1005411  
 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//1.0e-169:  
 537:99//AF041248  
 F-HEMBA1005426  
 F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-37:260:76//  
 25 AC006130  
 F-HEMBA1005447//CIT-HSP-2173N7.TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey se-  
 quence.//5.0e-133:631:98//B93234  
 F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related  
 30 C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete  
 sequence.//1.5e-118:868:83//AL022576  
 F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//1.2e-179:838:  
 99//AC005212  
 F-HEMBA1005472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING  
 35 DRAFT SEQUENCE.//3.4e-20:187:74//AL031985  
 F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SE-  
 QUENCE.//4.1e-22:445:65//AP000041  
 F-HEMBA1005475//CIT-HSP-2322D14.TR CIT-HSP Homo sapiens genomic clone 2322D14, genomic survey se-  
 quence.//6.7e-51:269:97//AQ026941  
 40 F-HEMBA1005497//HS\_3097\_A2\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3097 Col=10 Row=M, genomic survey sequence.//1.4e-66:345:96//AQ103810  
 F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence.//5.4e-178:818:  
 98//AC004957  
 F-HEMBA1005506//Mus musculus (clone 0EBF17) early B-cell factor (EBF) mRNA, complete cds.//2.6e-06:73:  
 98//L12147  
 45 F-HEMBA1005508//Homo sapiens clone hRPK.1\_A\_1, complete sequence.//0.00012:455:60//AC006196  
 F-HEMBA1005511//Homo sapiens MHC class 1 region.//3.3e-43:421:77//AF055066  
 F-HEMBA1005513//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//2.3e-20:352:  
 69//U71219  
 F-HEMBA1005517//Homo sapiens DNA for (CGG)n trinucleotide repeat region, isolate E7.//2.5e-08:431:62//  
 50 AJ001216  
 F-HEMBA1005518//M.musculus mRNA for paladin gene.//8.2e-90:651:81//X99384  
 F-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 7.8e-167:755:99//AC004913  
 F-HEMBA1005526//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//2.4e-42:475:73//  
 55 AC006241  
 F-HEMBA1005528//Mus musculus mCAF1 protein mRNA, complete cds.//1.2e-94:512:92//U21855  
 F-HEMBA1005530  
 F-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING

DRAFT SEQUENCE.//9.4e-87:422:99//AL034431  
 F-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//6.1e-41:486:68//  
 AC004743  
 F-HEMBA1005558//Drosophila melanogaster DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:  
 5 306:68//AC004377  
 F-HEMBA1005568//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153  
 F-HEMBA1005570//Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:  
 10 592:59//AE001407  
 F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932  
 F-HEMBA1005577//HS-1004-A1-E11 -MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic  
 clone Plate=CT 498 Col=21 Row=I, genomic survey sequence.//0.00034:254:64//B30971  
 F-HEMBA1005581//Rattus norvegicus mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531  
 15 F-HEMBA1005582//HS\_3242\_A1\_B07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3242 Col=13 Row=C, genomic survey sequence.//1.1e-13:91:98//AQ211275  
 F-HEMBA1005583  
 F-HEMBA1005588//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//8.7e-31:283:  
 20 75//AC006025  
 F-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.3e-158:748:  
 99//AC005746  
 F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP Homo sapiens genomic clone 2309F14, genomic survey se-  
 quence.//6.4e-30:194:91//AQ016527  
 F-HEMBA1005606//CIT-HSP-2326I6.TR CIT-HSP Homo sapiens genomic clone 2326I6, genomic survey se-  
 quence.//0.0014:132:70//AQ041484  
 25 F-HEMBA1005609//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-  
 33:249:85//AC005089  
 F-HEMBA1005616//Homo sapiens DNA sequence from PAC 43C13 on chromosome Xq21.1-Xq21.3. rab proteins  
 geranylgeranyltransferase component A 1 (rab escort protein 1) (REP-1) (choroideraemia protein) (TCD protein).//  
 30 6.5e-29:279:69//AL009175  
 F-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING  
 DRAFT SEQUENCE.//6.4e-90:158:87//AL031731  
 F-HEMBA1005627//RPCI11-34P9 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34P9, genomic survey se-  
 quence.//0.014:168:67//AQ045110  
 35 F-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.0e-149:736:93//AC004460  
 F-HEMBA1005632  
 F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-6p21.33. Contains ESTs.//  
 6.6e-38:452:67//Z98036  
 F-HEMBA1005666  
 40 F-HEMBA1005670//Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.//5.1e-59:687:74//  
 AC004850  
 F-HEMBA1005679//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-  
 47:357:85//AC005478  
 F-HEMBA1005680  
 45 F-HEMBA1005685//RPCI11-23D19.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23D19, genomic sur-  
 vey sequence.//0.99:228:63//AQ013742  
 F-HEMBA1005699//Human ligand for eph-related receptor tyrosine kinases (EPLG8) mRNA, complete cds.//1.4e-  
 72:406:92//U57001  
 F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.00040:190:66//X56513  
 50 F-HEMBA1005717//Plasmodium falciparum MAL3P1, complete sequence.//0.0099:260:63//Z97348  
 F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151:88//D14697  
 F-HEMBA1005737//Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.//5.6e-15:157:79//  
 AC005156  
 F-HEMBA1005746//RPCI11-63N8.TK RPCI11 Homo sapiens genomic clone R-63N8, genomic survey sequence.//  
 55 1.3e-18:113:100//AQ238535  
 F-HEMBA1005755//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs  
 and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.6e-56:764:70//Z97181  
 F-HEMBA1005765//Human DNA sequence from PAC 288L1 on chromosome 22q12-qter contains ESTs and pol-  
 ymorphic CA repeat (D22S1152).//1.1e-30:275:77//Z82196

F-HEMBA1005780//RPCI11-74E19.TJ RPCI11 Homo sapiens genomic clone R-74E19, genomic survey sequence.//0.0011:283:62//AQ268432  
 F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//0.14:326:61//AC004079  
 5 F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6.3e-10:706:59//X92523  
 F-HEMBA1005822//Mouse Bac 291G16, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.87:417:56//AC003020  
 F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 Fosmid Clone f39e1 In DGCR Region, complete sequence.//8.8e-42:370:79//AC000094  
 10 F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-42:690:67//AL022577  
 F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey sequence.//4.3e-07:253:59//  
 15 AL018749  
 F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone-2289L23, genomic survey sequence.//2.2e-68:333:99//B98952  
 F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL H191), complete sequence.//1.9e-57:  
 331:87//AC005351  
 20 F-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//5.1e-182:  
 864:98//AC004945  
 F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//3.0e-44:340:80//  
 AC004086  
 25 F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethyl-aniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL021026  
 30 F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44:328:77//AL031584  
 F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//1.3e-41:431:  
 77//AC005666  
 F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPCI4-761J14, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086  
 35 F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//  
 AC004974  
 F-HEMBA1005962//RPCI11-17O15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-17015, genomic survey sequence.//9.5e-36:315:84//B82821  
 40 F-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=1, genomic survey sequence.//9.3e-73:372:97//AQ147357  
 F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//  
 AF082516  
 F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//6.3e-07:  
 423:60//AE001408  
 45 F-HEMBA1005999//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//3.8e-09:360:  
 64//AC005599  
 F-HEMBA1006002  
 F-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//4.5e-83:495:90//AF036405  
 F-HEMBA1006031  
 50 F-HEMBA1006035  
 F-HEMBA1006036//Human (lambda) DNA for immunoglobulin light chain.//2.4e-59:652:74//D87009  
 F-HEMBA1006042//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//  
 2.1e-43:330:7011AC005386  
 F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
 55 DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC004153  
 F-HEMBA1006081  
 F-HEMBA1006090//, complete sequence.//4.5e-139:748:92//AC005500  
 F-HEMBA1006091//Homo sapiens gene encoding telethonin, exons 1 to 2, partial.//0.0091:346:62//AJ011098

- F-HEMBA1006100//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//2.8e-18:180:78//AC005880
- 5 F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte-Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.26:84:71//AL031177
- 10 F-HEMBA1006121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 691N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL031672
- 15 F-HEMBA1006124//CIT-HSP-2355B17.TF CIT-HSP Homo sapiens genomic clone 2355B17, genomic survey sequence.//0.044:225:61//AQ058966
- F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085
- 20 F-HEMBA1006138//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//7.5e-22:164:75//AL022162
- 25 F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500
- F-HEMBA1006155//H.sapiens CpG island DNA genomic Mse1 fragment, clone 119b6, forward read cpg119b6.ft1a.//1.0:85:72//Z64428
- 30 F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.1e-185:852:99//AF048693
- F-HEMBA1006173//striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt].//8.4e-50:642:73//S49400
- 35 F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PAC clone pDJ105i19, complete sequence.//1.4e-22:194:74//AC005318
- F-HEMBA1006198
- F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98//AF070557
- F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds.//8.2e-05:359:61//D86074
- 40 F-HEMBA1006252//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664
- F-HEMBA1006253
- F-HEMBA1006259//HS\_2231\_A1\_D10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722
- 45 F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//5.2e-27:156:85//AC004673
- F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80//X72791
- F-HEMBA1006278//Mus musculus poly(A) polymerase VI mRNA, complete cds.//2.1e-57:665:70//U58134
- 50 F-HEMBA1006283
- F-HEMBA1006284//Streptomyces fradiae tylactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//9.6e-06:623:60//U78289
- F-HEMBA1006291//HS\_2208\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804
- F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I89415
- 55 F-HEMBA1006309//Caenorhabditis elegans cosmid F01F1.//1.1e-21:420:63//U13070
- F-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183
- F-HEMBA1006328//Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds.//1.5e-46:485:73//L29074
- 60 F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//0.0032:61:91//B40563
- F-HEMBA1006344//HS-1009-A2-B02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420
- F-HEMBA1006347//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//1.6e-31:484:68//U71219
- 65 F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=11 Row=M, genomic survey sequence.//5.4e-15:95:100//B41671
- F-HEMBA1006359//Human ZNF43 mRNA.//1.4e-115:823:81//X59244
- 70 F-HEMBA1006364//Mouse mRNA for transforming growth factor-beta2.//2.7e-10:247:71//X57413

F-HEMBA1006377//Mus musculus chromosome 7, clone 19K5, complete sequence.//3.0e-57:401:81//AC002327  
 F-HEMBA1006380//CIT-HSP-2172K18.TF CIT-HSP Homo sapiens genomic clone 2172K18, genomic survey sequence.//1.3e-110:525:99//B92570  
 F-HEMBA1006381//HS-1045-B2-F10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 828 Col=20 Row=L, genomic survey sequence.//4.4e-05:163:70//B37813  
 F-HEMBA1006398//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.8e-62:370:86//AC004806  
 F-HEMBA1006416//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//3.7e-15:157:78//AC005179  
 5 F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen Ki-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DDX1003 and DDX1055, complete sequence.//1.2e-39:752:63//AL022165  
 10 F-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//2.4e-41:438:76//AF107885  
 F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//  
 15 20 0.027:293:64//AL031781  
 F-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//1.7e-50:310:80//Z93930  
 F-HEMBA1006438//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.051:440:59//X04465  
 F-HEMBA1006445//Felis catus ras p21 (H-ras) mRNA, partial cds.//1.0:238:59//U62088  
 25 F-HEMBA1006446//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//2.4e-05:702:58//AL031749  
 F-HEMBA1006461//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//8.6e-55:409:83//AC004560  
 F-HEMBA1006467//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.0:293:59//  
 30 35 AC006120  
 F-HEMBA1006471//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.4e-05:731:59//AC004709  
 F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP Homo sapiens genomic clone 2017H3, genomic survey sequence.//5.2e-60:435:83//B54247  
 F-HEMBA1006483//Homo sapiens chromosome 5, BAC clone 8e5 (LBNL H167), complete sequence.//2.9e-48:  
 40 45 50 55 286:84//AC004752  
 F-HEMBA1006485//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.96:283:  
 59//AC006031  
 F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.8e-14:259:67//AL022577  
 F-HEMBA1006489//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//6.6e-11:595:61//AL031283  
 F-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//6.0e-122:337:  
 100//AC005828  
 F-HEMBA1006494//Homo sapiens chromosome 7qtelo BAC E3, complete sequence.//3.8e-23:459:68//AF093117  
 F-HEMBA1006497//HS\_3023\_B2\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey sequence.//2.3e-81:433:95//AQ093846  
 F-HEMBA1006502//H.sapiens 7SL repeat (clones 2-19b).//1.6e-13:86:87//X62364  
 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//2.3e-139:470:98//AB014566  
 F-HEMBA1006521//Human BAC clone RG167B05 from 7q21, complete sequence.//4.3e-27:406:71//AC003991  
 F-HEMBA1006530//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//2.9e-27:408:65//AL031650  
 F-HEMBA1006535//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.028:599:60//AL034557  
 F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.//1.4e-171:  
 654:98//AF093419

F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene./.3.8e-104:811:80//Z73986  
 F-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds./.4.8e-99:386:82//U06944  
 F-HEMBA1006562//Human fructose-1,6-biphosphatase (FBP1) gene, exon 1./.0.012:322:60//U21925  
 5 F-HEMBA1006566//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces./.0.0026:580:58//AC005504  
 F-HEMBA1006569//Ovis aries beta actin mRNA, complete cds./.6.3e-08:231:70//U39357  
 F-HEMBA1006579//CIT-HSP-2380A22.TR CIT-HSP Homo sapiens genomic clone 2380A22, genomic survey sequence./.0.036:250:62//AQ197107  
 10 F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162./.1.0:225:63//AL021841  
 F-HEMBA1006595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE./.3.6e-50:689:69//AL022156  
 15 F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces./.1.9e-42:253:84//AC004166  
 F-HEMBA1006612//RPCI11-88F20.TJ RPCI11 Homo sapiens genomic clone R-88F20, genomic survey sequence./.1.1e-51:266:98//AQ286726  
 20 F-HEMBA1006617//HS\_2193\_B2\_H07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence./.1.1e-59:413:85//AQ299685  
 F-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudo-genes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence./.1.4e-35:257:89//AL023284  
 25 F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence./.9.6e-112:800:83//AC002036  
 F-HEMBA1006635//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE./.0.15:393:58//AL031745  
 F-HEMBA1006639//Petromyzon marinus polyadenylate binding protein (PABP) mRNA, complete cds./.9.6e-15:318:68//AF032896  
 30 F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces./.0.58:254:65//AC006148  
 F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, complete cds./.1.5e-37:108:88//U94479  
 F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence./.1.3e-154:671:96//AC005601  
 35 F-HEMBA1006653  
 F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence./.5.2e-110:254:93//AC005189  
 F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence./.1.4e-14:177:76//AC004554  
 40 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56./.5.5e-15:122:90//Y12065  
 F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete sequence./.0.098:218:63//AC004755  
 F-HEMBA1006682//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE./.1.4e-05:719:57//AL034346  
 45 F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence./.3.1e-22:151:78//AC006011  
 F-HEMBA1006696//CITBI-E1-2522D16.TF CITBI-E1 Homo sapiens genomic clone 2522D16, genomic survey sequence./.5.6e-17:324:66//AQ280738  
 F-HEMBA1006708  
 F-HEMBA1006709  
 50 F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces./.3.3e-08:136:79//AC005537  
 F-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence./.5.8e-162:497:98//AC005828  
 F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence./.7.4e-48:320:87//AC004796  
 55 F-HEMBA1006754//Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs./.4.1e-129:804:85//Z83850

F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//2.2e-162:766:99//AC005752  
 F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence.//1.2e-19:326:69//U73465  
 5 F-HEMBA1006779//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//1.4e-103:355:87//AL022727  
 F-HEMBA1006780//CIT-HSP-2359P7.TR CIT-HSP Homo sapiens genomic clone 2359P7, genomic survey sequence.//0.072:147:68//AQ077208  
 10 F-HEMBA1006789//nbxb0037I13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0037I13r, genomic survey sequence.//0.00011:288:63//AQ290474  
 F-HEMBA1006795//CIT-HSP-2307E3.TF CIT-HSP Homo sapiens genomic clone 2307E3, genomic survey sequence.//5.1e-80:420:96//AQ020511  
 F-HEMBA1006796//Human clone 23803 mRNA, partial cds.//4.5e-06:202:68//U79298  
 15 F-HEMBA1006807//Homo sapiens mRNA for SPOP.//1.2e-66:651:73//AJ000644  
 F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_O\_9, complete sequence.//6.0e-116:541:99//AC004797  
 F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//0.40:159:66//AC004262  
 20 F-HEMBA1006832//Homo sapiens (subclone 3\_g8 from P1 H25) DNA sequence, complete sequence.//1.8e-24:323:71//AC002196  
 F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10.//0.15:403:60//AB020872  
 F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.20:472:57//AE001369  
 25 F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence.//3.4e-79:641:76//AF046757  
 F-HEMBA1006885//HS\_2208\_B2\_G06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey sequence.//4.9e-18:206:76//AQ089246  
 F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//5.4e-07:298:65//AL031321  
 30 F-HEMBA1006914//S.pombe chromosome II cosmid c16H5.//0.00040:194:66//AL022104  
 F-HEMBA1006921//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//1.1e-174:813:99//AC006027  
 F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185.//0.0075:183:65//AF036704  
 35 F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A).//4.0e-06:739:57//X95275  
 F-HEMBA1006936  
 F-HEMBA1006938//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING DRAFT SEQUENCE.//1.1e-05:733:57//AL031747  
 F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-90:437:98//AJ010841  
 40 F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X. contains STS and polymorphic CA repeat.//0.67:217:62//Z82205  
 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.6e-143:740:94//AF004828  
 F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase.//2.8e-101:338:89//E06058  
 45 F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//7.1e-31:536:66//AC003071  
 F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE://9.5e-07:285:60//Z82209  
 F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence.//0.99:388:58//AC002328  
 50 F-HEMBA1007017//Sequence 3 from Patent WO9416067.//0.96:220:62//A39358  
 F-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//1.3e-124:838:83//X79088  
 F-HEMBA1007045  
 F-HEMBA1007051//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.17:343:60//Z99281  
 55 F-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.3e-67:659:74//U85056  
 F-HEMBA1007062//Tubulin gene.//1.0:113:67//A18572  
 F-HEMBA1007066//HS\_3116\_A2\_A03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=6 Row=A, genomic survey sequence.//0.80:214:62//AQ140467  
 F-HEMBA1007073//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library)

complete sequence./.9.3e-54:519:68//AC004242  
F-HEMBA1007078/CIT-HSP-2318N6.TF CIT-HSP Homo sapiens genomic clone 2318N6, genomic survey sequence./.8.7e-80:387:98//AQ044076  
F-HEMBA1007080  
5 F-HEMBA1007085//Streptomyces coelicolor cosmid 7A1./.3.5e-06:496:59//AL034447  
F-HEMBA1007087//Plasmodium falciparum MAL3P6, complete sequence./.7.4e-07:553:56//Z98551  
F-HEMBA1007112//HS\_2171\_A1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence./.1.0:172:61//AQ091865  
F-HEMBA1007113//Human DNA sequence from clone 1044O17 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence./.0.54:502:56//AL023875  
F-HEMBA1007121//Caenorhabditis elegans cosmid ZK430./.1.4e-08:265:64//U42833  
F-HEMBA1007129//CITBI-E1-2504A5.TF CITBI-E1 Homo sapiens genomic clone 2504A5, genomic survey sequence./.0.97:267:62//AQ264035  
10 F-HEMBA1007147//HS\_3208\_A2\_C04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=8 Row=E, genomic survey sequence./.9.1e-90:466:95//AQ176696  
F-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence./.6.0e-138:524:98//AC005239  
F-HEMBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence./.2.0e-20:157:87//AQ280780  
20 F-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds./.2.0e-62:318:97//AF062085  
F-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces./.1.6e-21:205:80//AC005911  
F-HEMBA1007194//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence./.1.3e-11:87:96//AQ187492  
25 F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds./.1.7e-156:478:98//D86987  
F-HEMBA1007206//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence./.0.024:342:63//AC004223  
F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds./.5.0e-176:839:98//AB018340  
F-HEMBA1007243//Chinese hamster hprt mRNA, complete cds./.4.3e-58:687:68//J00060  
30 F-HEMBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129).//.0.084:177:62//V00899  
F-HEMBA1007256//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE./.1.3e-75:490:88//AL022240  
F-HEMBA1007267//HS\_3218\_A1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey sequence./.2.9e-62:393:87//AQ181128  
35 F-HEMBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence./.1.1e-63:314:99//B95401  
F-HEMBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence./.3.1e-31:401:72//AC004638  
F-HEMBA1007281//HS\_3115\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey sequence./.5.0e-70:372:96//AQ186691  
40 F-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence./.1.2e-152:727:98//AL031003  
F-HEMBA1007300//Canis familiaris PDE5 mRNA for 3',5'-Cyclic GMP Phosphodiesterase, complete cds./.2.1e-21:542:63//AB008467  
45 F-HEMBA1007301//COL1A1-type I collagen pro alpha 1(I) chain propeptide {3' region} [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Mutant, 855 nt].//.1.7e-08:388:61//S64596  
F-HEMBA1007319//Genomic sequence from Mouse 9, complete sequence./.6.0e-84:390:75//AC000399  
F-HEMBA1007320  
50 F-HEMBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete sequence./.0.091:260:64//AC004485  
F-HEMBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces./.0.12:472:59//AC005140  
F-HEMBA1007341//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence./.1.5e-18:408:64//AC006120  
55 F-HEMBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces./.8.7e-25:500:62//AC005377  
F-HEMBA1007347//Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete sequence./.0.75:269:61//AC005738

F-HEMBB1000005//Homo sapiens chromosome Y, clone 264,M,20, complete sequence./.5.0e-05:441:60//AC004617  
F-HEMBB1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence./.1.0e-44:417:77//AC004491  
5 F-HEMBB1000018//HS\_2179\_B2\_E04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence./.0.012:87:77//AQ023250  
F-HEMBB1000024//Human DNA sequence from PAC 106I20 on chromosome 22q12-qter contains NADH pseudogene, ESTs, STS./.8.1e-11:461:61//Z81369  
F-HEMBB1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence./.0.96:198:62//AQ062938  
10 F-HEMBB1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs./.0.00049:276:64//AL009173  
F-HEMBB1000036//H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 302e2, reverse read 302e2.r./.0.0057:66:81//Z79857  
15 F-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds./.1.9e-100:450:98//AF084928  
F-HEMBB1000039//HS\_2167\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey sequence./.0.022:108:69//AQ092404  
20 F-HEMBB1000044//Borrelia burgdorferi (section 50 of 70) of the complete genome./.1.0e-07:486:61//AE001164  
F-HEMBB1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces./.5.3e-05:585:58//AC005507  
F-HEMBB1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene.  
25 Contains ESTs, STSs and GSSs, complete sequence./.5.8e-38:549:67//AL022170  
F-HEMBB1000054//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence./.7.0e-98:328:83//AC002349  
F-HEMBB1000055//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE./.3.7e-05:600:58//AB000880  
30 F-HEMBB1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces./.1.3e-48:472:78//AC005096  
F-HEMBB1000083  
F-HEMBB1000089//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE./.0.0036:679:56//AL031744  
35 F-HEMBB1000099//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence./.1.1e-15:312:68//AC005909  
F-HEMBB1000103//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence./.1.0e-37:316:74//AC006210  
F-HEMBB1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence./.3.1e-25:259:76//  
40 AF045450  
F-HEMBB1000119//Homo sapiens ASMTL gene./.1.2e-137:654:98//Y15521  
F-HEMBB1000136//Mycobacterium tuberculosis H37Rv complete genome; segment 127/162./.0.59:217:66//Z74697  
F-HEMBB1000141//Homo sapiens DNA from chromosome 19q13.1 cosmid f14121 containing ATP4A and GADPH-2 genes, genomic sequence./.8.4e-31:113:88//AD000090  
45 F-HEMBB1000144//Human BAC clone RG114A06 from 7q31, complete sequence./.4.4e-58:339:87//AC002542  
F-HEMBB1000173//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence./.9.4e-160:562:93//AC002996  
F-HEMBB1000175  
50 F-HEMBB1000198//HS\_3071\_A2\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence./.0.99:261:61//AQ137388  
F-HEMBB1000215//Homo sapiens chromosome 17, clone hRPK.481\_C\_4, complete sequence./.6.7e-17:138:86//AC005839  
F-HEMBB1000217//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds./.0.00083:287:  
55 60//U80808  
F-HEMBB1000218//Caenorhabditis elegans cosmid C52A11, complete sequence./.0.90:337:56//Z46792  
F-HEMBB1000226//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island./.1.7e-90:175:92//Z69890

F-HEMBB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence./.0.16:171:62//U07918  
 F-HEMBB1000244//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces./.4.8e-08:355:63//AC005522  
 5 F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds./.6.6e-155:735:98//AF075587  
 F-HEMBB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16./.0.58:396:59//M98818  
 10 F-HEMBB1000264//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds./.4.4e-32:100:100//U75968  
 F-HEMBB1000266//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence./.3.8e-16:176:78//AC004470  
 F-HEMBB1000272//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence./.0.011:379:58//AE001369  
 15 F-HEMBB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)./.0.92:272:61//AL022580  
 F-HEMBB1000284//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence./.0.00071:568:57//AC002366  
 20 F-HEMBB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like; zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene./.3.0e-13:439:65//Z98745  
 F-HEMBB1000312//Homo sapiens clone GS051M12, complete sequence./.0.031:252:65//AC005007  
 F-HEMBB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic survey sequence./.0.00033:173:65//AL026242  
 25 F-HEMBB1000318//HS\_3244\_B2\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence./.3.9e-85:438:95//AQ252951  
 F-HEMBB1000335//Homo sapiens chromosome 18, clone hRPK.24\_A\_23, complete sequence./.0.63:285:61//AC005968  
 F-HEMBB1000336  
 30 F-HEMBB1000337//Homo sapiens chromosome 4 clone B208G5 map 4q25, complete sequence./.0.0014:309:64//AC004051  
 F-HEMBB1000338//HS\_3108\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence./.3.8e-09:331:63//AQ140356  
 35 F-HEMBB1000339//Homo sapiens 12q24 PAC RPCI1-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence./.1.2e-52:295:77//AC002351  
 F-HEMBB1000341  
 F-HEMBB1000343//Plasmodium falciparum MAL3P3, complete sequence./.0.00081:397:61//Z98547  
 F-HEMBB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence./.9.1e-34:596:66//AL020989  
 40 F-HEMBB1000369//Genomic sequence from Human 17, complete sequence./.0.012:298:60//AC002090  
 F-HEMBB1000374//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence./.9.3e-69:294:89//U96409  
 F-HEMBB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence./.3.5e-54:352:88//AL034377  
 45 F-HEMBB1000391//Trichothecium roseum internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence./.0.011:168:67//U51982  
 F-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds./.2.6e-163:762:98//AF076838  
 F-HEMBB1000402//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence./.7.7e-15:466:63//AC002368  
 50 F-HEMBB1000404//Homo sapiens mRNA for myosin-IXA./.3.5e-65:324:98//AJ001714  
 F-HEMBB1000420//244Kb Contig from Human Chromosome 11p15.5 spanning D11S1 through D11S25, complete sequence./.0.013:399:62//AC001228  
 F-HEMBB1000434//Homo sapiens PAC clone 278C19 from 12q, complete sequence./.6.1e-83:571:84//AC004263  
 55 F-HEMBB1000438//RPCI11-21E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21E14, genomic survey sequence./.0.0030:295:63//B83110  
 F-HEMBB1000441//Homo sapiens Chromosome 22q12 Cosmid Clone II47g11, complete sequence./.2.5e-33:372:72//AC000035

F-HEMBB1000449//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//1.3e-51:534:72//Z83821  
 5 F-HEMBB1000455//Saccharomyces cerevisiae mitochondrion origin of replication (ori6) and oli1 gene, complete cds.//0.016:522:58//L36899  
 F-HEMBB1000472  
 F-HEMBB1000480  
 F-HEMBB1000487//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 128O3, WORKING DRAFT SEQUENCE.//0.00013:314:64//Z98742  
 10 F-HEMBB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//4.1e-110:529:98//AL034423  
 F-HEMBB1000491//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.10:187:65//AE001388  
 15 F-HEMBB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-06:637:58//AL022577  
 F-HEMBB1000510//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//3.1e-96:737:81//AC005553  
 20 F-HEMBB1000518//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.00014:163:68//AC004676  
 F-HEMBB1000523//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence.//0.41:349:56//AL010212  
 F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus.//6.6e-37:138:  
 25 96/Y11710  
 F-HEMBB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//3.9e-56:683:71//AB020860  
 F-HEMBB1000554//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//2.2e-51:282:84//AJ011929  
 30 F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds.//6.1e-32:537:65//AB018293  
 F-HEMBB1000564  
 F-HEMBB1000573//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.2e-33:268:73//AC005077  
 35 F-HEMBB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//5.8e-47:734:66//AL022476  
 F-HEMBB1000586//H.sapiens highly polymorphic microsatellite DNA.//0.030:147:67//X79883  
 40 F-HEMBB1000589//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.3e-41:278:83//AC002300  
 F-HEMBB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.1e-182:871:98//AC005184  
 F-HEMBB1000592//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #19.//0.012:  
 45 185:64//AF009074  
 F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence, complete sequence.//1.2e-131:353:93//AF053356  
 F-HEMBB1000598//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.1e-58:600:72//AC006207  
 50 F-HEMBB1000623//cDNA encoding Coliolus manganese peroxidase.//0.89:284:62//E12284  
 F-HEMBB1000630//Mus musculus clone NSAT47 nonsatellite RNA sequence.//1.9e-15:129:87//U26231  
 F-HEMBB1000631//Sequence 26 from patent US 5708157.//3.2e-27:180:88//I80057  
 F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds.//1.6e-48:811:65//AB002349  
 F-HEMBB1000637//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.1e-58:649:73//AC005478  
 55 F-HEMBB1000638//HS\_3051\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=M, genomic survey sequence.//0.0032:497:56//AQ155234  
 F-HEMBB1000643//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:791:68//AC005077

F-HEMBB1000649//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence./.5.2e-64:775:69//AC003009

F-HEMBB1000652//Homo sapiens chromosome 10 clone CRI-JC2048 map 10q22.1, WORKING DRAFT SEQUENCE, 4 unordered pieces./.2.7e-52:334:89//AC006186

5 F-HEMBB1000665//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence./.0.0062:426:60//AL024493

F-HEMBB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island./.9.6e-95:399:78/Z84488

10 F-HEMBB1000673//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence./.3.8e-50:293:92//AQ155121

F-HEMBB1000684//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING DRAFT SEQUENCE./.8.0e-65 :282:83//Z93241

F-HEMBB1000693//Homo sapiens neuroan1 mRNA, complete cds./.1.6e-118:575:97//AF040723

15 F-HEMBB1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces./.8.6e-07:251:61//AC005507

F-HEMBB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE./.2.9e-20:434:64//AL031118

20 F-HEMBB1000709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE./.0.26:184:65//AL034554

F-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds./.1.8e-129:692:93//U53475

F-HEMBB1000726//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence./.2.7e-40:304:80//U91321

25 F-HEMBB1000738//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence./.8.9e-35:582:63//AF011889

F-HEMBB1000749//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces./.6.2e-46:262:89//AC005849

30 F-HEMBB1000763//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE./.1.6e-99:316:98//AL034405

F-HEMBB1000770//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence./.0.044:325:60//AL022727

F-HEMBB1000774

35 F-HEMBB1000781//Sequence 3 from patent US 5753446./.1.2e-92:599:86//AR008277

F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds./.9.3e-64:672:71//AB014577

F-HEMBB1000790//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence./.2.4e-41:460:74//AC004801

F-HEMBB1000794//HS\_3034\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic survey sequence./.1.8e-74:378:97//AQ117099

40 F-HEMBB1000807//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39d7, reverse read cpg39d7.rt1a//8.5e-14:95:97//Z58412

F-HEMBB1000810//H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 303a8, complete read./.3.2e-05:138:71//Z79983

F-HEMBB1000821//HS\_2168\_B1\_A12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic survey sequence./.0.85 :208:60//AQ086361

45 F-HEMBB1000822//Human BAC clone GS113H23 from 5p15.2, complete sequence./.3.0e-06:361:60//AC003015

F-HEMBB1000826//Human BAC clone RG180F08 from 7q31, complete sequence./.1.1e-27:360:69//AC002431

F-HEMBB1000827

50 F-HEMBB1000831

F-HEMBB1000835//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence./.0.00098:234:63//AL023581

F-HEMBB1000840//Human Chromosome 11 Cosmid cSRSL97a6, complete sequence./.4.5e-61:328:79//U73649

55 F-HEMBB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence./.9.7e-144:809:87//AL021068

F-HEMBB1000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING

DRAFT SEQUENCE, 9 unordered pieces./.0.12:492:58//AC004157  
F-HEMBB1000870//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
DRAFT SEQUENCE, 9 unordered pieces./.0.0024:212:67//AC004157  
F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds./.1.5e-32:200:94//AF085351  
5 F-HEMBB1000883//HS\_3065\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3065 Col=8 Row=F, genomic survey sequence./.0.0017:152:66//AQ137687  
F-HEMBB1000887  
F-HEMBB1000888//CIT-HSP-2329A10.TR CIT-HSP Homo sapiens genomic clone 2329A10, genomic survey se-  
quence./.1.5e-31:172:98//AQ044369  
10 F-HEMBB1000890  
F-HEMBB1000893//Plasmodium falciparum MAL3P2, complete sequence./.9.5e-06:768:56//AL034558  
F-HEMBB1000908//Homo sapiens clone DJ1119N05, complete sequence./.4.5e-21:199:82//AC004968  
F-HEMBB1000910//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
DRAFT SEQUENCE./.0.72:366:59//AL034557  
15 F-HEMBB1000913//HS\_3078\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3078 Col=3 Row=F, genomic survey sequence./.9.9e-12:221:63//AQ144507  
F-HEMBB1000915//Homo sapiens DNA for (CGG)n trinucleotide repeat region, isolate P4./.1.2e-49:252:99//  
AJ001215  
F-HEMBB1000917//Homo sapiens chromosome 5, P1 clone 254f11 (LBNL H62), complete sequence./.2.3e-42:  
20 316:76//AC006077  
F-HEMBB1000927//Human BDR-2 mRNA for hippocalcin, complete cds./.3.6e-30:528:65//D16593  
F-HEMBB1000947//CpG0856B CpIOWAgDNA1 Cryptosporidium parvum genomic, genomic survey sequence./.  
0.81:262:62//AQ254493  
25 F-HEMBB1000959//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 346O6, WORKING  
DRAFT SEQUENCE./.1.2e-43:454:75//Z84487  
F-HEMBB1000973//Mus musculus schlafen2 (Slfn2) mRNA, complete cds./.8.3e-42:458:72//AF099973  
F-HEMBB1000975//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence./.  
0.98:196:63//AB005234  
F-HEMBB1000981  
30 F-HEMBB1000985//Homo sapiens chromosome 19, cosmid R29388, complete sequence./.2.9e-06:566:57//  
AC004476  
F-HEMBB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS./.  
0.099:391:57//Z98753  
F-HEMBB1000996//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-  
35 sequences (GSSs)./6.2e-33:227:80//Z94802  
F-HEMBB1001004  
F-HEMBB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence./.4.0e-13:164:  
79//AC002551  
F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence./.7.5e-13:229:  
40 69//AC002310  
F-HEMBB1001014//Homo sapiens chromosome 16, BAC clone 375G12 (LANL), complete sequence./.0.32:474:  
58//AC005751  
F-HEMBB1001020//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence./.  
2.6e-39:218:80//AF069291  
45 F-HEMBB1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence./.5.3e-05:656:59//AF070717  
F-HEMBB1001037//CIT-HSP-2358K16.TF CIT-HSP Homo sapiens genomic clone 2358K16, genomic survey se-  
quence./.6.6e-05:228:64//AQ080539  
F-HEMBB1001047//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from  
Xq28, complete sequence./.4.0e-27:385:71//U82671  
50 F-HEMBB1001051//H.sapiens mRNA for FAN protein./.1.2e-27:160:98//X96586  
F-HEMBB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces./.  
2.3e-89:180:91//AC006014  
F-HEMBB1001058//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Li-  
brary) complete sequence./.1.2e-41:468:74//AC006060  
55 F-HEMBB1001060//Human Tigger1 transposable element, complete consensus sequence./.4.3e-122:785:86//  
U49973  
F-HEMBB1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING  
DRAFT SEQUENCE./.7.1e-162:770:99//AL034375

F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//3.1e-146:736:95//AF034803  
 F-HEMBB1001096//Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene, partial cds.//0.00088:690:57//AF008210  
 5 F-HEMBB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//2.1e-76:368:99//AF049612  
 F-HEMBB1001105//CIT-HSP-2185N1.TR CIT-HSP Homo sapiens genomic clone 2185N1, genomic survey sequence.//1.0e-09:136:76//AQ002987  
 F-HEMBB1001112//Rattus rattus sec61 homologue mRNA, complete cds.//1.0e-108:909:76//M96630  
 10 F-HEMBB1001114//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//7.2e-07:459:59//AC005284  
 F-HEMBB1001117//HS\_2178\_B1\_E12\_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey sequence.//7.8e-50:331:86//AQ068244  
 F-HEMBB1001119//Human collagen type XII alpha-1 precursor (COL12A1) mRNA, complete cds.//1.6e-25:150:  
 15 98//U73778  
 F-HEMBB1001126  
 F-HEMBB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.8e-24:228:80//AC004673  
 F-HEMBB1001137  
 20 F-HEMBB1001142//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.0e-40:231:76//AC004617  
 F-HEMBB1001151//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.9e-47:640:67//AF015264  
 F-HEMBB1001153//CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.//0.76:136:67//AQ075724  
 25 F-HEMBB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypcan-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//9.9e-63:259:79//AL008712  
 F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds.//2.2e-34:509:66//D78334  
 F-HEMBB1001177//CIT-HSP-2321I17.TR CIT-HSP Homo sapiens genomic clone 2321I17, genomic survey sequence.//5.9e-27:320:75//AQ036473  
 30 F-HEMBB1001182//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//5.7e-06:62:96//B85188  
 F-HEMBB1001199  
 F-HEMBB1001208//HS\_2026\_B1\_C07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey sequence.//0.00018:134:70//AQ229237  
 35 F-HEMBB1001209//CITBI-E1-2521F23.TF CITBI-E1 Homo sapiens genomic clone 2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357  
 F-HEMBB1001210//HS\_3102\_A2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196  
 40 F-HEMBB1001218//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//1.0e-31:315:72//AL031291  
 F-HEMBB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504  
 F-HEMBB1001234//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39f9, forward read cpg39f9.ft1e//  
 45 4.0e-30:171:97//Z65435  
 F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754  
 F-HEMBB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 2375N19, genomic survey sequence.//0.0076:250:63//AQ109087  
 F-HEMBB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SE-  
 50 QUENCE.//0.0097:89:80//AP000032  
 F-HEMBB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 2320E5, genomic survey se-  
 quence.//3.7e-54:284:97//AQ037173  
 F-HEMBB1001267//Homo sapiens chromosome 17, clone hRPK.488\_L\_1, complete sequence.//3.5e-30:236:78//  
 AC005303  
 55 F-HEMBB1001271//HS\_3011\_A1\_G02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3011 Col=3 Row=M, genomic survey sequence.//5.2e-07:364:62//AQ214217  
 F-HEMBB1001282//CIT-HSP-2356J20.TF CIT-HSP Homo sapiens genomic clone 2356J20; genomic survey se-  
 quence.//1.8e-16:109:97//AQ060969

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F-HEMBB1001288//R.norvegicus mRNA for gephyrin./3.4e-18:194:77//X66366  
F-HEMBB1001289//Genomic sequence from Human 9q34, complete sequence./4.8e-66:434:74//AC000387  
F-HEMBB1001294//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence./2.0e-90:437:99//AQ155035  
5 F-HEMBB1001302  
F-HEMBB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 2053E15, genomic survey sequence./2.2e-07:370:61//B69144  
F-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds./5.7e-116:663:85//U92703  
10 F-HEMBB1001315//Homo sapiens chromosome 10 clone LA10NC01\_40\_G\_3 map 10q26.1-10q26.2, WORKING DRAFT SEQUENCE, 1 ordered pieces./2.5e-33:328:77//AC006096  
F-HEMBB1001317//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence./1.4e-122:680:91//AC006210  
15 F-HEMBB1001326//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence./2.8e-09:518:60//AC004129  
F-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c./3.7e-56:458:79//D63850  
F-HEMBB1001335//HS\_3055\_A1\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=19 Row=O, genomic survey sequence./1.0:222:63//AQ147384  
20 F-HEMBB1001337//Human PAC clone DJ0093I03 from Xq23, complete sequence./1.0e-74:319:85//AC003983  
F-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region./4.0e-135:856:87//U85056  
F-HEMBB1001346//Human familial Alzheimer's disease (STM2) gene, complete cds./3.3e-44:481:74//U50871  
F-HEMBB1001348//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence./1.8e-17:210:73//AC006041  
25 F-HEMBB1001356//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces./1.0:386:59//AC005079  
F-HEMBB1001364//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence./0.97:349:61//AC004662  
F-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete sequence./5.5e-161:766:98//AC005876  
30 F-HEMBB1001367//Homo sapiens chromosome 17, clone hRPC.906\_A\_24, complete sequence./3.0e-55:510:76//AC004408  
F-HEMBB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequence./0.048:244:64//AC005192  
35 F-HEMBB1001380//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence./2.5e-26:257:78//AC006204  
F-HEMBB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds./5.1e-99:571:89//AF071314  
F-HEMBB1001387//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene./7.1e-05:546:58//X02354  
40 F-HEMBB1001394//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence./4.0e-129:788:88//AC005023  
F-HEMBB1001410//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds./4.8e-11:632:59//AF045555  
F-HEMBB1001424//Mus musculus Chromosome 4 BAC clone BacB6, complete sequence./0.0012:435:59//AC003019  
45 F-HEMBB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces./3.8e-17:360:64//AC005482  
F-HEMBB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt].//4.1e-114:668:88//S65367  
F-HEMBB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence./2.3e-37:438:74//AB000931  
50 F-HEMBB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, complete cds./9.1e-92:550:88//L18966  
F-HEMBB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNL H142), complete sequence./0.00024:385:62//AC004768  
55 F-HEMBB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequence./0.84:577:57//AC005790  
F-HEMBB1001458//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces./8.0e-40:377:78//AC000382  
F-HEMBB1001463//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence./0.011:482:

59//AF001549  
F-HEMBB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence.//0.019:263:61//  
U91320

5 F-HEMBB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced  
form, complete cds.//1.0e-30:521:66//U92564

F-HEMBB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
1.3e-31:479:71//AC004873

10 F-HEMBB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.7e-  
51:680:70//AC005080

15 F-HEMBB1001527  
F-HEMBB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h In DGCR Region, complete se-  
quence.//1.3e-79:696:79//AC000089

F-HEMBB1001535//Oaries DNA for polymorphic marker 'OVINRA01' (339 bp).//0.00034:217:62//X89268

20 F-HEMBB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//0.54:266:  
60//AC004548

F-HEMBB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//4.6e-25:784:61//  
AC004262

25 F-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//6.9e-  
50:213:80//AC004605

30 F-HEMBB1001562//Homo sapiens clone NH0523H20, complete sequence.//0.46:269:60//AC005041

F-HEMBB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-  
gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//1.7e-107:620:83//AL020989

F-HEMBB1001565//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-50:734:67//  
AC004003

35 F-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and  
GSSs, complete sequence.//1.4e-166:816:97//AL031677

F-HEMBB1001586  
F-HEMBB1001588//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.6e-21:419:65//  
AC005261

40 F-HEMBB1001603  
F-HEMBB1001618//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin  
Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a  
Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker  
D6S416, complete sequence.//4.5e-29:422:72//Z99289

45 F-HEMBB1001619//HS\_3079\_B1\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3079 Col=7 Row=B, genomic survey sequence.//0.0010:77:79//AQ123388

F-HEMBB1001630//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-  
12:667:59//AC005089

50 F-HEMBB1001635//Plasmodium falciparum MAL3P7, complete sequence.//3.8e-05:475:57//AL034559

F-HEMBB1001637//Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the al-  
ternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively  
spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronat-  
riodilatin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myo-  
tubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.//  
9.2e-13:168:76//AL021155

F-HEMBB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//  
0.00097:721:58//AB006702

F-HEMBB1001653//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//0.15:276:63//  
AC002038

55 F-HEMBB1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, com-  
plete cds.//0.43:393:61//L14320

F-HEMBB1001668//F16C15-T7 IGF Arabidopsis thaliana genomic clone F16C15, genomic survey sequence.//  
0.040:275:60//B12308

F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//7.2e-171:803:98//AB014546

F-HEMBB1001684//Sequence 1 from patent US 5700927.//7.5e-124:883:81//I86429

F-HEMBB1001685//CIT-HSP-2287O9.TF CIT-HSP Homo sapiens genomic clone 2287O9, genomic survey se-  
quence.//2.3e-34:191:97//B99261

F-HEMBB1001695//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding

exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (*Drosophila*) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL009178

5 F-HEMBB1001704//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575

F-HEMBB1001706

F-HEMBB1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543

10 F-HEMBB1001717//*Saccharomyces cerevisiae* mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.1e-13:723:58//AJ223323

F-HEMBB1001735//Human PAC clone DJ0596O09 from 7p15, complete sequence.//1.3e-36:427:73//AC003074

F-HEMBB1001736//*S.pombe* chromosome II cosmid c4B4.//0.0085:479:57//AL023706

F-HEMBB1001747//*Homo sapiens* PAC clone DJ1002N02 from 7p21-p22, complete sequence.//4.0e-112:532:84//AC005376

15 F-HEMBB1001749//*Homo sapiens* chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.3e-98:395:82//AC005829

F-HEMBB1001753//*S.maximus* repeat region, 342bp.//4.2e-11:69:85//Z78099

F-HEMBB1001756//*Homo sapiens* full-length insert cDNA clone ZD86A11.//0.0015:302:62//AF088064

20 F-HEMBB1001760//*P.falciparum* complete gene map of plastid-like DNA (IR-A).//0.011:615:56//X95275

F-HEMBB1001762//CIT-HSP-2290J16.TF CIT-HSP *Homo sapiens* genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184

F-HEMBB1001785//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746

25 F-HEMBB1001797//Human heterogenous nuclear RNA W16W.//0.00012:83:86//X17272

F-HEMBB1001802//*Plasmodium falciparum* MAL3P7, complete sequence.//1.8e-11:538:60//AL034559

F-HEMBB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882

F-HEMBB1001816//*Homo sapiens* chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204

30 F-HEMBB1001831//*Homo sapiens* PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//2.3e-162:763:98//AF056209

F-HEMBB1001834//CIT-HSP-2291O12.TF CIT-HSP *Homo sapiens* genomic clone 2291O12, genomic survey sequence.//7.6e-08:73:94//AQ004168

35 F-HEMBB1001836//*Homo sapiens* 12q13.1 PAC RPCI-1228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC004801

F-HEMBB1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC004073

F-HEMBB1001850//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0027:812:58//AC005504

40 F-HEMBB1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581

F-HEMBB1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//1.7e-56:399:86//U07563

F-HEMBB1001868//*Rattus norvegicus* clone 923 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//6.1e-08:234:67//U01145

45 F-HEMBB1001869//*Homo sapiens* full-length insert cDNA clone YT86F01.//7.4e-87:432:97//AF085974

F-HEMBB1001872

F-HEMBB1001874//*Homo sapiens* clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.4e-14:631:61//AC005000

F-HEMBB1001875//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//0.93:415:57//Z82209

50 F-HEMBB1001880//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:729:60//Z93403

F-HEMBB1001899//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//0.0038:425:58//AL010216

55 F-HEMBB1001905//*S.pombe* chromosome III cosmid c330.//1.1e-23:520:62//AL031603

F-HEMBB1001906

F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//3.7e-82:672:81//U47742

F-HEMBB1001910//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./.0.0033:566:55//AC005505  
 F-HEMBB1001911//Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence./.1.0:581:58//AC004705  
 5 F-HEMBB1001915//Caenorhabditis elegans cosmid T05H10, complete sequence./.1.2e-16:283:67//Z47812  
 F-HEMBB1001921//Homo sapiens chromosome 17, clone hCIT.123\_J\_14, complete sequence./.3.4e-07:803:58//AC003950  
 F-HEMBB1001922//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence./.5.0e-06:756:56///AE001391  
 10 F-HEMBB1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat./.3.1e-45:609:73//AL009181  
 F-HEMBB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 10/11./.3.2e-158:745:99//AB020867  
 15 F-HEMBB1001944//, complete sequence./.4.1e-60:638:73//AC005815  
 F-HEMBB1001945//HS\_3185\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence./.1.0:280:58//AQ188882  
 F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds./.5.6e-20:333:66//AB002390  
 F-HEMBB1001950//Human lipocortin (LIP) 2 gene, upstream region./.0.0094:180:63//M62899  
 20 F-HEMBB1001952//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 101A4, WORKING DRAFT SEQUENCE./.5.4e-19:329:70//Z93341  
 F-HEMBB1001953//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence./.0.11:589:58//AC005284  
 F-HEMBB1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion channel, ESTs, CpG island./.9.8e-25:446:  
 25 67//Z98941  
 F-HEMBB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence./.2.8e-147:727:97//AC005736  
 F-HEMBB1001967//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces./.3.2e-56:650:71//AC004963  
 30 F-HEMBB1001973//Homo sapiens chromosome 12p13.3-clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces./.1.2e-42:327:84//AC005844  
 F-HEMBB1001983//CIT-HSP-2315M4.TF CIT-HSP Homo sapiens genomic clone 2315M4, genomic survey sequence./.8.8e-35:198:96//AQ028071  
 F-HEMBB1001988//D.polychroa microsatellite sequence (clone Dp 1C e12)./.4.5e-07:337:62//X92189  
 35 F-HEMBB1001990//HS\_3234\_A1\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=15 Row=M, genomic survey sequence./.0.039:279:59//AQ204689  
 F-HEMBB1001996//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE./.0.18:392:58//AL024507  
 F-HEMBB1001997//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces./.1.3e-  
 40 43:446:71//AC005069  
 F-HEMBB1002002//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./.0.077:444:58//AC004153  
 F-HEMBB1002005//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 963K23, WORKING DRAFT SEQUENCE./.3.4e-16:173:78//AL031685  
 45 F-HEMBB1002009//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces./.0.00033:790:56//AC005506  
 F-HEMBB1002015//Homo sapiens genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SE-  
 QUENCE./.6.7e-05 :126:76//AP000056  
 F-HEMBB1002042//Oncorhynchus mykiss cytochrome P450 (CYP4V1) mRNA, partial cds./.6.4e-33:402:69//  
 50 AF046012  
 F-HEMBB1002043  
 F-HEMBB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence./.3.0e-167:809:97//AC005740  
 F-HEMBB1002045  
 55 F-HEMBB1002049//Homo sapiens chromosome 17, clone hRPC.161\_P\_9, complete sequence./.0.87:177:65//AC006237  
 F-HEMBB1002050//Streptomyces coelicolor cosmid D78./.8.5e-08:644:58//AL034355  
 F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds./.2.5e-05:402:61//AB014512

F-HEMBB1002069  
F-HEMBB1002092/\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B331O8; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces././/7.8e-104:550:83//AC004064  
F-HEMBB1002094//Homo sapiens genomic DNA, 21q region, clone: 125H6N2, genomic survey sequence././/2.9e-49:302:83//AG001476  
5 F-HEMBB1002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence././/0.00023:542:61//AC004035  
F-HEMBB1002134//Human h-neuro-d4 protein mRNA, complete cds././/7.3e-43:533:70//U43843  
F-HEMBB1002139//HS-1048-A2-B02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
.10 Plate=CT 831 Col=4 Row=C, genomic survey sequence././/0.055:228:66//B38714  
F-HEMBB1002142//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P5, WORKING  
DRAFT SEQUENCE././/0.0095:276:64//AL031748  
F-HEMBB1002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces././/0.055:520:  
57//AC002421  
15 F-HEMBB1002189//Homo sapiens cosmid ICRFc104I0935Q8 from Xq28, complete sequence././/2.6e-05:311:63//  
AF002998  
F-HEMBB1002190//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces././/5.4e-05:647:59//AC005140  
F-HEMBB1002193//Sequence 5 from patent US 5709858././/1.8e-34:179:100//I80846  
20 F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10././/1.2e-23:405:67//X52332  
F-HEMBB1002218//HS\_2056\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2056 Col=17 Row=F, genomic survey sequence././/3.3e-45:245:97//AQ244711  
F-HEMBB1002232//Human chromosome 11 72g7 cosmid, complete sequence././/1.9e-21:314:70//U73648  
F-HEMBB1002247  
25 F-HEMBB1002249//Homo sapiens DNA sequence from BAC 34I8 on chromosome 6p21.3-22.1. Contains ZNF184  
gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fli-2, rat helix destabilizing protein, mouse Topoisomerase-inhibitor suppressed gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIKE pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene 1) genes. Contains ESTs,  
STSs and GSSs, complete sequence././/4.1e-45:327:83//AL021918  
30 F-HEMBB1002254//Human chromosome 16 BAC clone LANL cosmid-440E5, WORKING DRAFT SEQUENCE,  
2 unordered pieces././/9.8e-40:315:82//AC002506  
F-HEMBB1002255//Plasmodium falciparum MAL3P3, complete sequence././/0.0035:312:62//Z98547  
F-HEMBB1002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING  
DRAFT SEQUENCE, 3 unordered pieces././/0.013:469:59//AC005504  
35 F-HEMBB1002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence././/5.3e-  
18:527:61//AC004682  
F-HEMBB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence././/8.6e-139:818:88//  
U73642  
F-HEMBB1002306//HS\_3109\_A2\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
40 nomic clone Plate=3109 Col=2 Row=O, genomic survey sequence././/1.3e-75:371:98//AQ148164  
F-HEMBB1002327//HS\_3235\_B2\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3235 Col=20 Row=N, genomic survey sequence././/3.3e-83:418:97//AQ209752  
F-HEMBB1002329//CITBI-E1-2503J7.TR CITBI-É1 Homo sapiens genomic clone 2503J7, genomic survey se-  
quence././/3.3e-31:220:88//AQ263402  
45 F-HEMBB1002340  
F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein././/4.1e-154:724:98//AJ010841  
F-HEMBB1002358//Human thymidylate kinase (CDC8) mRNA, complete cds././/3.3e-36:192:98//L16991  
F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds././/1.8e-13:96:96//U55766  
50 F-HEMBB1002364//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 376D21, WORKING  
DRAFT SEQUENCE././/7.5e-24:202:71//Z98946  
F-HEMBB1002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
DRAFT SEQUENCE, 8 unordered pieces././/1.9e-06:674:56//AC004153  
F-HEMBB1002381//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence././/0.34:238:  
61//AC005222  
55 F-HEMBB1002383  
F-HEMBB1002387//CIT-HSP-2173E20.TR CIT-HSP Homo sapiens genomic clone 2173E20, genomic survey se-  
quence././/5.2e-17:434:66//B91052  
F-HEMBB1002409//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glycan-3

precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-56:324:88//AL008712  
 F-HEMBB1002415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING  
 DRAFT SEQUENCE.//8.9e-35:334:75//AL031319  
 F-HEMBB1002425//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//1.0e-36:317:76//  
 5 U62317  
 F-HEMBB1002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds.//4.3e-88:296:92//  
 U92010  
 F-HEMBB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING  
 10 DRAFT SEQUENCE.//2.7e-43:419:78//AL034349  
 F-HEMBB1002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
 1.3e-27:542:68//AC005534  
 F-HEMBB1002458//HS\_3246\_A2\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3246 Col=10 Row=M, genomic survey sequence.//3.2e-51:257:99//AQ217993  
 F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//1.9e-87:493:92//U43885  
 15 F-HEMBB1002489  
 F-HEMBB1002492//Arabidopsis thaliana BAC T15B16.//0.028:516:57//AF104919  
 F-HEMBB1002495//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complete sequence.//1.1e-16:297:  
 68//AC006141  
 F-HEMBB1002502//Homo sapiens clone DJ1163L11, complete sequence.//1.1e-91:675:82//AC005230  
 20 F-HEMBB1002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//2.7e-  
 11:648:60//AC004605  
 F-HEMBB1002510//HS\_3236\_B1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3236 Col=21 Row=P, genomic survey sequence.//1.2e-06:67:94//AQ205992  
 F-HEMBB1002520//Homo sapiens BAC clone NH0004N07 from Y, complete sequence.//1.2e-70:580:72//  
 25 AC006152  
 F-HEMBB1002522//Homo sapiens Xp22 bin 150 clone GSHB-223P11 (Genome Systems Human BAC library)  
 complete sequence.//5.6e-22:516:64//AC004553 F-HEMBB1002531  
 F-HEMBB1002534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING  
 DRAFT SEQUENCE.//6.9e-62:265:87//AL034346  
 30 F-HEMBB1002545//Human BAC clone RG128M16 from 7q21-7q22, complete sequence.//2.7e-44:200:82//  
 AC000059  
 F-HEMBB1002550//Homo sapiens PAC clone DJ0910I17 from 7q11.21-q11.23, complete sequence.//0.22:161:  
 68//AC004927  
 F-HEMBB1002556//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//7.5e-43:306:77//  
 35 AC004861  
 F-HEMBB1002579  
 F-HEMBB1002582//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING  
 DRAFT SEQUENCE.//0.00018:431:61//AL033520  
 F-HEMBB1002590//Yeast (S.cerevisiae) mitochondrial apocytochrome b gene, 3' flank.//0.78:147:64//J01471  
 40 F-HEMBB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 9E21, WORKING  
 DRAFT SEQUENCE.//3.6e-50:692:69//AL008639  
 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-151:710:98//AF089749  
 F-HEMBB1002601//Human BAC clone RG020D02 from 7q22, complete sequence.//1.5e-07:416:60//AC002381  
 F-HEMBB1002603//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//0.40:341:60//AC002454  
 45 F-HEMBB1002607//Mus musculus homeobox containing nuclear transcriptional factor Hmx1 (Hmx1) gene, com-  
 plete cds.//0.0042:460:60//AF009614  
 F-HEMBB1002610//Homo sapiens Chromosome 12q24 PAC RPCI3-462E2 (Roswell Park Cancer Institute Human  
 PAC library) complete sequence.//6.3e-23:559:63//AC003029  
 F-HEMBB1002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete sequence.//4.2e-17:441:63//  
 50 AC000025  
 F-HEMBB1002614//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//0.013:  
 324:56//AE001417  
 F-HEMBB1002617//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//2.1e-07:  
 441:60//AF001550  
 55 F-HEMBB1002623//C.hyalina microsatellite marker DNA (id ATCC4).//0.57:106:66//Z95304  
 F-HEMBB1002635//Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.//4.8e-22:127:100//  
 U34819  
 F-HEMBB1002664//HS\_2265\_A1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=2265 Col=11 Row=O, genomic survey sequence //0.54:115:67//AQ101557  
 F-HEMBB1002677//Homo sapiens (subclone 3\_d1 from P1 H25) DNA sequence, complete sequence //2.2e-49:  
 784:68//L81774  
 F-HEMBB1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23 //1.0:112:63//U04492  
 5 F-HEMBB1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 Plate=CT 772 Col=12 Row=M, genomic survey sequence //4.4e-07:86:84//B39748  
 F-HEMBB1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 Plate=CT 802 Col=20 Row=L, genomic survey sequence //0.98:183:61//B34077  
 F-HEMBB1002692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING  
 10 DRAFT SEQUENCE //0.00039:408:60//AL033525  
 F-HEMBB1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces //  
 7.3e-35:323:74//AC004955  
 F-HEMBB1002699//Mus musculus D6MM5e protein (D6Mm5e) and DOK protein (Dok) genes, complete cds; and  
 15 LOR2 protein (Lor2) gene, partial cds //0.031:325:62//AF084363  
 F-HEMBB1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic  
 clone Plate=CT 804 Col=2 Row=G, genomic survey sequence //1.8e-25:158:95//B34720  
 F-HEMBB1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding  
 carbonyl reductase and carbonyl reductase 3 (complete cds) //1.7e-137:534:96//AB003151  
 F-HEMBB1002712//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038  
 20 on chromosome X contains ESTs and STS //0.0019:612:58//Z71187  
 F-MAMMA1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3  
 3 unordered pieces //6.1e-43:354:81//AC003117  
 F-MAMMA1000019  
 F-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5) //2.0e-40:185:97//Z47553  
 25 F-MAMMA1000025//Homo sapiens PAC clone DJ0806A17 from 7p13-p14, complete sequence //1.0:211:65//  
 AC005483  
 F-MAMMA1000043//Human angiotensin I-converting enzyme (ACE) gene, intron 12 //0.075:204:65//M73275  
 F-MAMMA1000045//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a  
 30 gene similar to melanoma-associated antigen, EST; GSS and an inverted repeat, complete sequence //4.1e-122:  
 495:79//AL031073  
 F-MAMMA1000055//M.musculus mRNA for testin //2.1e-35:559:66//X78989  
 F-MAMMA1000057//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence //5.5e-121:703:  
 35 89//AC005829  
 F-MAMMA1000069//Homo sapiens minisatellite ceb1 repeat region //0.00013:329:60//AF048727  
 F-MAMMA1000084//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains  
 ESTs STS and CpG island //2.1e-53:445:79//Z93023  
 F-MAMMA1000085//Caenorhabditis elegans cosmid Y23H5A //0.0017:164:64//AF077541  
 F-MAMMA1000092//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence //1.2e-70:598:78//  
 40 AC004744  
 F-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence //1.1e-156:857:92//  
 AC003976  
 F-MAMMA1000117//HS\_3223\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3223 Col=16 Row=H, genomic survey sequence //5.4e-100:527:94//AQ221160  
 F-MAMMA1000129//ryanodine receptor //0.055 :492:59//A20359  
 45 F-MAMMA1000133  
 F-MAMMA1000134//HS\_3078\_B1\_C02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3078 Col=3 Row=F, genomic survey sequence //2.1e-93:462:97//AQ144362  
 F-MAMMA1000139//Homo sapiens Xp22 PAC RPC11-5G11 (from Roswell Park Cancer Center) complete se-  
 quence //3.3e-14:322:65//AC002369  
 50 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds //6.9e-25:148:97//AB014585  
 F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds //1.0e-29:  
 219:87//AF031924  
 F-MAMMA1000163  
 F-MAMMA1000171//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence //6.3e-14:92:88//  
 55 AC005393  
 F-MAMMA1000173//Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human  
 Drebrin //2.2e-114:698:87//U58884  
 F-MAMMA1000175//HS\_3050\_B1\_B03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3050 Col=5 Row=D, genomic survey sequence./.6.2e-73:357:99//AQ102678  
 F-MAMMA1000183//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE./.4.6e-94:904:73//AL023808  
 F-MAMMA1000198//Z.diploperennis repetitive DNA (clone ZEAR 266).//0.18:152:70//X53610  
 5 F-MAMMA1000221//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence./.0.017:99:75//AC004583  
 F-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE./.0.36:312:62//AL031283  
 10 F-MAMMA1000241//HS\_3217\_B1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=3 Row=D, genomic survey sequence./.1.9e-94:456:98//AQ193401  
 F-MAMMA1000251//Homo sapiens NF2 gene./.0.00092:270:64//Y18000  
 F-MAMMA1000254//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces./.0.0034:777:57//AC005140  
 15 F-MAMMA1000257//Homo sapiens DNA sequence from PAC 201D7 on chromosome 6p22.1-22.3. Contains EST and STS./.0.00036:230:65//AL022717  
 F-MAMMA1000264//Homo sapiens (subclone 9\_f5 from P1 H17) DNA sequence, complete sequence./.1.5e-30:499:68//L81612  
 F-MAMMA1000266//Bacillus licheniformis strain pMEL12 Bag320 satellite DNA./.0.28:218:64//AF034430  
 20 F-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence./.1.4e-157:788:96//AF001549  
 F-MAMMA1000277//Mycobacterium tuberculosis H37Rv complete genome; segment 48/162./.0.70:320:61//AL021897  
 F-MAMMA1000278//Sequence 23 from patent US 5708157./.9.3e-103:540:95//I80055  
 25 F-MAMMA1000279//Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, STS, GSS, complete sequence./.2.4e-49:262:77//AL031643  
 F-MAMMA1000284//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence./.1.1e-30:324:75//B03004  
 F-MAMMA1000287//Homo sapiens, clone hRPK.15\_A\_1, complete sequence./.2.7e-54:401:83//AC006213  
 30 F-MAMMA1000302//Drosophila melanogaster complete mitochondrial genome./.0.0051:307:61//U37541  
 F-MAMMA1000307//Homo sapiens chromosome 12p13.3 clone RPCI5-1154L15, WORKING DRAFT SEQUENCE, 67 unordered pieces./.0.15:449:59//AC006205  
 F-MAMMA1000309//cDNA coding human apolipoprotein E3./.0.00010:691:58//E00359  
 F-MAMMA1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 798A17, WORKING DRAFT SEQUENCE./.0.27:301:60//AL031274  
 35 F-MAMMA1000313  
 F-MAMMA1000331//Human Chromosome 16 BAC clone CIT987SK-A-735G6, complete sequence./.9.8e-06:151:71//AC002400  
 F-MAMMA1000339  
 40 F-MAMMA1000340//HS\_2181\_B2\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181 Col=14 Row=L, genomic survey sequence./.4.3e-05:181:68//AQ024288  
 F-MAMMA1000348//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence./.5.3e-30:575:66//AC004139  
 F-MAMMA1000356//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces./.1.8e-52:264:76//AC005052  
 45 F-MAMMA1000360//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence./.6.5e-91:569:88//AC004879  
 F-MAMMA1000361//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat./.1.4e-42:315:83//Z98950  
 50 F-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE./.2.9e-114:516:89//AL022345  
 F-MAMMA1000385//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence./.6.9e-26:377:71//AQ279944  
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds./.3.7e-148:710:98//AB015132  
 55 F-MAMMA1000395  
 F-MAMMA1000402//Homo sapiens clone DJ0718N17, complete sequence./.4.0e-115:845:85//AC005999  
 F-MAMMA1000410//HS\_3245\_A1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=3 Row=E, genomic survey sequence./.9.6e-42:350:80//AQ205768

F-MAMMA1000413//HS\_3223\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=2 Row=L, genomic survey sequence./1.6e-48:318:89//AQ188456  
 F-MAMMA1000414//HS\_2027\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey sequence./1.4e-46:286:92//AQ231369  
 5 F-MAMMA1000416//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence./9.4e-33:310:72//AC004640  
 F-MAMMA1000421//Homo sapiens clone DJ1129D05, complete sequence./3.3e-29:223:84//AC005630  
 F-MAMMA1000422  
 F-MAMMA1000423//Drosophila yakuba mitochondrial DNA molecule./2.2e-10:639:57//X03240  
 10 F-MAMMA1000424//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence./4.6e-47:556:68//AC003973  
 F-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds./8.0e-99:545:92//AF062484  
 F-MAMMA1000431//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces./4.8e-41:289:79//AC005283  
 15 F-MAMMA1000444//Human DNA sequence from clone 714B7 on chromosome 22q12.2-13.2 Contains CYTO-CHROME C OXIDASE VIIb precursor like pseudogene and ESTs, complete sequence./2.3e-34:291:80//Z99755  
 F-MAMMA1000446  
 F-MAMMA1000458//Mus musculus clone OST9003, genomic survey sequence./5.0e-53:231:84//AF046620  
 20 F-MAMMA1000468//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE./0.75:303:60//Z93017  
 F-MAMMA1000472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE./4.0e-41:403:77//AL033543  
 F-MAMMA1000478//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces./9.5e-54:369:77//AC005081  
 25 F-MAMMA1000483//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence./3.6e-34:332:77//AC004381  
 F-MAMMA1000490//Homo sapiens 12q13.1 PAC RPCI1-90J4 (Roswell Park Cancer Institute Human PAC library) complete sequence./8.9e-128:822:87//AC003686  
 30 F-MAMMA1000500//CIT-HSP-231905.TF CIT-HSP Homo sapiens genomic clone 2319O5, genomic survey sequence./4.8e-29:175:94//AQ044812  
 F-MAMMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxyysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence./5.7e-45:334:82//AL022336  
 35 F-MAMMA1000516//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat./2.9e-43:529:69//Z92545  
 F-MAMMA1000522//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence./2.0e-14:380:63//AL022576  
 40 F-MAMMA1000524//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence./1.4e-22:420:66//AC006101  
 F-MAMMA1000559//Human HepG2 3' region cDNA, clone hmd3f08./5.4e-29:168:97//D16922  
 F-MAMMA1000565//RPCI11-61K6.TJRPCI11 Homo sapiens genomic clone R-61K6, genomic survey sequence./1.7e-120:561:100//AQ194238  
 45 F-MAMMA1000567//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island./3.1e-43:387:80//Z81370  
 F-MAMMA1000576//Homo sapiens BAC clone RG442F18 from 2, complete sequence./1.2e-30:237:75//AC005104  
 F-MAMMA1000583//RPCI11-60M22.TJ RPCI11 Homo sapiens genomic clone R-60M22, genomic survey sequence./9.6e-102:487:99//AQ198091  
 50 F-MAMMA1000585//Homo sapiens clone UWGC:djs14 from 7p14-15, complete sequence./5.2e-39:370:78//AC006195  
 F-MAMMA1000594//Homo sapiens chromosome 19, cosmid R31646, complete sequence./3.9e-43:328:83//AC005338  
 55 F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481\_C\_4, complete sequence./1.5e-32:259:82//AC005839  
 F-MAMMA1000605//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE./2.4e-59:318:83//AL031297

F-MAMMA1000612//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence./.4.8e-30:171:96//AQ116793  
 F-MAMMA1000616//HS\_3176\_A1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3176 Col=11 Row=l, genomic survey sequence./.4.7e-28:287:79//AQ300310  
 5 F-MAMMA1000621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING DRAFT SEQUENCE./.0.015:478:58//AL034371  
 F-MAMMA1000623  
 F-MAMMA1000625//DNA encoding Hepatitis C virus antigen./.0.93:196:61//E06898  
 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds./.0.95:365:59//AF023674  
 10 F-MAMMA1000664//HS\_3096\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3096 Col=3 Row=F, genomic survey sequence./.2.7e-51:257:99//AQ145137  
 F-MAMMA1000669//Homo sapiens chromosome 19, cosmid R26908, complete sequence./.2.0e-66:586:67//AC004785  
 15 F-MAMMA1000670//HS\_2243\_B2\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=16 Row=B, genomic survey sequence./.8.7e-05:94:80//AQ153650  
 F-MAMMA1000672//Mus musculus clone OST8270, genomic survey sequence./.3.9e-64:471:81//AF046705  
 F-MAMMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds./.1.2e-07:186:67//U27489  
 20 F-MAMMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2; neurofibromatosis 1 (NF1) exons 28-49; ecotropic viral integration site 2B (EVI2B) exons 1-2; ecotropic viral integration site 2A (EVI2A) exons 1-2; adenylate kinase (AK3) exons 1-2./.3.0e-53:653:70//L05367  
 F-MAMMA1000707//CIT-HSP-2302019.TR CIT-HSP Homo sapiens genomic clone 2302019, genomic survey sequence./.1.8e-08:131:77//AQ017947  
 F-MAMMA1000713//Rattus norvegicus clonal polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats./.0.062:134:67//U00762  
 25 F-MAMMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end./.1.0:266:61//X15028  
 F-MAMMA1000718//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence./.3.6e-05:289:60//B95401  
 F-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence./.4.4e-184:842:98//AC005781  
 30 F-MAMMA1000723//Homo sapiens clone DJ0892G19, complete sequence./.8.8e-05:430:60//AC004917  
 F-MAMMA1000731//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence./.3.8e-55:796:66//AC004274  
 F-MAMMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a./.6.6e-77:555:74//AF064859  
 35 F-MAMMA1000733//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE./.0.98:479:58//AL031749  
 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds./.7.3e-168:802:98//AF100141  
 F-MAMMA1000738//S.cerevisiae chromosome XIV reading frame ORF YNL132w./.8.6e-31:626:63//Z71408  
 F-MAMMA1000744//Gorilla Alu-repetitive sequence in beta-globin gene cluster./.2.7e-54:410:82//X06123  
 40 F-MAMMA1000746//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-10F4, complete sequence./.3.7e-109:779:83//AC004158  
 F-MAMMA1000752//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces./.1.2e-20:444:63//AC005075  
 F-MAMMA1000760//Homo sapiens clone RG015P03, complete sequence./.1.5e-44:403:79//AC005048  
 45 F-MAMMA1000761//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces./.2.3e-22:159:81//AC004166  
 F-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence./.1.3e-51:789:68//AC005703  
 F-MAMMA1000776//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS./.5.7e-40:238:78//Z95116  
 50 F-MAMMA1000778//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE./.7.6e-29:222:84//AL031118  
 F-MAMMA1000782//Human 2,4-dienoyl-CoA reductase gene, exon 9./.0.90:137:62//U94987  
 F-MAMMA1000798//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C124C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces./.0.00058:163:71//AC003656  
 55 F-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence./.6.3e-151:714:99//

AC005339  
F-MAMMA1000824//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-104:503:99//AC005912  
F-MAMMA1000831//Homo sapiens clone UWGC:g1211a139, complete sequence.//0.76:302:58//AC005502  
5 F-MAMMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.//1.9e-54:322:68//AC002456  
F-MAMMA1000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755  
F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817  
10 F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.13:439:59//AC004710  
F-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557  
F-MAMMA1000851//Gallus domesticus filamin gene 5' region, partial cds.//0.86:193:63//U00146  
15 F-MAMMA1000855//Human minisatellite region detected by myoglobin 33-repeat probe, clone lambda 33.10.//0.081:229:62//M30549  
F-MAMMA1000856//B.taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:253:60//Z22747  
F-MAMMA1000859//Sequence 6 from Patent WO9722695.//2.3e-79:533:82//A63553  
F-MAMMA1000862  
20 F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050  
F-MAMMA1000865  
F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2385J8, genomic survey sequence.//0.00017:158:70//AQ240906  
25 F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA repeat, STS, complete sequence.//1.0:121:68//AL022152  
F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185:90//AF015152  
F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75//AL022336  
30 F-MAMMA1000880//Homo sapiens full-length insert cDNA clone ZD54A10.//5.2e-26:143:100//AF086327  
F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801  
F-MAMMA1000897//R.norvegicus mRNA for plasma protein.//4.8e-07:479:58//Y11283  
35 F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, genomic survey sequence.//0.94:115:66//B61433  
F-MAMMA1000906//HS\_3110\_B2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey sequence.//2.5e-63:548:78//AQ182819  
F-MAMMA1000908//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397  
40 F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-09:596:58//AL034560  
F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence.//6.6e-07:249:66//889575  
F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence.//2.9e-43:415:66//AC004917  
45 F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence.//6.1e-44:235:78//B47296  
F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299  
F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.8e-14:175:76//AL031117  
50 F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0082:684:56//AC005308  
F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.//3.3e-30:530:67//AC004643  
F-MAMMA1000957//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//1.3e-72:390:94//AQ155121  
55 F-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-58:318:86//AC006001  
F-MAMMA1000968//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the

TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.4e-18:396:65//AL022394

5 F-MAMMA1000975//Human DNA sequence from clone 344I7 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence.//1.4e-79:690:77//AL024458

F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//0.089:214:66//AC004991

10 F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.1e-58:458:82//AC000114

F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12. Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406

F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.24:166:68//AL022401

15 F-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.6e-103:139:99//AJ011929

F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds.//6.5e-48:465:76//AF070567

20 F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Homo sapiens genomic clone 2501L21, genomic survey sequence.//1.0:175:62//AQ241701

F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:753:6//1AF061444

25 F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence.//7.9e-24:256:76//AC002990

F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 2284N21, genomic survey sequence.//0.96:78:75//AQ000903

30 F-MAMMA1001041//chicken mRNA for alpha-actinin, complete cds.//2.8e-09:355:63//D26597

F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457

F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125

35 F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169

F-MAMMA1001073//HS\_3046\_A2\_G08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420

F-MAMMA1001074//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733

40 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749

F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//2.0e-22:334:69//AC006120

F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155

45 F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087

F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05 :594:60//AC005256

50 F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019

F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045

F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637

55 F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence.//3.3e-21:237:73//AF047825

F-MAMMA1001133//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//0.97:202:63//Z95116

F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//1.6e-84:406:82//S70011  
 F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//1.3e-14:182:76//AL022339  
 F-MAMMA1001145//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038  
 5 on chromosome X contains ESTs and STS.//5.2e-87:714:78//Z71187  
 F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 2341D13 genomic survey sequence.//0.00051:249:61//AQ055735  
 F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//2.2e-30:410:70//AC004518  
 10 F-MAMMA1001162//Homo sapiens full-length insert cDNA clone ZA79C01.//2.4e-13:87:100//AF086123  
 F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds.//9.3e-15:432:60//U31629  
 F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//6.8e-57:670:  
 72//AC005696  
 F-MAMMA1001191  
 15 F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//1.5e-117:759:84//U29156  
 F-MAMMA1001202  
 F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.5e-161:764:98//AC005412  
 20 F-MAMMA1001206//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//5:1e-30:535:65//AC004099  
 F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//8.4e-182:860:  
 98//AC005393  
 F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.7e-58:690:70//AC004875  
 25 F-MAMMA1001222//Mouse loricrin mRNA, complete cds.//2.7e-07:624:58//M34398  
 F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence.//0.91:177:66//AC005726  
 F-MAMMA1001244  
 30 F-MAMMA1001249//Human 28S ribosomal RNA pseudogenes and alu repeat region sequence.//6.7e-09:502:58//U67616  
 F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//5.0e-37:342:80//Z99495  
 F-MAMMA1001259  
 35 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//8.7e-40:659:64//AB014561  
 F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//4.9e-43:265:81//AC004453  
 F-MAMMA1001271//Salmo salar DNA for a cryptic repeat.//2.6e-06:311:63//AJ012206  
 F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
 40 6.6e-70:327:83//AC004840  
 F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-05:276:66//AC003035  
 F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//3.6e-98:199:98//AL022314  
 F-MAMMA1001296//RPCI11-38B4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38B4, genomic survey sequence.//4.7e-33:292:71//AQ030084  
 F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.6e-182:860:  
 45 98//AC005703  
 F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.9e-70:163:97//Z93244  
 F-MAMMA1001322//Human DNA sequence from clone 774I24 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS, complete sequence.//2.6e-19:379:68//AL031290  
 50 F-MAMMA1001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 197L1, WORKING DRAFT SEQUENCE.//4.5e-131:751:90//AL031390  
 F-MAMMA1001330

F-MAMMA1001341//Sus scrofa.//1.6e-36:420:73//Z46906  
 F-MAMMA1001343//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//1.1e-05:818:58//AL031744  
 F-MAMMA1001346  
 5 F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.0e-44:505:74//AC004086  
 F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit a mRNA, complete cds.//1.5e-07:415:58//M86826  
 F-MAMMA1001397//Human DNA sequence from clone 462D8 on chromosome 22q11.21-12.1 Contains EST, STS  
 10 and GSS, complete sequence.//1.6e-23 :209:75//AL022332  
 F-MAMMA1001408//HS\_3242\_A1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=21 Row=O, genomic survey sequence.//2.7e-07:181:69//AQ207300  
 F-MAMMA1001411//Homo sapiens autosomal dominant polycystic kidney disease type II protein (PKD2) gene, exon 14.//0.98:120:68//AF004872  
 15 F-MAMMA1001419//HS\_2053\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=23 Row=L, genomic survey sequence.//1.9e-75 :424:93//AQ244585  
 F-MAMMA1001420//Homo sapiens chromosome 4 clone B203C23 map 4q25, complete sequence.//2.4e-09:199:70//AC004049  
 F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SE-  
 20 QUENCE, 4 unordered pieces.//5.1e-42:558:69//AC004529 F-MAMMA1001442//Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence.//0.0019:516:56//AE001400  
 F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.6e-42:486:70//AC003684  
 F-MAMMA1001452//RPCI11-48022.TJ RPCI11 Homo sapiens genomic clone R-48O22, genomic survey se-  
 25 quence.//5.3e-87:423:98//AQ199294  
 F-MAMMA1001465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//0.00038:114:75//AL033543  
 F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//4.1e-99:604:87//L31783  
 F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.  
 30 //1.0e-13:158:77//AC005486  
 F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17).//9.6e-52:438:81//X04366  
 F-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B7, WORKING DRAFT SEQUENCE.//3.7e-152:720:99//AL031714  
 35 F-MAMMA1001510//Human PAC clone DJ438O4 from 22q12.1-qter, complete sequence.//1.1e-05:371:61//AC002378  
 F-MAMMA1001522  
 F-MAMMA1001547  
 F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.3e-128:614:98//AB007931  
 40 F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//0.97:154:68//AF001548  
 F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//1.8e-95:529:91//M61764  
 F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin  
 45 heavy chain gene, EST, CA repeat, STS, GSS, complete sequence.//1.8e-07:104:84//Z98949  
 F-MAMMA1001600//HS\_3022\_A2\_H01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=2 Row=O, genomic survey sequence.//1.6e-66:405:90//AQ163791  
 F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA re-  
 peat, Ninenin like sequence, complete sequence.//0.00043:715:58//AL008626  
 F-MAMMA1001606//jd114 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 2G6,  
 50 genomic survey sequence.//0.19:266:62//B13685  
 F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds.//9.7e-54:442:69//AF053630  
 F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNasel-hypersensitive site.//0.14:221:62//M29833  
 F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2  
 55 ordered pieces.//2.0e-47:611:71//AC005412  
 F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds.//1.1e-42:611:67//U57796  
 F-MAMMA1001635//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//4.0e-35:407:70//AC000118

F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.44:245:63//AL022577  
 5 F-MAMMA1001654//Mouse transcriptional control element.//0.0025:189:63//M17284  
 F-MAMMA1001663//CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 2165E16, genomic survey sequence.//9.7e-05:146:66//B95491  
 F-MAMMA1001670//HS\_3136\_A1\_G06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence.//3.1e-28:237:85//AQ148779  
 10 F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614  
 F-MAMMA1001679//HS\_3054\_A1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=O, genomic survey sequence.//1.0:89:70//AQ106118  
 15 F-MAMMA1001683//Spermatozopsis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970  
 F-MAMMA1001686//HS\_3219\_B1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence.//0.00072:180:65//AQ180345  
 F-MAMMA1001692//HS\_3047\_B1\_B10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228  
 20 F-MAMMA1001711//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-42:316:82//AC004845  
 F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 2347A14, genomic survey sequence.//1.1e-60:413:87//AQ059125  
 F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//1.8e-133:646:97//AF095687  
 25 F-MAMMA1001735//chicken brain tubulin beta chain mRNA.//3.5e-110:740:84//J00913  
 F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS.//0.98:416:57//Z72001  
 F-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence.//3.2e-16:194:75//AC006017  
 30 F-MAMMA1001744//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//0.0036:181:66//AL030998  
 F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//1.2e-60:822:68//AF070718  
 35 F-MAMMA1001751//Human potassium channel KCNO1 mRNA, complete cds.//1.2e-35:583:65//U90065  
 F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//8.4e-102:627:87//AF041338  
 F-MAMMA1001757//HS\_2058\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=8 Row=F, genomic survey sequence.//1.7e-24:173:88//AQ243865  
 40 F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//6.6e-76:349:87//AL022722  
 F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.23:633:57//M97514  
 F-MAMMA1001768//Bovine herpesvirus 1 complete genome.//2.3e-11:547:60//AJ004801  
 50 F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-76:509:78//AC004801  
 F-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.7e-106:744:82//X85991  
 F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence.//6.0e-20:228:75//AC002563  
 F-MAMMA1001785  
 F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs and GSSs, complete sequence.//5.0e-05:152:74//Z99129  
 55 F-MAMMA1001790//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//4.5e-53:318:80//AC005845

F-MAMMA1001806//Homo sapiens chromosome 19, cosmid R29368, complete sequence./.1.0:131:67//  
 AC004262  
 F-MAMMA1001812//Human Chromosome X clone bWXD187, complete sequence./.3.0e-34:257:83//AC004383  
 F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 from 7q21.2-q22, complete sequence./.5.2e-61:516:  
 79//AC004128  
 F-MAMMA1001817//Homo sapiens 12q24 PAC RPCI1-261P5 (Roswell Park Cancer Institute Human PAC library)  
 complete sequence./.3.1e-32:295:78//AC004031  
 F-MAMMA1001818//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete  
 sequence bases 1.333303./.0.71:179:67//AJ011930  
 F-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene./.3.0e-91:726:79//Y13148  
 F-MAMMA1001824//HS\_3108\_A1\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3108 Col=23 Row=M, genomic survey sequence./.3.4e-05:119:74//AQ107508  
 F-MAMMA1001836//Homo sapiens chromosome 18, clone hRPK.537\_E\_1, complete sequence./.3.4e-45:312:  
 85//AC006211  
 F-MAMMA1001837//Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds./.4.5e-51:480:75//  
 AF052042  
 F-MAMMA1001848//CITBI-E1-2516P17.TF CITBI-E1 Homo sapiens genomic clone 2516P17, genomic survey  
 sequence./.1.0e-100:486:98//AQ279620  
 F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmids R30072 and R28588, ge-  
 nomic sequence, complete sequence./.5.1e-07:197:67//AC002390  
 F-MAMMA1001854  
 F-MAMMA1001858//RPCI11-11L22.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11L22, genomic survey  
 sequence./.0.091:161:65//B75631  
 F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence./.2.6e-09:397:61//AC003013  
 F-MAMMA1001868//HS\_2196\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2196 Col=24 Row=B, genomic survey sequence./.5.8e-13:86:100//AQ032455  
 F-MAMMA1001874//H.sapiens CpG island DNA genomic Mse1 fragment, clone 63h5, reverse read cpg63h5.rtla./.  
 1.0:127:63//Z62129  
 F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-  
 sequences (GSSs)./.1.7e-19:372:67//Z94802  
 F-MAMMA1001880//RPCI11-90K3.TJ RPCI11 Homo sapiens genomic clone R-90K3, genomic survey sequence./.  
 6.6e-11:362:62//AQ283465  
 F-MAMMA1001890//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING  
 DRAFT SEQUENCE./.1.8e-45:317:86//AL021707  
 F-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING  
 DRAFT SEQUENCE./.2.7e-23:255:77//Z82207  
 F-MAMMA1001908//HS\_2225\_A1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2225 Col=5 Row=A, genomic survey sequence./.5.4e-08:264:62//AQ301597  
 F-MAMMA1001931//HS\_3049\_B2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3049 Col=18 Row=H, genomic survey sequence./.1.7e-47:295:90//AQ100157  
 F-MAMMA1001956//H.sapiens DNA sequence./.0.056:233:66//Z22493  
 F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds./.0.99:173:68//AF106656  
 F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chro-  
 mosome X contains ESTs glycerol kinase pseudogene./.5.3e-63:479:78//Z73986  
 F-MAMMA1001970//Homo Sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence./.1.4e-126:699:  
 93//AC003071  
 F-MAMMA1001992//HS\_3078\_A1\_A09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3078 Col=17 Row=A, genomic survey sequence./.3.3e-08:257:65//AQ143646  
 F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214\_O\_I, complete sequence./.1.5e-07:244:  
 62//AC005224  
 F-MAMMA1002011//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3252 Col=9 Row=D, genomic survey sequence./.1.3e-07:170:69//AQ304711  
 F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered piec-  
 es./.2.1e-34:315:79//AC004803  
 F-MAMMA1002033//HS\_3023\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3023 Col=8 Row=M, genomic survey sequence./.4.3e-69:366:94//AQ105493  
 F-MAMMA1002041//Genomic sequence from Human 9q34, complete sequence./.5.3e-85:439:82//AC001227  
 F-MAMMA1002042//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence./.1.4e-20:314:70//

AC005669  
F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPCII1-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence./.6.8e-14:526:62//AC005906

5 F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiuinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence./1.1e-47:648:71//AL030996

10 F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence./2.4e-19:256:74//AC004869

F-MAMMA1002068//Homo sapiens, clone hRPK.2\_A\_1, complete sequence./5.4e-41:407:78//AC006197

F-MAMMA1002078//Human DNA sequence from PAC 106I20 on chromosome 22q12 Contains ESTs and STS, complete sequence./0.021:333:64//Z81313

15 F-MAMMA1002082  
F-MAMMA1002084//Caenorhabditis elegans cosmid F28C12, complete sequence./0.032:469:58//Z93380

F-MAMMA1002093//HS\_3050\_B1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey sequence./1.0:77:71//AQ105997

F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR./8.3e-10:464:60//AF017308

20 F-MAMMA1002118  
F-MAMMA1002125//Homo sapiens chromosome 17, clone HCIT217L10, complete sequence./1.0e-35:619:68//AC003962

F-MAMMA1002132//RPCI11-78F11.TJ RPCI11 Homo sapiens genomic clone R-78F11, genomic survey sequence./1.0e-90:357:97//AQ286460

25 F-MAMMA1002140//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence./1.6e-45:583:64//AC004216

F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds./6.0e-11:192:70//M88338

F-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE./0.0028:570:59//AL021391

30 F-MAMMA1002153//HS\_3005\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=7 Row=G, genomic survey sequence./4.9e-41:213:99//AQ132213

F-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE./1.2e-45:303:78//AL031431

F-MAMMA1002156

35 F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo sapiens genomic clone 2508P18, genomic survey sequence./7.1e-42:255:92//AQ266165

F-MAMMA1002170//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence./2.0e-81:604:81//AC004448

40 F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence./3.2e-43:333:83//AC004212

F-MAMMA1002198//H.sapiens thiol-specific antioxidant protein mRNA./1.0e-34:121:98//Z22548

F-MAMMA1002209//HS\_2197\_B1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey sequence./9.6e-18:163:84//AQ210058

45 F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR./6.3e-08:435:60//AF017308

F-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds./1.8e-124:752:87//AF032667

F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unorderd pieces./0.67:356:59//AC004710

50 F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds./9.3e-140:836:87//U38253

F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence./1.4e-145:691:98//AC005666

F-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence./6.0e-138:660:98//AC005600

55 F-MAMMA1002267//Homo sapiens chromosome 2, P1 clone 777H5 (LBNL H27), complete sequence./0.066:333:60//AC003676

F-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds./1.1e-39:404:74//AF068748

F-MAMMA1002269//HS\_3163\_B1\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3163 Col=5 Row=H, genomic survey sequence //1.0:150:63//AQ171576  
 F-MAMMA1002282//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence //1.5e-22:315:  
 67//AC003108  
 F-MAMMA1002292//B.garinii (strain TIs1) p83/100 gene (partial) //0.73:200:64//X81533  
 5 F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces //  
 1.6e-56:408:75//AC006023  
 F-MAMMA1002294//Sequence 2 from Patent WO9516779 //1.8e-06:401:62//A45258  
 F-MAMMA1002297  
 F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence //0.0056:  
 10 525:61//AC004221  
 F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 2345B2, genomic survey se-  
 quence //1.2e-90:446:98//AQ053994  
 F-MAMMA1002308//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING  
 15 DRAFT SEQUENCE //1.3e-35:329:78//AL031680  
 F-MAMMA1002310//Human gastric (H<sup>+</sup> + K<sup>+</sup>)-ATPase gene, complete cds //0.0060:301:60//J05451  
 F-MAMMA1002311//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syn-  
 drome region, WORKING DRAFT SEQUENCE, 3 unordered pieces //8.6e-50:327:69//AC004737  
 F-MAMMA1002312//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and  
 20 STS //1.3e-09:741:58//Z86064  
 F-MAMMA1002317  
 F-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence //1.9e-158:746:99//  
 AC005756  
 F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence //5.3e-52:  
 25 617:70//AC004796  
 F-MAMMA1002329//Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete cds //0.22:143:67//  
 U93871  
 F-MAMMA1002332//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING  
 30 DRAFT SEQUENCE //1.6e-31:287:74//AL034402  
 F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162 //2.5e-09:674:59//  
 AL022022  
 F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases  
 35 1.41604 //2.1e-57:522:77//AJ011932  
 F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence //2.0e-14:258:69//  
 AC004129  
 F-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORK-  
 40 ING DRAFT SEQUENCE //7.8e-132:723:91//AL022100  
 F-MAMMA1002352//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 128O3, WORKING  
 DRAFT SEQUENCE //5.8e-17:326:70//Z98742  
 F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces //  
 45 1.1e-14:399:63//AC004825  
 F-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 109G6, WORKING  
 DRAFT SEQUENCE //3.7e-43:420:75//AL023879  
 F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
 50 DRAFT SEQUENCE, 8 unordered pieces //0.0022:534:59//AC004153  
 F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC  
 Library) complete sequence //5.3e-18:156:75//AC005831  
 F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome  
 4p16.3, contains EST //4.9e-43:353:69//Z68885  
 F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs  
 55 and a GSS, complete sequence //1.8e-22:282:74//AL008719  
 F-MAMMA1002362//Platemys spixii CR1-like LINE, partial sequence //0.00058:83:79//D82938  
 F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey se-  
 quence //4.4e-10:85:92//AQ196889  
 F-MAMMA1002384//RPCI11-80J20.TV RPCI11 Homo sapiens genomic clone R-80J20, genomic survey se-  
 quence //2.7e-56:286:98//AQ284134  
 F-MAMMA1002385//CIT-HSP-2328G13.TF CIT-HSP Homo sapiens genomic clone 2328G13, genomic survey se-  
 quence //5.5e-46:335:84//AQ043985  
 F-MAMMA1002392//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence //8.5e-29:273:78//

AC004888  
F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//8.2e-09:287:63//AL023 875

5 F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var1) gene, complete cds.//9.6e-08:730:57//L40608

F-MAMMA1002417//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.1e-06:181:72//AL034402

F-MAMMA1002427//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//1.3e-51:593:72//AC004604

10 F-MAMMA1002428  
F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.3e-56:388:81//Z93023

F-MAMMA1002446//CIT-HSP-2324O22.TR CIT-HSP Homo sapiens genomic clone 2324O22, genomic survey sequence.//2.3e-56:302:95//AQ027479

15 F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.1e-54:190:94//AC005229

F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds.//0.00045:457:60//U14005

F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//9.7e-33:709:60//U10556

20 F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.092:506:58//AC004671

F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2-unordered pieces.//0.025:100:76//AC005077

25 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.9e-118:560:98//AF055460

F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.5e-22:297:73//AC005913

F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//7.2e-10:330:64//AC002477

30 F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon.//0.0080:124:72//L49359

F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.4e-160:775:97//AF065214

F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74\_E\_22 complete sequence.//1.9e-41:345:80//AC005696

35 F-MAMMA1002554  
F-MAMMA1002556  
F-MAMMA1002566

F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 2296N17, genomic survey sequence.//1.7e-07:76:90//AQ006579

40 F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GAA C27.//2.7e-08:195:70//AB018507

F-MAMMA1002585  
F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence.//2.1e-26:361:69//AC005019

45 F-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING DRAFT SEQUENCE.//1.3e-34:550:69//AL034548

F-MAMMA1002598//H.sapiens mRNA for ribosomal protein L7.//1.1e-21:123:100//X57958

F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//0.0018:358:61//AC005220

50 F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//2.1e-13:336:63//AC004861

F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.14:229:64//AC005486

F-MAMMA1002618  
F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.5e-71:319:85//AJ010598

55 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds.//1.5e-20:157:90//AF041449

F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//8.3e-06:137:72//AE000660

F-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING

DRAFT SEQUENCE//1.9e-171:819:98//AL031727  
 F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence//4.8e-85:478:78//AC003093  
 F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds//5.6e-09:499:62//U10063  
 F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds//3.6e-115:785:82//AF055666  
 5 F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence//1.5e-45:291:90//  
 AC002038  
 F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds//6.6e-06:661:  
 59//L41919  
 F-MAMMA1002655//HS\_2003\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 10 nomic clone Plate=2003 Col=22 Row=A, genomic survey sequence//9.0e-15:198:74//AQ224233  
 F-MAMMA1002662  
 F-MAMMA1002665//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence//1.4e-37:235:84//  
 AC005029  
 F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds//0.00027:272:64//U22398  
 15 F-MAMMA1002673  
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//3.7e-161:752:99//D86987  
 F-MAMMA1002685//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 394I7, WORKING  
 DRAFT SEQUENCE//6.2e-45:510:70//AL023585  
 F-MAMMA1002698//HS\_3024\_B1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 20 nomic clone Plate=3024 Col=11 Row=F, genomic survey sequence//1.7e-10:155:75//AQ072214  
 F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds//5.9e-75:509:83//  
 AF018261  
 F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds//1.2e-159:749:99//AB011399  
 F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of  
 25 the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence//3.0e-57:347:79//AL031053  
 F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence//3.4e-31:484:69//  
 AC005030  
 F-MAMMA1002721//CIT-HSP-2350M5.TR CIT-HSP Homo sapiens genomic clone 2350M5, genomic survey se-  
 quence//1.4e-06:265:63//AQ061245  
 30 F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2  
 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene.  
 Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence//0.18:386:58//AL023584  
 F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-  
 35 aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/  
 fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS//3.2e-05:362:63//Z83821  
 F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence//0.00010:  
 535:58//AE001368  
 F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence//1.2e-182:880:  
 97//AC005856  
 40 F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human  
 PAC Library) complete sequence//2.7e-175:829:98//AC006055  
 F-MAMMA1002754//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered  
 pieces//3.1e-31:372:75//AC004676  
 F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//3.3e-26:151:98//AB007902  
 45 F-MAMMA1002764//Human Chromosome 11 Cosmid cSR166a1, complete sequence//5.2e-49:355:81//U73636  
 F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20A22, genomic survey  
 sequence//6.7e-13:155:76//B92153  
 F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey se-  
 quence//9.7e-21:151:90//AQ028244  
 50 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene,  
 complete cds//5.6e-105:179:99//U07561  
 F-MAMMA1002780//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-08, com-  
 plete sequence//0.071:277:58//Z98546  
 F-MAMMA1002782//HS\_3213\_B2\_B08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 55 nomic clone Plate=3213 Col=16 Row=D; genomic survey sequence//0.00018:219:63//AQ175845  
 F-MAMMA1002796  
 F-MAMMA1002807//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; com-  
 plete sequence//6.9e-22:332:69//AC002404

F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-11:483:62//AC003035  
 F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//1.0e-64:320:83//AC002553  
 5 F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//2.8e-47:413:80//AC004875  
 F-MAMMA1002835  
 F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence.//1.1e-39:164:83//B14462  
 10 F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//1.9e-62:373:81//U58883  
 F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds.//1.7e-135:635:99//AB018353  
 F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic survey sequence.//6.7e-17:383:66//B11616  
 F-MAMMA1002858  
 15 F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9, genomic survey sequence.//8.3e-81:392:99//AQ081566  
 F-MAMMA1002869//Sequence 1 from patent US 5552529.//2.2e-86:696:78//I25863  
 F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds.//0.029:370:59//L12388  
 20 F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-23M23, genomic survey sequence.//1.8e-20:271:74//B86518  
 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds.//1.2e-28:680:61//D45027  
 F-MAMMA1002886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380A1, WORKING DRAFT SEQUENCE.//0.00040:505:57//Z97653  
 25 F-MAMMA1002887//HS\_3238\_B2\_G08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence.//5.5e-79:401:97//AQ219814  
 F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes.//4.6e-35:136:73//AF109906  
 F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence.//5.7e-14:450:60//AC004096  
 30 F-MAMMA1002895//H.sapiens CpG island DNA genomic Mse1 fragment, clone 46b6, forward read cpg46b6.ft1a.//3.7e-36:190:100//Z58616  
 F-MAMMA1002908//Penaeus monodon microsatellite locus Pmo27.//1.1e-05:195:62//AF068828  
 F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence.//1.0e-13:457:61//AC002402  
 35 F-MAMMA1002930//Homo sapiens Xp22 BAC GS HB-512P14 (Genome Systems Human BAC library) complete sequence.//0.25:260:62//AC004467  
 F-MAMMA1002937//H.sapiens ZNF74-1 mRNA.//6.3e-13:577:59//X71623  
 F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds.//5.1e-193:910:98//AB014598  
 F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence.//2.7e-23:174:77//AC004032  
 40 F-MAMMA1002947//Rhodobacter capsulatus strain SB1003, partial genome.//1.3e-09:475:61//AF010496  
 F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5.//0.0029:314:60//AF019366  
 F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//4.0e-10:194:71//Z94056  
 45 F-MAMMA1002972//H.sapiens CpG island DNA genomic Mse1 fragment, clone 2g10, forward read cpg2g10.ft1aa.//0.38:156:66//Z55272  
 F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//2.9e-41:234:79//AC005919  
 F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//1.7e-05:322:  
 50 63//AL022098  
 F-MAMMA1002987//CITBI-E1-2514J12.TR CITBI-E1 Homo sapiens genomic clone 2514J12, genomic survey sequence.//0.0064:135:66//AQ275871  
 F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-145D12, genomic survey sequence.//2.8e-31:201:89//B01998  
 55 F-MAMMA1003004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y237C10, WORKING DRAFT SEQUENCE.//1.6e-10:180:73//AL031601  
 F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleotide repeat polymorphism at the D11S488 locus.//3.5e-12:435:61//L04732

F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds./.2.3e-50:734:67//U79139  
 F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence./.1.2e-86:341:79//  
 AC003694  
 5 F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence./.2.6e-  
 13:443:61//AC003661  
 F-MAMMA1003019//HS\_3221\_A1\_A01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3221 Col=1 Row=A, genomic survey sequence./.2.8e-51:299:92//AQ184271  
 F-MAMMA1003026  
 10 F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence./.  
 0.0037:134:73//AC005214  
 F-MAMMA1003035//RPCI11-11P4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey se-  
 quence./.1.1e-07:66:100//B74936  
 F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence./.2.1e-19:220:76//AC004671  
 15 F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36.2. Contains ESTs, poly-  
 morphic CA repeat, tRNA and endogenous retrovirus./.9.5e-91:469:78//Z98257  
 F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS,  
 complete sequence./.0.21:289:61//AL031321  
 F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds./.1.7e-  
 20 139:663:98//AF077952  
 F-MAMMA1003049  
 F-MAMMA1003055//HS\_3014\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3014 Col=20 Row=L, genomic survey sequence./.4.2e-05:215:64//AQ164940  
 25 F-MAMMA1003056//HS\_3221\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3221 Col=24 Row=H, genomic survey sequence./.1.4e-16:206:74//AQ302772  
 F-MAMMA1003057//M.domesticus MD6 mRNA./.8.5e-128:654:94//X54352  
 F-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING  
 DRAFT SEQUENCE./.1.0:142:71//AL034371  
 F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence./.1.7e-42:  
 30 373:78//AC004796  
 F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds./.2.6e-42:288:88//AF042166  
 F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds./.1.6e-12:  
 477:64//U72634  
 F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds./.3.4e-121:789:  
 35 85//AF071316  
 F-MAMMA1003127//R.norvegicus MYR1 mRNA for myosin I heavy chain./.9.4e-58:423:83//X68199  
 F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds./.0.62:  
 676:58//U67916  
 F-MAMMA1003140  
 40 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein./.2.2e-80:397:97//Y15062  
 F-MAMMA1003150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING  
 DRAFT SEQUENCE./.7.3e-123:266:88//AL021579  
 F-MAMMA1003166//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING  
 DRAFT SEQUENCE./.1.6e-33:143:82//Z99716  
 45 F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs,  
 complete sequence./.0.50:216:61//Z95400  
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds./.4.8e-65:385:92//D31886  
 F-NT2RM1000032  
 F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating protein (SCAP) mRNA, complete cds./.6.3e-  
 50 135:565:84//U67060  
 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds./.1.1 e-106:542:95//AB014590  
 F-NT2RM1000039//Mouse genetic suppressor element mRNA./.0.080:239:60//L27155  
 F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds./.8.4e-96:535:91//D87671  
 F-NT2RM1000059//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING  
 55 DRAFT SEQUENCE./.1.0:257:59//AL031600  
 F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene, partial cds./.0.54:306:63//U37520  
 F-NT2RM1000080//Sequence 2 from patent US 5763589./.1.5e-115:566:97//AR012692  
 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds./.1.8e-114:550:97//AB014561

F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequence./.0.63:180:65//AC005594  
 5 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds./.0.027:126:70//AF007155  
 F-NT2RM1000119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING  
 DRAFT SEQUENCE./.0.022:644:58//Z97630  
 F-NT2RM1000127//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence./.1.6e-45:254:94//AQ195884  
 F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds./.5.5e-153:778:95//AB018335  
 10 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds./.1.1e-90:448:97//AF044959  
 F-NT2RM1000153//Human Nott linking clone 924A081D, genomic survey sequence./.5.9e-07:66:96//U49890  
 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds./.0.025:126:70//AF007155  
 F-NT2RM1000187//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence./.1.1e-05:56:98//AQ261184  
 15 F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds./.1.6e-38:711:65//D64009  
 F-NT2RM1000242  
 F-NT2RM1000244//HS\_2229\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2229 Col=7 Row=E, genomic survey sequence./.2.0e-13:95:95//AQ298474  
 20 F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206\_C\_20, complete sequence./.0.023:225:61//AC006070  
 F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence./.8.5e-24:473:64//Z68336  
 F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds./.6.4e-69:455:85//AF035940  
 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds./.6.5e-57:460:80//D50920  
 25 F-NT2RM1000271  
 F-NT2RM1000272  
 F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRNA, complete cds./.6.7e-97:430:92//U11927  
 F-NT2RM1000300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING  
 30 DRAFT SEQUENCE./.2.1e-96:170:100//Z93097  
 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds./.8.1e-127:708:92//D63880  
 F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cds./.5.7e-34:182:99//D79205  
 F-NT2RM1000341//Homo sapiens full-length insert cDNA clone YP11F06./.1.3e-100:504:97//AF085879  
 35 F-NT2RM1000354//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence./.1.6e-11:201:73//AQ218494  
 F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds./.1.8e-77:578:82//U76253  
 F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces./.9.4e-113:367:97//AC004821  
 F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4./.6.1e-14:362:62//Y08302  
 40 F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, complete cds./.1.0:482:58//U26679  
 F-NT2RM1000394//M.musculus mRNA for histone H3.3A./.1.7e-94:549:89//Z85979  
 F-NT2RM1000399  
 F-NT2RM1000421//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence./.3.6e-08:195:72//AQ032737  
 45 F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds./.3.7e-84:418:97//AF084928  
 F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds./.1.3e-35:525:69//D79989  
 F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence./.4.6e-73:533:83//AC004993  
 50 F-NT2RM1000553  
 F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA./.2.3e-110:555:97//AF070542  
 F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces./.1.3e-123:477:100//AC004873  
 55 F-NT2RM1000623//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence./.8.2e-06:75:89//AQ032737  
 F-NT2RM1000648//Halobium cutirubrum L11, L1, L10 and L12 equivalent ribosomal protein gene cluster./.1.3e-06:414:61//X15078  
 F-NT2RM1000661//Homo sapiens cap-binding protein 4EHP mRNA, complete cds./.9.3e-54:275:97//AF047695

F-NT2RM1000666//HS\_2016\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey sequence././/5.7e-13:199:73//AQ227865  
5 F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence././/2.7e-94:499:94//AL031133  
F-NT2RM1000672  
F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds././/2.2e-119:582:98//AB015348  
F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence././/0.95:284:61//AL032627  
10 F-NT2RM1000702//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence././/0.073:290:58//AQ089514  
F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase././/4.8e-65:435:85//AJ004832  
F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds././/8.0e-126:690:92//AB011139  
15 F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds././/2.5e-66:524:83//AF027208  
F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303././/0.92:395:58//AJ011930  
F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds././/2.1e-70:  
407:92//L39210  
F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces././/  
20 6.6e-36:98:93//AC000380  
F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4././/9.3e-22:  
126:99//X52233  
F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
DRAFT SEQUENCE, 8 unordered pieces././/7.1e-09:540:59//AC004153  
25 F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein././/4.0e-81:497:88//Z97207  
F-NT2RM1000802  
F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds././/3.7e-63:490:84//AF027208  
F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA././/7.2e-153:749:96//AF070542  
30 F-NT2RM1000829//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence././/0.74:215:67//AQ099134  
F-NT2RM1000833//Canis familiaris sec61 homologue mRNA, complete cds././/5.1e-114:683:88//M96629  
F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic survey sequence././/1.1e-26:279:74//  
AL018762  
F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial././/9.3e-148:726:97//AJ010840  
35 F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exon 2././/0.97:124:65//AB008378  
F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone NRLA143D././/1.2e-31:172:98//K95834  
F-NT2RM1000874//Homo sapiens KE05 protein mRNA, complete cds././/2.8e-131:632:97//AF064605  
F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence././/1.2e-98:214:99//AC004228  
40 F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds././/2.7e-156:762:97//  
AF082516  
F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds././/2.0e-17:310:67//AB014561  
F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds././/  
3.2e-95:469:83//U58280  
45 F-NT2RM1000898  
F-NT2RM1000905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING  
DRAFT SEQUENCE././/1.8e-74:188:98//Z97630  
F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces././/5.7e-  
148:601:98//AC004873  
50 F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces././/  
0.071:392:60//AC004846  
F-NT2RM1000962//H.sapiens CpG island DNA genomic Mse1 fragment, clone 140d1, forward read  
cpg140d1.ft1a././/4.1e-35:187:99//Z56803  
F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 or-  
55 dered pieces././/1.1e-23:266:77//AC005959  
F-NT2RM1001003//Homo sapiens alpha-catenin-like protein mRNA, complete cds././/4.0e-160:760:98//U97067  
F-NT2RM1001008//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds././/1.7e-  
11:602:61//U52064

F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//3.9e-93:645:86//Z95125  
 5 F-NT2RM1001044//S.pombe chromosome III cosmid c320.//0.90:128:66//AL022245  
 F-NT2RM1001059//Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.//3.8e-53:  
 261:80//AC005915  
 F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey se-  
 quence.//0.64:285:59//B94391  
 F-NT2RM1001072//HS\_3115\_B1\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 10 nomic clone Plate=3115 Col=13 Row=H, genomic survey sequence.//7.3e-23:140:95//AQ147905  
 F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence.//5.0e-50:186:98//  
 AC005263  
 F-NT2RM1001082//Sequence 1 from Patent WO9718303.//2.1e-144:736:95//A62731  
 F-NT2RM1001085//CIT-HSP-2310F21.TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey se-  
 quence.//8.8e-45:235:97//AQ020757  
 15 F-NT2RM1001092//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489  
 F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964  
 F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5'UTR).//0.0014:349:61//Z95973  
 F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//  
 20 AC004678  
 F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//  
 AF024624  
 F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//  
 AC004755  
 25 F-NT2RM2000006//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING  
 DRAFT SEQUENCE.//5.3e-150:724:98//AL031291  
 F-NT2RM2000013//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:  
 749:69//X58826  
 F-NT2RM2000030//Homo sapiens clone DJ0708P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//  
 30 2.1e-97:270:77//AC004863  
 F-NT2RM2000032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
 DRAFT SEQUENCE.//1.9e-25:172:76//AL034379  
 F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DXS6791 and DXS8038 on  
 35 chromosome X contains ESTs.//5.0e-05:325:65//Z73418  
 F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:  
 117:68//L12269  
 F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-  
 RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//  
 40 0.38:312:62//AF109905  
 F-NT2RM2000101  
 F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mRNA, complete cds.//3.8e-58:297:  
 97//M12303  
 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:  
 98//AF067224  
 45 F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey se-  
 quence.//2.2e-33:191:95//B93289  
 F-NT2RM2000239//F rubripes GSS sequence, clone 156P04aG12, genomic survey sequence.//8.9e-44:445:69//  
 AL018549  
 50 F-nnnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//  
 AF075292  
 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162  
 F-NT2RM2000259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING  
 DRAFT SEQUENCE.//0.0013:305:63//AL031658  
 F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//  
 55 AF073934  
 F-NT2RM2000287//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones  
 A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Se-  
 quencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SE-

QUENCE, 50 unordered pieces.//1.3e-11:96:86//AC003656  
 F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864

5 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132  
 F-NT2RM2000363//RPCI11-90B10.TJ RPCI11 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300  
 F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//1.2e-94:599:86//U48251

10 F-NT2RM2000371//RPCI11-57I4.TJ RPCI11 Homo sapiens genomic clone R-57I4, genomic survey sequence.//1.1e-52:312:91//AQ083343  
 F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:196:91//X70514  
 F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.99:345:58//AE001274

15 F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973  
 F-NT2RM2000407//Mus musculus semaphorin Vla mRNA, complete cds.//1.4e-131:439:88//AF030430  
 F-NT2RM2000420//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204  
 F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022

20 F-NT2RM2000452//HS\_3009\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794  
 F-NT2RM2000469//HS\_2019\_A1\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041  
 F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.5e-15:386:63//AB018290

25 F-NT2RM2000502  
 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//5.1e-171:824:97//AF061243  
 F-NT2RM2000522  
 F-NT2RM2000540  
 F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC004466

30 F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132  
 F-NT2RM2000567//Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.//3.0e-06:664:58//AF083252  
 F-NT2RM2000569//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681

35 F-NT2RM2000577//RPCI11-43G22.TJ RPCI11 Homo sapiens genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391  
 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987  
 F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC004466

40 F-NT2RM2000594//Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626  
 F-NT2RM2000599//O.sativa osr40g3 gene.//0.30:585:56//Y08988  
 F-NT2RM2000609  
 F-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776  
 F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952

45 F-NT2RM2000624  
 2.9e-06:231:64//Z82061  
 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272  
 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558  
 F-NT2RM2000639//RPCI11-69E5.TJ RPCI11 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491  
 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576

55 F-NT2RM2000669  
 F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.1e-106:748:82//AC002038  
 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:64//D86984

F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594:98//AB015342  
 F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244  
 F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815:89//U25691  
 F-NT2RM2000795//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING  
 5 DRAFT SEQUENCE.//1.0e-78:723:76//AL021392  
 F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228  
 F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.//1.1e-05:361:62//  
 AC005017  
 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//8.7e-184:847:99//AB015046  
 10 F-NT2RM2000952  
 F-NT2RM2000984//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-  
 RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//  
 7.6e-41:239:76//AF109905  
 F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 2333N18, genomic survey se-  
 15 quence.//1.1e-11:298:66//AQ035862  
 F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120:627:91//U21855  
 F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//6.8e-118:690:88//  
 AF071314  
 F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.3e-  
 20 145:614:99//AC004873  
 F-NT2RM2001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING  
 DRAFT SEQUENCE.//2.7e-95:461:99//AL034380  
 F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//7.2e-  
 24:726:62//U52064  
 25 F-NT2RM2001141  
 F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the  
 CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase com-  
 ponent A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, com-  
 plete sequence.//0.98:300:62//AL022401  
 30 F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//  
 1.2e-147:741:96//AC005488  
 F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial  
 cds.//0.026:408:59//U66829  
 35 F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-  
 135:627:98//AC004987  
 F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700  
 F-NT2RM2001221//Chimpanzee (P.paniscus) involucrin, complete cds.//0.53:670:55//M26514  
 F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M65150  
 F-NT2RM2001243  
 40 F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey  
 sequence.//0.0011:274:59//AQ276184  
 F-NT2RM2001256//M.musculus mRNA for 200 kD protein.//2.3e-129:742:90//X80169  
 F-NT2RM2001291//CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey se-  
 quence.//4.6e-09:156:72//B57734  
 45 F-NT2RM2001306//RPCI11-2815.TP RPCI-11 Homo sapiens genomic clone RPCI-11-2815, genomic survey se-  
 quence.//0.069:234:64//B84850  
 F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.1e-22:111:  
 81//AC005919  
 F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340:58//AE001118  
 50 F-NT2RM2001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 209H1, WORKING  
 DRAFT SEQUENCE.//3.7e-44:340:85//Z84465  
 F-NT2RM2001345//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:290:58//AQ089514  
 F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-60:365:87//  
 55 U56429  
 F-NT2RM2001370//Homo sapiens PAC clone DJ0815D20 from 7p11-p13, complete sequence.//0.98:415:58//  
 AC004899  
 F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2-GGT Region, complete

sequence.//4.0e-54:394:75//AC004033  
 F-NT2RM2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033520  
 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1e-96:453:99//AJ007509  
 5 F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.//7.1e-91:601:83//AB000113  
 F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete sequence.//0.81:200:69//AC005624  
 10 F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2.//3.8e-16:316:65//Z99708  
 F-NT2RM2001544  
 F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//3.3e-24:318:67//AL032657  
 F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//2.1e-26:582:64//M34551  
 15 F-NT2RM2001582//M.musculus red-1 gene.//1.4e-102:581:90//X92750  
 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65//AB007902  
 F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:736:90//AF032667  
 F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431  
 20 F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//8.6e-118:779:85//M96630  
 F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//1.5e-50:561:71//AC004691  
 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//9.2e-153:740:98//AB014518  
 F-NT2RM2001637//F.rubripes GSS sequence, clone 155D22bD8, genomic survey sequence.//2.5e-13:224:64//Z91020  
 25 F-NT2RM2001641//CIT-HSP-2347F23.TF CIT-HSP Homo sapiens genomic clone 2347F23, genomic survey sequence.//1.3e-67:340:98//AQ060913  
 F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds.//1.4e-110:459:89//M96629  
 F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.2e-153:807:93//AF023451  
 30 F-NT2RM2001659//nbxb0002cE07f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002J13f, genomic survey sequence.//1.0:485:56//AQ051653  
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//3.7e-172:802:99//AF044195  
 F-NT2RM2001668  
 35 F-NT2RM2001670//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.2e-18:279:70//AJ003147  
 F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA; complete cds.//1.6e-137:683:94//U21157  
 40 F-NT2RM2001675//RPCI11-51J16.TJ RPCI11 Homo sapiens genomic clone R-51J16, genomic survey sequence.//1.0:394:58//AQ053677  
 F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAI project).//0.87:220:61//AL021890  
 F-NT2RM2001688//B.parapertussis bvg locus (transcription regulators of virulence factors) with bvgA and bvgS genes.//1.0:286:62//X52948  
 45 F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 345H13, genomic survey sequence.//3.2e-53:241:82//B59854  
 F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, clone Mu2.//1.2e-05:306:58//M10668  
 50 F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//6.0e-06:548:59//AL021920  
 F-NT2RM2001699//HS\_3195\_8B2\_DO1\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3195 Col=2 Row=H, genomic survey sequence.//2.7e-07:322:61//AQ189056  
 55 F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.//7.8e-05:354:58//Z95556  
 F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//7.5e-42:335:81//AC004469  
 F-NT2RM2001716

F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//4.2e-08:536:58//AC004290  
 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence.//1.4e-26:163:95//AF052123  
 F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//6.2e-111:530:98//AB007931  
 5 F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPCI704E14135Q2.//3.1e-102:248:95//AJ010598  
 F-NT2RM2001743  
 F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.11:138:66//Z68117  
 F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cds.//9.4e100:418:88//M96629  
 10 F-NT2RM2001768//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993  
 F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.3e-66:680:72//AC006116  
 F-NT2RM2001782  
 F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb).//0.027:384:60//Z48053  
 15 F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770  
 F-NT2RM2001797//HS\_3045\_AT\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 Col=1 Row=G, genomic survey sequence.//1.4e-74:381:97//AQ129456  
 F-NT2RM2001800  
 20 F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.3e-178:827:99//AF044195  
 F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR.//1.0:290:58//AF053126  
 F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//3.3e-16:109:95//B89870  
 25 F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//5.8e-62:819:68//AC004274  
 F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//3.6e-131:738:90//AF013759  
 F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.1e-57:422:79//  
 30 AC002347  
 F-NT2RM2001855//HS\_3224\_A1\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3224 Col=13 Row=O, genomic survey sequence.//0.00012:68:91//AQ205285  
 F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the  
 35 gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.068:102:70//AL031177  
 F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between markers DXS366 and DXS87 on chromosome X.//0.0029:500:59//Z68328  
 40 F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//1.9e-187:866:97//AB014610  
 F-NT2RM2001896//S.cerevisiae chromosome III complete DNA sequence.//8.6e-30:613:63//X59720  
 F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.9e-176:859:97//AB007931  
 F-NT2RM2001930//M.musculus mRNA for semaphorin G.//4.7e-117:730:85//X97818  
 F-NT2RM2001935//Sequence 11 from Patent WO9610637.//1.0:356:60//A50028  
 45 F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence.//6.9e-138:653:98//AF091080  
 F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700  
 F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.//  
 50 0.42:179:65//AC005825  
 F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//3.8e-20:123:98//  
 AF089816  
 F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR004981  
 F-NT2RM2001997//Human HepG2 partial cDNA, clone hmd1b08m5.//9.6e-25:160:95//D16955  
 F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding  
 55 carbonyl reductase and carbonyl reductase 3 (complete cds).//0.88:380:60//AB003151  
 F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//AC002407  
 F-NT2RM2002014  
 F-NT2RM2002030//Mus musculus glutamine:fructose-6-phosphate amidotransferase mRNA, complete cds.//

1.5e-89:822:74//U00932  
F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M26132  
F-NT2RM2002055  
5 F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421:63//  
AF073936  
F-NT2RM2002091//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING  
DRAFT SEQUENCE.//4.6e-160:771:98//AL034380  
F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776:98//AJ010840  
F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//  
10 2.4e-143:684:98//AF030435  
F-NT2RM2002128//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete  
cds.//7.0e-27:330:73//U13152  
F-NT2RM2002142//Danio rerio gastrulation specific (G12) mRNA, complete cds.//6.3e-10:135:80//U27121  
F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//4.2e-143:800:  
15 92//AF084928  
F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds.//5.2e-164:787:97//AB007936  
F-NT2RM2002580//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//7.4e-  
13:337:62//AC004423  
F-NT2RM4000024//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.2e-62:  
20 801:70//X58826  
F-NT2RM4000027//Caenorhabditis elegans cosmid F09E5.//0.36:336:60//U37429  
F-NT2RM4000030//H.sapiens CpG island DNA genomic Mse1 fragment, clone 56h10, forward read  
cpg56h10.ft1a.//9.3e-22:127:100//Z55685  
F-NT2RM4000046//Curcurbita maxima 25S - 18S rDNA intergenic spacer.//4.1e-05:386:60//X13059  
25 F-NT2RM4000061  
F-NT2RM4000085//B.taurus mRNA for nuclear DNA helicase II.//1.9e-10:485:59//X82829  
F-NT2RM4000086  
F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds.//  
4.2e-23:345:69//AF060865  
30 F-NT2RM4000139//R.norvegicus trg mRNA.//1.4e-56:708:69//X68101  
F-NT2RM4000155//CIT-HSP-2282N15.TR CIT-HSP Homo sapiens genomic clone 2282N15, genomic survey se-  
quence.//3.0e-09:88:90//AQ000070  
F-NT2RM4000156//H.sapiens HPBRII-7 gene.//2.0e-21:586:60//X67336  
F-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.7e-143:810:  
35 90//D12646  
F-NT2RM4000169//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746:57//AC004157  
F-NT2RM4000191//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:  
60//AF051726  
40 F-NT2RM4000197  
F-NT2RM4000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING  
DRAFT SEQUENCE.//0.67:461:60//AL031667  
F-NT2RM4000200  
F-NT2RM4000202//H.sapiens CpG island DNA genomic Mse1 fragment, clone 34c2, forward read cpg34c2.ft1a.//  
45 1.7e-27:190:90//Z65361  
F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//1.4e-182:856:98//AB018255  
F-NT2RM4000215//S.cerevisiae MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:  
62//J03852  
F-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//  
50 4.6e-102:233:94//AC005383  
F-NT2RM4000233//Mus musculus semaphorin VIa mRNA, complete cds.//1.6e-135:835:86//AF030430  
F-NT2RM4000244//RPCI11-24P15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P15, genomic survey  
sequence.//5.5e-08:422:62//B86757  
F-NT2RM4000251//Mus musculus clone UWGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete  
55 sequence.//0.98:207:60//AC005855  
F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PAC clone pDJ1081b4 containing human mRNA for T-  
cell glycoprotein CD6, complete sequence.//5.2e-41:707:65//AC003689  
F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//7.9e-153:609:93//

M99438  
 F-NT2RM4000324  
 F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds./.3.9e-44:727:68//AF022085  
 5 F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds./.1.0e-143:801:90//AF090430  
 F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence./.6.1e-80:503:86//AF046700  
 F-NT2RM4000354//HS\_2221\_A2\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence./.1.0e-20:180:83//AQ253449  
 10 F-NT2RM4000356  
 F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds./.1.6e-133:628:99//AB014542  
 F-NT2RM4000368//RPCI11-91B5.TJ RPCI11 Homo sapiens genomic clone R-91B5, genomic survey sequence./.5.0e-12:431:61//AQ283217  
 F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, complete cds./.7.4e-86:845:72//AF059485  
 15 F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 9965./.2.5e-34:767:61//D44597  
 F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds./.1.5e-15:114:94//AB015046  
 F-NT2RM4000421  
 F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence./.1.5e-37:295:82//AC005921  
 20 F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds./.3.9e-94:740:78//AF062476  
 F-NT2RM4000457//CIT-HSP-2346B17.TR CIT-HSP Homo sapiens genomic clone 2346B17, genomic survey sequence./.1.5e-22:149:92//AQ062111  
 F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial./.1.3e-76:386:97//AJ010952  
 25 F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A, /./1.1e-22:356:67//AB000459  
 F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence./.0.53:198:70//AC005908  
 F-NT2RM4000511  
 F-NT2RM4000514  
 30 F-NT2RM4000515//CIT-HSP-2285L3.TR CIT-HSP Homo sapiens genomic clone 2285L3, genomic survey sequence./.0.0012:200:66//AQ000113  
 F-NT2RM4000520  
 F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds./.2.9e-31:732:64//M58297  
 F-NT2RM4000532//HS\_3231\_B1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence./.1.3e-59:362:90//AQ192093  
 35 F-NT2RM4000534  
 F-NT2RM4000585//CITBI-E1-2508I18.TR CITBI-E1 Homo sapiens genomic clone 2508I18, genomic survey sequence./.1.1e-34:208:93//AQ260706  
 F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence./.8.3e-34:180:99//AQ004125  
 40 F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence./.1.2e-09:203:66//AC005288  
 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds./.5.3e-14:305:68//AB002390  
 F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence./.8.4e-16:109:94//B89870  
 F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase./.2.3e-59:721:68//Z46786  
 F-NT2RM4000674  
 F-NT2RM4000689//CIT-HSP-2381O13.TF CIT-HSP Homo sapiens genomic clone 2381O13, genomic survey sequence./.2.6e-31:174:97//AQ110303  
 50 F-NT2RM4000698  
 F-NT2RM4000700  
 F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds./.1.1e-89:744:77//AF022789  
 F-NT2RM4000717  
 55 F-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE./.2.1e-140:299:99//AL034379  
 F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds./.3.8e-158:743:98//AB018303  
 F-NT2RM4000741

F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism./.7.1e-95:754:  
77//M99593

5 F-NT2RM4000764  
F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12./.0.30:523:60//AF078790

F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds./.5.5e-172:810:98//AB007920

10 F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 22q12-qter. contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCRFS1) exon, ESTs, STS, CA repeat and CpG island./.0.0057:163:69//Z82206

F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence./.6.9e-39:237:94//  
AC005306

F-NT2RM4000795//Rattus norvegicus neuroligin 3 mRNA, complete cds./.5.9e-97:857:74//U41663

15 F-NT2RM4000796//HS\_3214\_B1\_F11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence./.1.1e-14:254:68//AQ175988

F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds./.6.2e-  
78:816:72//AF023451

F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds./.0.33:276:63//M63109

F-NT2RM4000820//, complete sequence./.2.6e-142:450:97//AC005406

20 F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence./.1.9e-52:  
501:71//AC004373

F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence./.1.0:477:56//  
AC005940

F-NT2RM4000852  
F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete sequence./.3.4e-29:229:83//  
AC003957

25 F-NT2RM4000887  
F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete  
cds./.2.1e-20:407:64//AB011004

F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces./.0.  
41:311:64//AC004929

30 F-NT2RM4000971//RPCI11-53H3.TJ RPCI11 Homo sapiens genomic clone R-53H3, genomic survey sequence./.1.  
0:208:64//AQ053735

F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence./.1.3e-19:207:  
78//AC005245

35 F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone 2506B10, genomic survey se-  
quence./.1.4e-73:361:98//AQ263651

F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds./.5.1e-170:803:98//AB018272

F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds./.3.3e-125:584:99//AB014539

40 F-NT2RM4001032//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds./.0.00034:777:58//U47276

F-NT2RM4001047//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858

F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds./.3.1e-102:859:76//M96629

45 F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey se-  
quence./.4.6e-78:379:99//AQ044479

F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone  
cSRL-71b1, genomic survey sequence./.1.1e-12:152:75//B05776

F-NT2RM4001116  
F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence./.1.9e-136:717:93//  
AC004593

50 F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-  
ORF2, oleC-ORF3, oleC-ORF4, and oleC-PRF5) genes, complete cds; 3427 base-pairs./.0.0083:368:60//L06249

F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds./.3.9e-120:764:85//U04706

F-NT2RM4001160  
F-NT2RM4001187

F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey se-  
quence./.6.2e-12:181:72//B53378

55 F-NT2RM4001200//H.sapiens HZF10 mRNA for zinc finger protein./.1.3e-66:799:69//X78933

F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds./.4.2e-152:707:99//  
AF004828

F-NT2RM4001204

F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds.//1.6e-62:715:  
70//AF005381

F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884

5 F-NT2RM4001258//HS\_3171\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3171 Col=18 Row=N, genomic survey sequence.//2.5e-18:215:77//AQ149676

F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl  
pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//4.9e-28:526:  
66//AL022163

10 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-77:474:89//Z46973

F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11./.1.2e-16:230:73//U97002

F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e-41:642:66//D89016

F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence  
recovered from 5' end of P element, genomic survey sequence.//0.0040:141:68//AQ025127

15 F-NT2RM4001344//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORK-  
ING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388

F-NT2RM4001347

F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//  
0.10:400:61//AC004786

20 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799

F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs,  
STSs and GSSs and genomic marker D22S56, complete sequence.//0.99:255:59//AL021393

F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SE-  
QUENCE.//0.027:336:58//AP000023

25 F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, com-  
plete cds.//5.9e-124:783:85//AF020526

F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:  
71//AF050183

F-NT2RM4001414//Homo sapiens full-length insert cDNA clone ZE16C11./.9.1e-76:363:100//AF086563

30 F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-  
47:623:69//AC004226

F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala  
ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein  
FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and iso-  
leucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901

35 F-NT2RM4001454

F-NT2RM4001455

F-NT2RM4001483//Human zinc finger protein ZNF136./.3.2e-36:329:78//U09367

F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//1.2e-155:724:99//AB014585

40 F-NT2RM4001519//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
DRAFT SEQUENCE, 4 unordered pieces.//0.00019:418:59//AC004688

F-NT2RM4001522//Human HepG2 3' region MboI cDNA, clone hmd6a08m3.//1.4e-16:130:88//D17274

F-NT2RM4001557

F-NT2RM4001565

F-NT2RM4001566

45 F-NT2RM4001569//HS\_2050\_B1\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2050 Col=15 Row=F, genomic survey sequence.//2.7e-09:109:84//AQ234720

F-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.2e-127:740:89//  
AF071317

F-NT2RM4001592//M.musculus mRNA of enhancer-trap-locus 1.//7.3e-117:710:88//X69942

50 F-NT2RM4001594//Homo sapiens chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered  
pieces.//0.34:388:59//AC002355

F-NT2RM4001597//M.musculus red-1 gene.//6.2e-139:788:90//X92750

F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//3.3e-162:750:99//AB018334

55 F-NT2RM4001611//Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592.//2.5e-05:490:58//  
D90910

F-NT2RM4001629//Mus musculus palmytoylated protein p55 mRNA, complete cds.//0.65:186:64//U38196

F-NT2RM4001650//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0435P12;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.99:422:59//AC004689

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds./.2.6e-81:449:93//AB002320  
 F-NT2RM4001666  
 F-NT2RM4001682//Mus musculus clone OST9187, genomic survey sequence./.3.2e-35:240:87//AF046699  
 F-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING  
 5 DRAFT SEQUENCE./.1.9e-151:564:97//AL031447  
 F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds./.7.0e-85:748:74//D86957  
 F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,  
 complete sequence./.1.2e-91:488:94//AL034430  
 F-NT2RM4001731//Orang-utan in volucrin gene, complete cds./.0.40:530:59//M25312  
 10 F-NT2RM4001741//Mouse mRNA for talin./.1.1e-129:737:90//X56123  
 F-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING  
 DRAFT SEQUENCE./.2.3e-49:320:89//AL031709  
 F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence./.6.3e-64:379:76//AC005831  
 15 F-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1./.3.7e-146:871:87//Z83868  
 F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds./.2.3e-173:803:99//AB018270  
 F-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence./.2.0e-165:593:99//AC006017  
 F-NT2RM4001810  
 20 F-NT2RM4001813//Homo sapiens BAC clone NH0364H22 from 2, complete sequence./.7.1e-31:176:84//  
 AC005036  
 F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds./.  
 4.4e-34:195:95//M37712  
 F-NT2RM4001823//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds./.3.3e-51:490:75//U49046  
 F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds./.5.6e-74:688:  
 25 72//U28687  
 F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete se-  
 quence./.1.0:406:60//AC000076  
 F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alternatively spliced isoform 2,  
 complete cds./.1.6e-131:831:86//AF033275  
 30 F-NT2RM4001842//HS\_3163\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3163 Col=20 Row=M, genomic survey sequence./.1.5e-05:355:60//AQ168513  
 F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11./.4.0e-23:823:60//U70855  
 F-NT2RM4001858//Notophthalmus viridescens NvTbox1 mRNA, partial cds./.6.4e-11:266:66//U64433  
 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC./.6.9e-149:704:98//Y17711  
 35 F-NT2RM4001876//F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence./.5.7e-48:600:68//  
 Z88651  
 F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sapiens genomic clone 2348J1, genomic survey se-  
 quence./.0.0025:61:88//AQ060809  
 F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region./.2.5e-29:535:67//X98335  
 40 F-NT2RM4001922//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2237 Col=19 Row=E, genomic survey sequence./.2.2e-73:364:98//AQ033732  
 F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence./.  
 4.9e-10:269:63//AB005248  
 F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence./.7.6e-152:311:  
 45 100//AC005207  
 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds./.1.1e-170:808:98//AF098162  
 F-NT2RM4001953///\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces./.2.7e-45:310:86//AC004046  
 F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
 50 non-small cell lung cancer, segment 11/11./.1.6e-107:622:90//AB020868  
 F-NT2RM4001969//R.norvegicus mRNA for IP63 protein./.3.9e-24:221:76//X99330  
 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds./.1.0e-61:527:76//AB018341  
 F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X./.5.8e-07:  
 502:60//Z82253  
 55 F-NT2RM4001987//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey se-  
 quence./.2.6e-33:177:99//AQ051701  
 F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence./.0.019:65:90//  
 AC005921

F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence.//1.0:527:57//L15344  
 F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glycan-3  
 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712  
 F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//  
 5 U01882  
 F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-  
 44:473:76//AC005283  
 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540  
 F-NT2RM4002062//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORK-  
 10 ING DRAFT SEQUENCE, 8 unordered pieces.//0.0031:298:59//AC005122  
 F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//1.1e-147:705:98//  
 U82267  
 F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:69//D83783  
 F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//1.1e-  
 15 53:295:76//AC005216  
 F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//7.8e-25:277:75//AF072758  
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.0e-23:588:61//  
 AF059569  
 F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1.//3.1e-68:544:69//X60789  
 20 F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.0e-121:762:  
 86//D12646  
 F-NT2RM4002128//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312  
 F-NT2RM4002140  
 25 F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//1.8e-49:736:65//  
 AC004152  
 F-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.5e-70:454:85//AF035940  
 F-NT2RM4002161//Homo sapiens mRNA for LAFPTPase, isoform 1, partial.//4.2e-151:763:96//AJ130763  
 F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete genome.//2.1e-16:580:60//  
 30 AE000540  
 F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains  
 ESTs.//1.0e-07:792:61//AL008636  
 F-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//3.2e-132:782:87//AF030430  
 F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//  
 35 1.5e-40:292: 84//L14684  
 F-NT2RM4002213  
 F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U67160  
 F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//1.0:428:58//  
 AC004448  
 40 F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-  
 60:294:81//AB005959  
 F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006I18aG12, genomic survey sequence.//3.3e-12:217:  
 67//AL024779  
 F-NT2RM4002278//HS\_3089\_A1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 45 nomic clone Plate=3089 Col=9 Row=I, genomic survey sequence.//1.9e-64:381:92//AQ121653  
 F-NT2RM4002281  
 F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey se-  
 quence.//9.0e-49:336:86//AQ042515  
 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457  
 50 F-NT2RM4002301//Human Notl linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881  
 F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-  
 gene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and  
 D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822  
 F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865  
 55 F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64849  
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//2.8e-149:708:98//AB014549  
 F-NT2RM4002374//Homo sapiens 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC  
 library) complete sequence.//0.00040:312:63//AC002978

F-NT2RM4002383//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE./.6.8e-29:378:66//AL031284

5 F-NT2RM4002390

F-NT2RM4002398//CIT-HSP-2288N22.TR CIT-HSP Homo sapiens genomic clone 2288N22, genomic survey sequence./.3.4e-35:184:100//AQ001110

10 F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome./.2.0e-16:468:59//AE001092

F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence./.1.6e-16:123:91//U89336

15 F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands./.9.6e-64:467:84//Z92845

F-NT2RM4002452

F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence./.2.2e-24:201:86//Z85988

20 F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence./.1.3e-45:487:70//AC004690

F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds./.2.7e-163:777:98//AF083255

25 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds./.2.3e-93:464:97//AB014591

F-NT2RM4002493

F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces./.3.5e-41:442:75//AC005484

30 F-NT2RM4002504//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence./.3.8e-31:233:87//AL031577

F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence./.7.7e-08:274:62//AL027162

F-NT2RM4002532

F-NT2RM4002534

35 F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds./.3.8e-53:394:81//AF072759

F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds./.6.4e-160:902:89//AF022962

F-NT2RM4002567//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence./.8.5e-31:220:88//AQ263402

40 F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 mRNA, complete cds./.5.2e-05:199:65//AF049344

F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence./.0.89:275:61//AC004875

F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence./.3.7e-44:768:64//AC005454

45 F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces./.7.8e-34:574:65//AC005122

F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds./.3.9e-111:582:95//AB013385

F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//1.1e-153:747:96//AJ012449

50 F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE./.1.6e-125:243:88//AP000047

F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence./.9.6e-09:414:59//Z92784

F-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12./.2.8e-183:548:91//X98834

F-NT2RP1000101//H.sapiens CpG island DNA genomic Mse1 fragment, clone 28b4, forward read cpg28b4.ft1a./.6.0e-27:163:95//Z60555

55 F-NT2RP1000111//CIT-HSP-2307O14.TR CIT-HSP Homo sapiens genomic clone 2307O14, genomic survey sequence./.1.2e-11:128:81//AQ016069

F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds./.1.0e-38:324:81//M86699

F-NT2RP1000124//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE./.0.59:476:59//AL034557

F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor./.2.7e-35:535:681//E08546

F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds./.6.7e-05:77:90//AF011792

F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces./.

1.9e-20:431:64//AC006030  
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence././/2.5e-138:679:97//AF070535  
 F-NT2RP1000191  
 F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds././/5.3e-05:220:61//  
 5 D89496  
 F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence././/4.7e-51:  
 508:69//AC004373  
 F-NT2RP1000259  
 F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA, complete cds././/7.8e-142:866:  
 10 88//AF042383  
 F-NT2RP1000324//RPCI11-81O21.TJ RPCI11 Homo sapiens genomic clone R-81O21, genomic survey se-  
 quence././/2.8e-29:182:92//AQ285136  
 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, com-  
 plete cds././/4.2e-147:693:98//AF053551  
 15 F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence././/1.4e-08:281:61//Z75525  
 F-NT2RP1000348//H.sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpg12f1.rt1c././/  
 1.7e-09:71:100//Z56610  
 F-NT2RP1000357  
 F-NT2RP1000358 5.7e-16:403:61//AC005456  
 20 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds././/9.8e-125:497:86//AB014538  
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds././/1.8e-176:877:  
 96//AF064594  
 F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp././/4.6e-106:700:84//AJ001558  
 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds././/9.4e-178:710:98//AB011159  
 25 F-NT2RP1000416  
 F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds././/1.0:198:60//L40178  
 F-NT2RP1000439//HS\_2182\_A1\_D06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2182 Col=11 Row=G, genomic survey sequence././/2.1e-68:441:87//AQ024305  
 F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SE-  
 30 QUENCE././/3.8e-57:185:88//AP000047  
 F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence././/2.7e-132:204:99//  
 AC004453  
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete se-  
 quence././/4.9e-80:196:95//AC002985  
 35 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds././/1.9e-55:440:80//U47634  
 F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a  
 Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloro-  
 plast 30S ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691  
 and STSs././/2.6e-92:562:88//Z99297  
 40 F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds././/2.0e-130:622:98//D87686  
 F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes, complete cds's././/0.11:360:  
 58//M81648  
 F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces././/4.9e-  
 34:209:93//AC004895  
 45 F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds././/1.2e-  
 08:331:63//U26264  
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds././/4.4e-81:295:92//  
 AF017418  
 F-NT2RP1000577//HS\_2228\_B2\_C05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 50 nomic clone Plate=2228 Col=10 Row=F, genomic survey sequence././/1.9e-31:179:75//AQ185128  
 F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds././/4.7e-34:223:90//U31620  
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene,  
 complete sequence././/1.6e-18:229:65//AC004770  
 F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds././/9.3e-89:584:84//M62419  
 55 F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete se-  
 quence././/1.0:203:63//Z85989  
 F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence././/0.0034:350:61//  
 AC005943

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F-NT2RP1000688//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//5.2e-10:120:80//X69907  
F-NT2RP1000695  
F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//I30536  
F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-  
5 19:188:81//AC004932  
F-NT2RP1000730  
F-NT2RP1000733//Human chromosome 16p13-1 BAC clone CIT987SK-551G9 complete sequence.//1.3e-30:  
315:75//U95742  
F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete  
10 cds.//8.0e-122:604:96//AF101434  
F-NT2RP1000746//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//1.5e-83:466:92//AQ186344  
F-NT2RP1000767//Homo sapiens full-length insert cDNA clone ZD81B04.//2.8e-21:144:91//AF086442  
F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//  
15 AF054840  
F-NT2RP1000796//T.thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//M71213  
F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown  
gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic  
marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244  
20 F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:  
424:96//AF048837  
F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//  
AF047020  
F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.41. Contains the  
25 HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE  
pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs,  
complete sequence.//8.7e-169:842:96//AL022398  
F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//3.3e-15:196:76//  
U96629  
30 F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence.//1.6e-144:724:96//AC004812  
F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//  
AF054840  
F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//6.7e-106:551:95//AF064094  
F-NT2RP1000902//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING  
35 DRAFT SEQUENCE.//0.0097:55:100//Z82199  
F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R).//1.3e-30:174:97//Z94761  
F-NT2RP1000916  
F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon.//0.19:103:72//L49362  
F-NT2RP1000944//HS\_2179\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
40 nomic clone Plate=2179 Col=24 Row=F, genomic survey sequence.//0.032:140:63//AQ065269  
F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//3.7e-53:461:78//  
U62483  
F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
clone cSRL-143G4, genomic survey sequence.//0.030:89:78//B01950  
45 F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence.//3.9e-11:445:61//Z49068  
F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.3e-57:326:92//AC004263  
F-NT2RP1000966//Human nucleolin gene, complete cds.//3.4e-64:197:981/M60858  
F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sapiens genomic clone 2314B10, genomic survey se-  
quence.//0.32:137:68//AQ017126  
50 F-NT2RP1000988//Human chromosome 3p21.1 gene sequence.//8.0e-72:665:80//L13435  
F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene,  
partial cds.//1.3e-31:497:65//U34925  
F-NT2RP1001013//HS\_3068\_B1\_809\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3068 Col=17 Row=D, genomic survey sequence.//1.0e-24:414:66//AQ127667  
55 F-NT2RP1001014//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//0.00052:83:81//AQ304711  
F-NT2RP1001033//Homo sapiens chromosome 17, clone hRPC-1073\_F\_15, complete sequence.//1.3e-134:241:  
99//AC004686

F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence./.2.5e-59:451:83//AC004993  
 F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds./.4.5e-93:476:96//U82267  
 5 F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces./.6.6e-54:217:89//AC004938  
 F-NT2RP1001113  
 F-NT2RP1001173  
 F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds./.8.1e-26:373:681/U79139  
 10 F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces./.3.5e-32:388:73//AC006039  
 F-NT2RP1001199  
 F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1./.2.0e-29:166:96//AF081508  
 F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence./.7.3e-50:128 :  
 15 99//AC002036  
 F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds./.4-3e-91:344:93//AF029914  
 F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's-/0.54:292:63//L44140  
 F-NT2RP1001294  
 20 F-NT2RP1001302  
 F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor./.1.5e-07:335:64//X15750  
 F-NT2RP1001311//RPCI11-67O14.TK RPCI11 Homo sapiens genomic clone R-67O14, genomic survey se-  
 quence./.0.26:80:75//AQ239291  
 F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin  
 25 heavy chain (FTH), complete sequence./.8.8e-75:304:98//AC004228  
 F-NT2RP1001361//B.taurus CI-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647  
 F-NT2RP1001385  
 F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds./.1.4e-72:535:83//  
 AF071316  
 30 F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cy-  
 tochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14  
 subunit, ESTs, CA repeat, STS, GSS./.5.8e-105:570:94//AL021878  
 F-NT2RP1001424  
 35 F-NT2RP1001432  
 F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence./.1.7e-84:422:97//AF052149  
 F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds./.1.3e-47:471:73//AF069737  
 F-NT2RP1001466//HS\_3006\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=3006 Col=16 Row=G, genomic survey sequence./.0.56:289:60//AQ154336  
 F-NT2RP1001475//H.sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375  
 F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds./.1/4-0e-87:563:85//L11316  
 F-NT2RP1001494  
 F-NT2RP10015431//Drosophila melanogaster DNA sequence (P1 DS01142 (D148)), complete sequence./.1.9e-  
 45 27:387:67//AC004280  
 F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds./.8.0e-63:314:98//  
 AF054840  
 F-NT2RP1001569//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds./.1.2e-  
 68:514:81//U17343  
 F-NT2RP100T616//Human clone 23665 mRNA sequence./.7.6e-40:496:74//U90913  
 50 F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 2059N5, genomic survey se-  
 quence./.2.4e-45:305:88//B69912  
 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence./.1.5e-135:685:96//AF091081  
 F-NT2RP2000006//HS\_3061\_B2\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 55 nomic clone Plate=3061 Col=6 Row=F, genomic survey sequence./.1.9e-17:394:67//AQ178856  
 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds./.3.5e-14:241:68//AB002390  
 F-NT2RP2000008//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING  
 DRAFT SEQUENCE./.1.7e-34:147:99//AL034424  
 F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence./.1.4e-32:345:75//

AC005066  
 F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic survey sequence.//5.0e-41:445:72//  
 Z88655  
 F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.9e-76:383:97//AB018290  
 5 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//  
 2.4e-95:467:97//AF061749  
 F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 2328J24, genomic survey se-  
 quence.//3.3e-39:236:91//AQ043092  
 F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds.//3.2e-50:311:90//D78610  
 10 F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:766:66//AF059485  
 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//2.0e-118:  
 597:95//AC005754  
 F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017:423:60//AC006037  
 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//2.1e-77:278:97//  
 15 AF050079  
 F-NT2RP2000079//H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k.//  
 3.2e-33:197:95//Z55440  
 F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:98//AB018338  
 F-NT2RP2000091//HS\_2228\_A2\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 20 nomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:55:90//AQ146363  
 F-NT2RP2000097  
 F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.5e-  
 05:482:60//AC004961  
 F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-22:274:69//  
 25 AC003973  
 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//4.9e-114:551:97//AB018356  
 F-NT2RP2000120//HS\_3000\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365  
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//4.2e-119:  
 30 607:96//AF054177  
 F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//  
 AC004827  
 F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419  
 F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP  
 35 (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs,  
 complete sequence.//0.45:377:58//AL034370  
 F-NT2RP2000157//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library)  
 complete sequence.//4.0e-73:317:87//AC005924  
 F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey se-  
 40 quence.//3.0e-14:123:90//AQ263431  
 F-NT2RP2000173  
 F-NT2RP2000175  
 F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-06:152:66//  
 AL007295  
 45 F-NT2RP2000195//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative  
 unknown genes, ESTs, STSs and GSSs, complete sequence.//7.6e-62:170:99//AL023581  
 F-NT2RP2000205  
 F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmids R29828 and F25496, complete se-  
 quence.//7.2e-80:170:90//AC003030  
 50 F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//5.5e-  
 64:400:85//AC004382  
 F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-  
 SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-  
 55 3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island,  
 ESTs and STSs.//2.2e-07:280:66//Z97632  
 F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//8.8e-  
 30:508:67//U88401  
 F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.0e-79:504:

87//AC004066  
 F-NT2RP2000248  
 F-NT2RP2000257//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORKING DRAFT SEQUENCE//0.0078:286:60//AL021388  
 5 F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey sequence//5.7e-82:416:97//AQ059184  
 F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence//4.5e-29:310:73//AC006116  
 F-NT2RP2000274  
 10 F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor//6.3e-20:260:73//X74904  
 F-NT2RP2000288  
 F-NT2RP2000289  
 F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and - 9//4.6e-69:744:70//M27877  
 15 F-NT2RP2000298//*Streptomyces coelicolor* cosmid 2E9//4.4e-05:502:59//AL021530  
 F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces//2.1e-13:173:76//AC006082  
 F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence//8.3e-144:731:95//AL022398  
 20 F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence//1.9e-102:555:90//AL034430  
 F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds//6.4e-105:639:87//M25757  
 25 F-NT2RP2000337//HS\_2060\_B1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2060 Col=1 Row=J, genomic survey sequence//0.78:218:60//AQ243333  
 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//3.6e-129:627:97//U83981  
 F-NT2RP2000369//HS\_2182\_B1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=21 Row=D, genomic survey sequence//2.5e-87:421:99//AQ024835  
 30 F-NT2RP2000412//Human DNA sequence from PAC 124O9 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs//0.72:170:65//AL021327  
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//5.0e-66:375:93//L28010  
 F-NT2RP2000420//Homo sapiens full-length insert cDNA YQ86E07//9.2e-77:423:93//AF075093  
 35 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//2.1e-126:609:96//AF102265  
 F-NT2RP2000438//CITBI-E1-2519O19.TR CITBI-E1 Homo sapiens genomic clone 2519O19, genomic survey sequence//0.96:61:78//AQ276878  
 F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence//7.1e-17:341:67//AC004691  
 40 F-NT2RP2000459//H.sapiens mRNA for imogen 38//5.7e-21:158:87//Z68747  
 F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs//3.2e-11:160:73//Z92844  
 F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence//0.0031:187:66//AC005229  
 45 F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence//8.8e-07:179:64//AL026277  
 F-NT2RP2000516//*Mus musculus* t complex testis-specific protein (Tctex2) gene, wild type, promoter sequence//0.19:72:81//U21671  
 50 F-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE//5.0e-115:570:96//AL022318  
 F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds//8.4e-37:196:98//AB005543  
 F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence//0.81:354:60//AC005321  
 55 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//1.3e-149:732:97//AB014514  
 F-NT2RP2000644//HS\_3211\_A1\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211 Col=11 Row=K, genomic survey sequence//3.6e-42:282:86//AQ175486  
 F-NT2RP2000656

F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence./0.57:141:66//AQ278386  
 F-NT2RP2000668  
 F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces./  
 5 4.3e-22:433:62//AC004916  
 F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence./2.7e-22:270:75//AC005913  
 F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces./1.4e-32:574:64//AC005122  
 10 F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence./4.8e-113:546:98//AC004540  
 F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces./  
 15 0.97:115:70//AC004965  
 F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds./9.7e-16:162:77//U62293  
 F-NT2RP2000764//HS\_2254\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey sequence./0.071:45:95//AQ068887  
 F-NT2RP2000809  
 20 F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite./0.040:158:64//AF069698  
 F-NT2RP2000814  
 F-NT2RP2000816  
 F-NT2RP2000819  
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds./1.1e-26:390:70//AB002292  
 F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2./1.2e-44:255:93//Y09479  
 25 F-NT2RP2000845  
 F-NT2RP2000863//Human partial cDNA sequence, clone x874;./5.9e-29:173:94//Z47045  
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds./2.4e-140:732:94//AB018284  
 F-NT2RP2000892  
 F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds./3.4e-129:610:98//AB018266  
 30 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence./1.8e-37:212:84//AC005014  
 F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island./1.6e-126:682:93//Z69890  
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds./5.8e-112:533:98//AB018298  
 35 F-NT2RP2000965  
 F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence./9.2e-101:505:96//AL021393  
 F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence./1.6e-72:498:  
 40 82//AC005277  
 F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence./7.4e-12:171:  
 77//AC002394  
 F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence./1.2e-37:390:76//  
 45 AC004167  
 F-NT2RP2001044//HS\_2253\_B1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence./0.21:276:61//AQ069224  
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488./3.2e-144:696:97//  
 AB007957  
 F-NT2RP2001065  
 50 F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds./4.3e-104:775:81//  
 U91561  
 F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds./3.7e-69:488:82//AF000423  
 F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS./7.4e-11:490:61//  
 Z86063  
 F-NT2RP2001119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING  
 55 DRAFT SEQUENCE./5.1e-30:316:76//AL031596  
 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds./1.1e-31:519:63//D87072  
 F-NT2RP2001137//HS\_2193\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence./1.8e-11:136:78//AQ032187

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F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence./.6.2e-29:247:78//AC000076  
5 F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence./.0.23:207:66//AL009178  
10 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds./.2.3e-112:567:96//AB007949  
F-NT2RP2001174//RPCI11-58L2.TK RPCI11 Homo sapiens genomic clone R-58L2, genomic survey sequence./.7.6e-07:196:64//AQ237306  
F-NT2RP2001196  
F-NT2RP2001218  
15 F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1./.1.1e-09:320:65//U92893  
F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein./.6.1e-71:681:72//X51760  
F-NT2RP2001245//HS\_3062\_B1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence./.1.5e-05:268:63//AQ143177  
20 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds./.2.5e-106:514:97//AB018353  
F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence./.0.32:183:64//AE001430  
F-NT2RP2001290//M.musculus mRNA for I47 clone./.8.6e-102:641:86//X61455  
25 F-NT2RP2001295//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE./.0.20:171:63//AL022594  
F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds./.0.98:253:58//M22967  
F-NT2RP2001327//Human B12 protein mRNA, complete cds./.5.8e-29:359:71//M80783  
30 F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 2335A5, genomic survey sequence./.1.3e-65:366:94//AQ038539  
F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease./.3.8e-31:325:77//AJ003147  
F-NT2RP2001366//H.sapiens CpG island DNA genomic Mse1 fragment, clone 4e11, forward read cpg4e11.f1a./.1.7e-12:98:92//Z61305  
35 F-NT2RP2001378//HS\_3054\_B2\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence./.9.8e-17:131:89//AQ100721  
F-NT2RP2001381//Arabidopsis thaliana BAC T2L5./.0.080:434:59//AF096371  
F-NT2RP2001392//S.pristinaespiralis snbC gene & nb; snbDE gene./.0.019:267:59//Y11548  
40 F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat./.1.9e-16:133:78//Z93242  
F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds./.1.3e-63:419:84//AF080219  
F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds./.3.1e-98:747:79//U76759  
F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds./.3.7e-34:269:85//AF015454  
45 F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence./.3.2e-13:164:78//AC003065  
F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence./.3.0e-06:136:71//AF046702  
F-NT2RP2001440//cDNA sequence coding for gamma protein./.7.9e-83:553:86//E02350  
F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A)./.1.5e-09:829:57//X95275  
50 F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor./.1.3e-136:766:90//X75931  
F-NT2RP2001450  
F-NT2RP2001467  
F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence./.7.9e-14:151:80//AQ109561  
55 F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds./.2.6e-22:462:64//AF005355  
F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1./.2.0e-136:657:97//Y14494  
F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence./.1.2e-37:357:64//AC004596  
F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds./.1.6e-103:384:94//AF035586  
F-NT2RP2001560  
F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488./.4.4e-123:590:98//

AB007957  
F-NT2RP2001576//*Schistocerca americana* Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.038:  
580:58//U32943  
F-NT2RP2001581//*Mus musculus* semaphorin VIa mRNA, complete cds.//6.5e-09:222:66//AF030430  
5 F-NT2RP2001597//*Homo sapiens* alpha2-C4-adrenergic receptor gene, complete cds.//0.0057:361:60//U72648  
F-NT2RP2001601//*Homo sapiens* mRNA for KIAA0797 protein, partial cds.//7.2e-137:647:98//AB018340  
F-NT2RP2001613  
F-NT2RP2001628//*H.sapiens* (xs128) mRNA, 380bp.//1.7e-15:279:68//Z36784  
10 F-NT2RP2001634//*Homo sapiens* alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//5.4e-123:606:  
96//AF030233  
F-NT2RP2001660//*Homo sapiens* putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-  
NA, complete cds.//4.2e-144:687:97//AF058718  
F-NT2RP2001663//*H.sapiens* mRNA for 2-phosphopyruvate-hydrolase-alpha-enolase.//1.0e-36:372:74//X84907  
15 F-NT2RP2001675//*S.pombe* chromosome I cosmid c2G11.//0.070:507:59//Z54354  
F-NT2RP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//2.0e-60:232:96//  
AC005259  
F-NT2RP2001678//HS\_2007\_A2\_A04\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* ge-  
nomic clone Plate=2007 Col=8 Row=A, genomic survey sequence.//7.3e-62:370:91//AQ269699  
20 F-NT2RP2001699//RPCI11-57B17.TK RPCI11 *Homo sapiens* genomic clone R-57B17, genomic survey se-  
quence.//0.99:141:63//AQ115592  
F-NT2RP2001720//*Homo sapiens* PAC clone DJ0167F23 from 7p15, complete sequence.//9.4e-117:604:95//  
AC004079  
F-NT2RP2001721//*Homo sapiens* DNA sequence from clone 466I8 on chromosome Xq11.1-13.2. Contains an  
25 unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoag-  
ulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete se-  
quence.//1.0:273:61//AL030998  
F-NT2RP2001740//*Homo sapiens* Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete se-  
quence.//1.0:356:62//AC000090  
F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds.//3.7e-18:151:86//D14697  
30 F-NT2RP2001762//*Homo sapiens* chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.0e-  
145:715:97//AC004783  
F-NT2RP2001813//*Plasmodium falciparum* chromosome 2, section 15 of 73 of the complete sequence.//0.38:340:  
60//AE001378  
F-NT2RP2001839//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D\_ *Homo sapiens* ge-  
35 nomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347  
F-NT2RP2001861//*Homo sapiens* mRNA for paraplegin.//0.89:146:71//Y16610  
F-NT2RP2001869//*Homo sapiens* ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219  
F-NT2RP2001876//*Cyprinus carpio* mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//  
40 AB012309  
F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,  
complete sequence.//1.8e-87:496:92//AL031864  
F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//9.2e-112:633:90//  
M74161  
45 F-NT2RP2001900//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone R08A5,  
WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281  
F-NT2RP2001907//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 97f11, forward read cpg97f11.ft1a.//  
4.2e-26:206:84//Z64125  
50 F-NT2RP2001926//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
DRAFT SEQUENCE, 4 unorderd pieces.//5.5e-06:621:59//AC004688  
F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid *Homo sapiens* genomic clone  
cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856  
F-NT2RP2001943//*Drosophila melanogaster* cosmid 25E8.//0.00036:248:60//AL009196  
F-NT2RP2001946//*Homo sapiens* clone NH0140K04, complete sequence.//3.8e-78:232:99//AC005033  
55 F-NT2RP2001947//*Homo sapiens* full-length insert cDNA clone ZD81B04.//2.0e-28:172:94//AF086442  
F-NT2RP2001969//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 152a8, reverse read  
cpg152a8.rt1a.//1.0e-20:123:99//Z59378  
F-NT2RP2001976

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F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds./.0.0023:235:62//AB011117  
F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds./.3.1e-35:180:80//L22022  
F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds./.9.8e-61:314:97//AB018299  
F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence./.0.76:189:  
5 65//AC005895  
F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces./.2.9e-  
12:160:79//AC004825  
F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence./.0.0014:123:73//AC004029  
F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete  
10 sequence./.2.2e-86:722:77//AC004552  
F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon  
of a putative new gene and STSs and GSs, complete sequence./.0.13:350:61//AL033375  
F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w./.9.7e-11:480:60//Z73301  
F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds./.6.5e-97:610:86//  
15 U87306  
F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=adducin  
beta subunit 63 kda isoform/membrane skeleton protein {alternatively spliced, exon 10 to 13 region} [human,  
Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083  
F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence./.1.0e-127:643:96//AF052183  
20 F-NT2RP2002078//F12O16-T7.1 IGF Arabidopsis thaliana genomic clone F12016, genomic survey sequence./.  
0.14:191:64//AQ249805  
F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence./.0.0094:325:60//AC004917  
F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein./.9.8e-111:533:97//AJ007509  
F-NT2RP2002105//H.sapiens CpG island DNA genomic Mse1 fragment, clone 10h8, forward read cpg10h8.ft1a./.  
25 2.4e-29:178:94//Z58857  
F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey se-  
quence./.2.5e-32:202:92//B64468  
F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds./.0.095:319:59//  
M25874  
30 F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds./.1.0:258:63//D85923  
F-NT2RP2002172//HS\_3020\_B1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3020 Col=3 Row=P, genomic survey sequence./.1.2e-11:124:82//AQ093169  
F-NT2RP2002185//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey se-  
quence./.2.8e-18:109:100//AQ201833  
35 F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-sc1) mRNA, complete cds./.2.7e-36:363:78//U09215  
F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds./.9.5e-  
82:477:89//AF032872  
F-NT2RP2002208  
40 F-NT2RP2002219//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
DRAFT SEQUENCE./.1.0:378:58//AL034557  
F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
DRAFT SEQUENCE, 5 unordered pieces./.0.60:560:56//AC005308  
F-NT2RP2002235//P.falciparum glutamic acid-rich protein gnen, complete cds./.0.59:341:60//J03998  
F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds./.3.5e-81:398:87//U22394  
45 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds./.6.6e-50:315:89//AF005418  
F-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING  
DRAFT SEQUENCE./.9.7e-67:340:89//AL033527  
F-NT2RP2002270//RPCI11-77C23.TV RPCI11 Homo sapiens genomic clone R-77C23, genomic survey se-  
quence./.2.9e-18:79:93//AQ268098  
50 F-NT2RP2002292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING  
DRAFT SEQUENCE./.1.0:290:60//AL031033  
F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds./.1.5e-93:467:96//  
AF069532  
F-NT2RP2002316//HS\_2171\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
55 nomic clone Plate=2171 Col=22 Row=H, genomic survey sequence./.7.3e-94:463:97//AQ119673  
F-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds./.3.9e-123:640:95//AB015594  
F-NT2RP2002333  
F-NT2RP2002373//F.rubripes GSS sequence, clone 026F10aB8, genomic survey sequence./.0.46:234:61//

Z87330  
F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds././/9.4e-138:673:  
97//AF038958  
F-NT2RP2002394//P.falciparum complete gene map of plastid-like DNA (IR-A).//.0.79:421:56//X95275  
5 F-NT2RP2002408//F.rubripes GSS sequence, clone 080G11aA8, genomic survey sequence././/5.7e-15:220:71//  
AL015615  
F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9././/7.1e-71:582:80//AJ223742  
F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3././/0.0018:210:67//AF016682  
F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1././/2.8e-18:295:67//U88169  
10 F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence././/1.9e-06:  
281:66//AC004381  
F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds././/0.039:207:63//D42045  
F-NT2RP2002475  
15 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds././/2.4e-123:607:96//  
AB005289  
F-NT2RP2002498//Arabidopsis thaliana BAC F3D13././/0.73:395:57//AF069300  
F-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence././/7.2e-18:134:90//AC006213  
F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds././/1.2e-157:761:97//AB018334  
F-NT2RP2002520  
20 F-NT2RP2002537  
F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRAFT SEQUENCE, 7 un-  
ordered pieces././/0.83:252:60//AC004127  
F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma  
(polg) gene, complete sequence././/5.9e-93:186:99//AC005317  
25 F-NT2RP2002591//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING  
DRAFT SEQUENCE././/4.0e-38:175:78//Z98304  
F-NT2RP2002595//Sequence 2 from patent US 5763220././/1.5e-84:430:95//AR012155  
F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds././/1.9e-43:282:87//U19181  
F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, partial cds././/1.5e-11:99:90//AF051310  
30 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp././/5.6e-27:460:63//  
Y10806  
F-NT2RP2002621  
F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region and exon 1././/0.023:322:60//D90397  
F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete se-  
35 quence././/3.9e-149:794:94//AC005384  
F-NT2RP2002701//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING  
DRAFT SEQUENCE././/9.2e-10:129:75//AL034380  
F-NT2RP2002706//S.griseus secA gene././/1.3e-05:311:63//Y10980  
F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds././/2.5e-40:631:65//AB014572  
40 F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds././/4.8e-65:600:73//AF041107  
F-NT2RP2002736//S.pombe chromosome II cosmid c887././/0.17:352:58//AL033388  
F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) mating type surface protein (PSSP15) gene, complete cds;  
ORF, 5' end././/0.0073:274:66//M94861  
F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds././/7.5e-29:628:62//D89016  
45 F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library)  
complete sequence././/3.6e-31:568:67//AC005296  
F-NT2RP2002752//Human BAC clone RG317M02 from 7p15-p21, complete sequence././/1.7e-08:206:63//  
AC002433  
50 F-NT2RP2002753//Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs././/2.8e-71:195:  
89//Z82171  
F-NT2RP2002769//Streptomyces fradiae tylactone synthase, starter module and modules 1-7, (tylG) gene, com-  
plete cds././/0.0016:412:60//U78289  
F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sapiens genomic clone 2059C5, genomic survey se-  
quence././/6.8e-18:186:79//B69837  
55 F-NT2RP2002800  
F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene,  
WORKING DRAFT SEQUENCE, 11 unordered pieces././/1.2e-41:134:94//AC006078  
F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA, partial cds, clone

TRB-4//0.85:93:68//M18845  
 F-NT2RP2002862//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence //5.0e-67:390:91//AQ186344  
 F-NT2RP2002880  
 5 F-NT2RP2002891//CIT-HSP-2310O14.TF CIT-HSP Homo sapiens genomic clone 2310O14, genomic survey sequence //0.11:53:90//AQ019792  
 F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds //0.66:194:65//D16511  
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds //2.3e-135:628:99//AF038392  
 10 F-NT2RP2002929//F.rubripes GSS sequence, clone 123I23aA1, genomic survey sequence //3.9e-06:66:83//AL017246  
 F-NT2RP2002939  
 F-NT2RP2002954  
 F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds //1.3e-47:411:79//U62483  
 15 F-NT2RP2002979//CIT-HSP-2340D12.TF CIT-HSP Homo sapiens genomic clone 2340D12, genomic survey sequence //4.6e-96:476:97//AQ057233  
 F-NT2RP2002980//Sequence 20 from Patent EP0705842 //4.0e-13:100:94//A52230  
 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds //2.4e-09:272:61//AF059569  
 20 F-NT2RP2002987//Homo sapiens (subclone 6\_d9 from P1 H21) DNA sequence, complete sequence //1.0e-22:293:67//AC000958  
 F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds //4.0e-74:502:84//AF025424  
 25 F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces //2.3e-46:474:76//AC004765  
 F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence //4.2e-23:202:82//AC005703  
 F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs //3.4e-59:330:82//Z83822  
 30 F-NT2RP2003099//HS\_3008\_B2\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey sequence //1.4e-71:362:96//AQ089786  
 F-NT2RP2003108//Sequence 59 from patent US 5773577 //0.95:123:69//AR014362  
 F-NT2RP2003117//HS\_2034\_B2\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey sequence //1.5e-88:461:96//AQ230797  
 35 F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds //4.3e-46:470:72//AF079765  
 F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence //5.7e-10:436:61//AC005329  
 40 F-NT2RP2003129//P.thunbergii cab gene //0.00044:541:60//X61915  
 F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence //5.0e-78:393:97//AQ012976  
 F-NT2RP2003157//Human DNA sequence from cDNA 16pHQG;16 from chromosome 16p13.3 //5.4e-07:137:71//Z84716  
 45 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds //1.8e-111:581:93//D67025  
 F-NT2RP2003161//CITBI-E1-2506E20.TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence //0.0025:156:67//AQ262657  
 F-NT2RP2003164  
 50 F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds //1.4e-43:334:79//U91328  
 F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds //0.91:346:62//U50040  
 55 F-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE //1.7e-108:511:90//AL031597  
 F-NT2RP2003206  
 F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA //2.9e-136:726:93//X74794  
 F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds //2.6e-51:348:

86//AF023657  
 F-NT2RP2003237//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE//2.6e-56:415:83//AL031447  
 5 F-NT2RP2003243//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence//2.1e-16:112:93//AQ047107  
 F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds//6.0e-114:696:87//L38481  
 F-NT2RP2003272//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence//3.8e-16:110:94//AQ201833  
 10 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.5e-145:714:96//AB014525  
 F-NT2RP2003280//RPCI11-14I2.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-14I2, genomic survey sequence//6.4e-77:400:95//B85286  
 F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence//5.3e-29:287:73//AQ041024  
 15 F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//1.5e-54:508:74//AC003973  
 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds//6.1e-85:416:97//AB006572  
 F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphatase//0.60:309:64//X62722  
 20 F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds//1.0e-45:442:75//AF055666  
 F-NT2RP2003308//D.melanogaster crn mRNA//1.1e-63:697:70//X58374  
 F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence//0.040:145:64//AC005288  
 F-NT2RP2003339  
 25 F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence//0.12:275:60//AL034559  
 F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence//0.83:225:63//AC005510  
 F-NT2RP2003391  
 30 F-NT2RP2003393//HS\_3218\_A2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence//0.021:93:79//AQ204356  
 F-NT2RP2003394  
 F-NT2RP2003401  
 F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds//4.2e-61:533:75//M96630  
 35 F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE//2.1e-49:301:72//AP000023  
 F-NT2RP2003446  
 F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4//0.0018:366:60//AJ235272  
 F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, 40 complete sequence//7.5e-16:189:68//AC004770  
 F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end//1.9e-25:197:85//M21977  
 F-NT2RP2003499 2.1e-08:408:61//AB000826  
 F-NT2RP2003506//Homo sapiens cloné NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces//1.9e-33:192:96//AC005236  
 45 F-NT2RP2003511//Ceratopteris richardii mRNA for CRHB11, partial cds//1.0:328:60//AB013801  
 F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//7.3e-76:403:93//D87460  
 F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PDGF-B chain (PDGF= platelet-derived growth factor)//1.5e-24:151:95//X03702  
 F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end//1.3e-101:564:91//M21977  
 50 F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6//2.0e-40:315:75//Z80899  
 F-NT2RP2003543  
 F-NT2RP2003559//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.rt1a//1.1e-20:122:99//Z56144  
 F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds//8.8e-27:664:63//M34551  
 55 F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//4.1e-113:541:98//AB007931  
 F-NT2RP2003581  
 F-NT2RP2003596//F.rubripes GSS sequence, clone 036L10aF12, genomic survey sequence//J1.9e-11:210:65//AL012756

F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//1.9e-123:587:  
 98//AF030233  
 F-NT2RP2003629  
 F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminc acid synthetase.//7.8e-88:582:84//  
 5 AJ006215  
 F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//  
 5.6e-47:335:83//AC005081  
 F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete se-  
 quence.//1.2e-06:133:74//AC003684  
 10 F-NT2RP2003691//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 525L6, WORKING  
 DRAFT SEQUENCE.//1.7e-47:337:81//AL023807  
 F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, complete cds.//1.3e-65:458:82//U44803  
 F-NT2RP2003704//H.sapiens CpG island DNA genomic Mse1 fragment, clone 2a9, reverse read cpg2a9.rt1e.//  
 3.8e-17:170:84//Z60615  
 15 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-108:518:98//AB011097  
 F-NT2RP2003713//HS\_2016\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2016 Col=9 Row=D, genomic survey sequence.//1.3e-11:102:90//AQ226895  
 F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.4e-27:249:78//  
 AC003973  
 20 F-NT2RP2003727//RPCI11-77I19.TV RPCI11 Homo sapiens genomic clone R-77I19, genomic survey sequence.//  
 3.4e-26:294:74//AQ268303  
 F-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.6e-  
 74:194:91//AC004951  
 F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12, complete sequence.//1.7e-  
 25 92:165:96//AC003964  
 F-NT2RP2003760//B.primitiveus mRNA for coat protein gamma-cop.//4.5e-76:696:73//X92987  
 F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence.//1.0:109:69//AB013275  
 F-NT2RP2003769  
 30 F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence.//3.0e-96:467:  
 98//AC004771  
 F-NT2RP2003777  
 F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//7.2e-107:731:82//S70011  
 F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 2326L12, genomic survey se-  
 quence.//7.0e-20:124:95//AQ038761  
 35 F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//8.9e-06:151:74//  
 AC004491  
 F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.//  
 0.018:145:69//AC005167  
 40 F-NT2RP2003857//HS\_3227\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3227 Col=8 Row=M, genomic survey sequence.//0.96:257:61//AQ303467  
 F-NT2RP2003859  
 F-NT2RP2003871//Homo sapiens 12q24 PAC RPCI1-74B13 (Roswell Park Cancer Institute Human PAC library)  
 complete sequence.//2.0e-12:369:65//AC002375  
 45 F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2514D6, genomic survey se-  
 quence.//0.13:167:64//AQ265722  
 F-NT2RP2003912//nek1=serine/threonine- and tyrosine-specific protein kinase [mice, erythroleukemia cells, mR-  
 NA, 4263 nt].//1.3e-136:838:86//S45828  
 F-NT2RP2003952  
 50 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.1e-28:165:96//  
 AB014458  
 F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alter-  
 natively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B  
 55 and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSRE, p58/GTA,  
 Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal  
 Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae)  
 bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G  
 protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs,  
 complete sequence.//2.6e-24:298:74//AL031282

- F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783:96//AB018347  
 F-NT2RP2003984  
 F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.7e-26:260:77//AC000382
- 5 F-NT2RP2003988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681  
 F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693:91//AL023580  
 F-NT2RP2004014
- 10 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//5.8e-83:427:87//AC004780  
 F-NT2RP2004042  
 F-NT2RP2004066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134O19, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555
- 15 F-NT2RP2004081  
 F-NT2RP2004098//HS\_2216\_A1\_B12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey sequence.//1.0e-07:86:84//AQ145694  
 F-NT2RP2004124//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.0e-25:155:94//AQ136993
- 20 F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence.//1.0:220:62//AB007645  
 F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.93:480:56//AC002493  
 F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61//AC005140
- 25 F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) gene, complete cds.//1.0:162:66//AF028235  
 F-NT2RP2004172//S.pombe chromosome II cosmid c24E9.//1.7e-06:466:59//AL021816  
 F-NT2RP2004187//Homo sapiens full-length insert cDNA YQ86E07.//3.5e-17:354:64//AF075093
- 30 F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//9.4e-53:397:82//AF003998  
 F-NT2RP2004196  
 F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to exons 23 through 34.//0.0023:386:61//M60676  
 F-NT2RP2004226//HS\_2186\_A1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2186 Col=5 Row=G, genomic survey sequence.//7.8e-58:370:87//AQ063813
- 35 F-NT2RP2004232//H.sapiens mRNA for protein kinase C mu.//1.2e-34:448:67//X75756  
 F-NT2RP2004239//Homo sapiens lck mRNA for protein kinase, complete cds.//5.2e-108:510:99//AB015718  
 F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).//1.1e-12:489:61//AP000006
- 40 F-NT2RP2004242  
 F-NT2RP2004245  
 F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462:62//AL034446  
 F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299:64//AC005781
- 45 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735:97//AF000416  
 F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//0.98:267:59//AC004423  
 F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519
- 50 F-NT2RP2004347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650  
 F-NT2RP2004364  
 F-NT2RP2004365  
 F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//0.92:427:57//AL031864  
 F-NT2RP2004373//Homo sapiens cosmids Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493:65//AF035397

F-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence./.2.9e-11:83:96//AQ063969  
 F-NT2RP2004392  
 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence./.1.1e-171:875:95//  
 5 AC005164  
 F-NT2RP2004399//Homo sapiens SYBL1 gene./.1.4e-24:467:64//AJ004799  
 F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence./.0.00074:455:59//AF069441  
 F-NT2RP2004412//H.sapiens CpG island DNA genomic Mse1 fragment, clone 34g4, reverse read cpg34g4.rt1a./.  
 10 5.0e-27:154:98//Z65369  
 F-NT2RP2004425  
 F-NT2RP2004463//Streptomyces coelicolor cosmid 2E9./.0.0053:196:65//AL021530  
 F-NT2RP2004476//Drosophila melanogaster cosmid 67A9./.5.2e-15:377:63//AL034388  
 F-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence./.4.3e-100:497:  
 15 97//AC005591  
 F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence./.2.3e-07:815:57//AL034556  
 F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence./.8.5e-138:718:95//AC004890  
 F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds./.1.4e-137:687:96//AB011163  
 F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey se-  
 20 quence./.2.1e-85 :484:91//AQ239555  
 F-NT2RP2004568//H.vulgare GAA-satellite DNA./.2.0e-07:292:62//Z50100  
 F-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING  
 DRAFT SEQUENCE./.4.5e-44:512:72//AL023755  
 F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds./.1.0:344:  
 25 56//AF092908  
 F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H13r, genomic  
 survey sequence./.0.053:324:60//AQ258020  
 F-NT2RP2004600  
 F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence./.0.12:109:73//  
 30 AC005176  
 F-NT2RP2004614  
 F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein./.2.6e-102:496:98//AJ006291  
 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds./.1.6e-153:728:98//AB007929  
 F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces./.  
 35 0.092:239:61//AC005805  
 F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3-27.3. Contains an EST and  
 GSSs, complete sequence./.1.0:236:61//AL031312  
 F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds./.1.3e-59:327:94//AB014525  
 F-NT2RP2004709//HS\_2033\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=2033 Col=8 Row=J, genomic survey sequence./.1.9e-15:187:74//AQ230714  
 F-NT2RP2004710//HS\_3185\_82\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3185 Col=14 Row=H, genomic survey sequence./.9.9e-10:110:84//AQ172885  
 F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds./.6.4e-117:582:96//AB007947  
 F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X./.0.14:138:71//Z78022  
 45 F-NT2RP2004767//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65c11, reverse read  
 cpg65c11.rt1a./.1.3e-24:217:81//Z62210  
 F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds./.1.6e-45:541:71//AF024636  
 F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence./.5.8e-13:  
 697:59//AE001398  
 50 F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybridscreen./.5.0e-53:353:84//  
 U56252  
 F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds./.  
 1.5e-116:594:95//AF058953 F-NT2RP2004802  
 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds./.2.1e-101:495:97//AF054179  
 55 F-NT2RP2004841//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on  
 chromosome X contains EST CA repeat and an endogenous retroviral like element./.7.6e-82:531:84//Z72519  
 F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040O17bA3, genomic survey sequence./.0.96:183:64//  
 AL025645

F-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence././/4.8e-142:710:96//AC004383  
 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds././/2.0e-82:418:95//AB007144  
 F-NT2RP2004936  
 5 F-NT2RP2004959//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence././/3.5e-25:218:83//AQ150183  
 F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds././/2.5e-59:339:79//U56732  
 F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds././/3.6e-19:187:72//U91328  
 10 F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence././/0.0020:297:61//Z98551  
 F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds././/0.22:162:69//L29029  
 F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4, genomic survey sequence././/0.13:273:61//B12642  
 15 F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds././/1.5e-20:431:65//D63478  
 F-NT2RP2004999  
 F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase././/0.019:240:63//X63375  
 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds././/6.0e-159:782:97//AB014515  
 F-NT2RP2005003//H.sapiens Staf50 mRNA././/3.1e-42:430:75//X82200  
 20 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds././/1.4e-98:501:96//AF100141  
 F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence././/1.0:209:63//AC004849  
 F-NT2RP2005020  
 F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces././/  
 25 3.0e-43:98:93//AC000380  
 F-NT2RP2005031//HS\_2052\_B2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=20 Row=N, genomic survey sequence././/0.019:363:61//AQ231464  
 F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene././/0.70:174:65//U64454  
 F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence././/0.20:519:57//  
 30 AC005696  
 F-NT2RP2005108  
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds././/2.0e-103:495:98//AB014564  
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)././/2.9e-27:157:98//  
 X98743  
 35 F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5././/  
 0.00024:547:59//AJ223012  
 F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence././/  
 0.95:191:62//AC004527  
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds././/2.6e-89:447:96//AF045583  
 40 F-NT2RP2005147//HS\_3184\_A1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=1 Row=I, genomic survey sequence././/0.10:294:60//AQ252226  
 F-NT2RP2005159//H.sapiens CpG island DNA genomic Mse1 fragment, clone 132g6, forward read  
 cpg132g6.ft1a././/1.1e-13:93:97//Z59162  
 F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1././/2.6e-20:394:64//U13070  
 45 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein././/1.4e-125:633:96//AJ007509  
 F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds././/0.00016:316:  
 60//U80808  
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence././/0.51:52:92//  
 AC005189  
 50 F-NT2RP2005239//S.pombe chromosome II cosmid c21D10././/1.3e-22:356:67//AL031536  
 F-NT2RP2005254  
 F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3; clone NL197R)././/0.58:132:65//X87513  
 F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds././/9.0e-103:656:85//D30666  
 F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds././/3.4e-37:302:84//L26335  
 55 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds././/7.1e-122:604:96//  
 AF060219  
 F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein././/4.0e-140:670:98//AJ007590  
 F-NT2RP2005293//HS\_3245\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454  
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576  
 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds.//8.2e-22:166:90//  
 U11701  
 5 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
 cds.//0.39:353:62//AF032387  
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138  
 F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//  
 Z92844  
 10 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//4.7e-99:489:  
 96//AF072247  
 F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358  
 F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97:83//M77184  
 F-NT2RP2005407  
 15 F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence.//0.014:235:  
 62//AC005346  
 F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey se-  
 quence.//4.0e-107:532:97//AQ055548  
 F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//  
 20 1.0:239:61//B97865  
 F-NT2RP2005457//B.taurus CI-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647  
 F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat,  
 STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679  
 F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//6.5e-  
 25 18:152:75//AC006116  
 F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of  
 a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo)  
 gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2,  
 TBPII, TNF-R2, CD120B, TNFBR). Contains ESTs, STSs, GSSs, genomic marker D1S434 and a ca repeat poly-  
 30 morphism, complete sequence.//4.4e-12:89:97//AL031276  
 F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//4.3e-40:463:73//  
 AC004130  
 F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//  
 3.2e-115:228:99//AC006030  
 35 F-NT2RP2005491//HS\_2253\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2253 Col=20 Row=M, genomic survey sequence.//4.6e-23:234:80//AQ116847  
 F-NT2RP2005495  
 F-NT2RP2005496//HS\_3064\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436:98//AQ143097  
 40 F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503:78//M64931  
 F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//  
 0.86:183:63//AC005880  
 F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160:65//U82695  
 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:  
 45 444:92//AF092563  
 F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112:99//AB018307  
 F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-06:282:60//M14993  
 F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747:97//AJ012449  
 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618:98//AB007963  
 50 F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277:89//AF046734  
 F-NT2RP2005555//HS\_2188\_A2\_D04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-05:195:65//AQ086723  
 F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA,  
 complete cds.//2.5e-44:473:71//AF062529  
 55 F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//0.99:213:65//AC005016  
 F-NT2RP2005600//H.sapiens CpG island DNA genomic Mse1 fragment, clone 172d12, reverse read  
 cpg172d12.rt1a.//0.32:134:63//Z57359  
 F-NT2RP2005605

F-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//9.8e-91:447:97//AF062085  
 F-NT2RP2005622  
 F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:61//U10556  
 5 F-NT2RP2005637//NAT1 (NAT1\*10)=acetyltransferase 1 (3' region, polyadenylation polymorphism) [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt].//0.22:156:65//S78829  
 F-NT2RP2005640//Mouse U6 RNA gene.//5.5e-19:249:76//X06980  
 F-NT2RP2005645//HS\_2201\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ066763  
 10 F-NT2RP2005651//H.sapiens DNA sequence.//0.00037:150:66//Z22493  
 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626  
 F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:98//AF064605  
 F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//  
 AF089814  
 15 F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405  
 F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836  
 F-NT2RP2005694  
 F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPCI11-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC005183  
 20 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342  
 F-NT2RP2005719//R.norvegicus mRNA for metallothionein-III.//0.86:117:64//X89603  
 F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367  
 F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//  
 AC002528  
 25 F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//  
 5.1e-41:138:95//AC005627  
 F-NT2RP2005732//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING  
 DRAFT SEQUENCE.//0.61:303:60//Z93017  
 F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270  
 30 F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342  
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//  
 AF068868  
 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//  
 AF082516  
 35 F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853  
 F-NT2RP2005767//G.gallus PB1 gene.//2.1e-73:544:80//X90849  
 F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836  
 F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds.//1.2e-121:649:88//  
 D11336  
 40 F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds.//0.96:184:60//AB015853  
 F-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING  
 DRAFT SEQUENCE.//1.9e-63:222:96//AL034423  
 F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//  
 AF010579  
 45 F-NT2RP2005812  
 F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I.//0.031:358:59//X74103  
 F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086  
 F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873  
 F-NT2RP2005853//RPCI11-24D4.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24D4, genomic survey  
 50 sequence.//6.4e-13:130:85//AQ013490  
 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:  
 829:98//AF092564  
 F-NT2RP2005859//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 914P20, WORKING  
 DRAFT SEQUENCE.//0.25:174:62//AL034553  
 55 F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103I24aF4, genomic survey sequence.//7.8e-06:92:79//  
 AL027276  
 F-NT2RP2005886//HS\_3187\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3187 Col=16 Row=G, genomic survey sequence.//7.1e-95:494:95//AQ155885

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F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds./.2.7e-32:660:66//L11316  
F-NT2RP2005901//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, reverse read cpg15b5.rt1a./.0.0026:66:84//Z54729  
5 F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence./.6.4e-49:481:75//AC004241  
F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds./.6.6e-61:657:73//U63840  
F-NT2RP2005942//H.sapiens PAP mRNA./.1.6e-46:618:67//X76770  
F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence./.1.0e-48:533:71//AC005207  
10 F-NT2RP2006023//HS\_3048\_A1\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence./.2.1e-25:167:91//AQ126553  
F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence./.3.9e-06:102:74//B51912  
F-NT2RP2006043//Human intercrine-alpha (hIRH) mRNA, complete cds./.1.9e-05:418:59//U19495  
15 F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55./.0.0035:226:65//AF016861  
F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5./.3.9e-11:121:85//D17047  
F-NT2RP2006071  
F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence./.0.46:264:59//  
20 AF027207  
F-NT2RP2006100//Human Chromosome X, complete sequence./.3.2e-94:488:95//AC004073  
F-NT2RP2006103//HS\_2254\_A2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey sequence./.5.7e-27:156:96//AQ129602  
25 F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence./.11.2e-62:655:71//AC000378  
F-NT2RP2006141//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE./.1.2e-69:316:98//AL034405  
F-NT2RP2006166//Homo sapiens chromosome 4 clone B32I8, complete sequence./.3.1e-45:387:81//AC004063  
30 F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lec4A cell line point mutant mRNA, complete cds./.0.99:111:73//U62587  
F-NT2RP2006186//Homo Sapiens mRNA for KIAA0654 protein, partial cds./.7.8e-113:567:96//AB014554  
F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence./.2.8e-28:718:62//AC005232  
F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66  
unordered pieces./.6.5e-83:239:94//AC006057  
35 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein./.1.4e-116:618:93//X96484  
F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence./.2.0e-18:118:97//AQ012480  
F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds./.7.6e-102:635:86//  
U49055  
40 F-NT2RP2006258//RPCI11-9N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-9N9, genomic survey sequence./.8.6e-05:181:63//B71615  
F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK./.0.44:111:71//X97630  
F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,8.5,9,10,11,12,13] genes./.2.0e-05:501:59//X97257  
F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds./.2.7e-138:679:97//AF035262  
F-NT2RP2006320//P.falciparum pfmdr1 gene./.0.00013:425:60//X56851  
45 F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence./.4.1e-19:545:62//  
AC003973  
F-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745I14, WORKING DRAFT SEQUENCE./.8.9e-18:131:90//AL033532  
F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence./.6.2e-125:602:  
50 98//AC004893  
F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence./.2.1e-06:241:65//  
AC005514  
F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence./.7.8e-06:148:  
70//AL029590  
55 F-NT2RP2006393//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and  
pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence./.6.8e-06:167:70//AL022727  
F-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE./.4.2e-92:363:84//AL023808

F-NT2RP2006441  
F-NT2RP2006454//Sequence 8 from Patent WO9517522./2.9e-06:180:66//A45338  
F-NT2RP2006456  
F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein./3.4e-148:545:98//AJ006266  
5 F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding ch1-ch4 and secretion domains, partial cds./0.061:201:66//U50149  
F-NT2RP2006472  
F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence./8.8e-10:273:66//Z93929  
10 F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6./0.71:174:59//U40965  
F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds./6.6e-114:669:90//AF038966  
F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1./6.0e-26:  
15 503:63//M20855  
F-NT2RP2006573//Molluscum contagiosum virus subtype 1, complete genome./0.44:134:71//U60315  
F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033./5.0e-16:140:85//U50537  
F-NT2RP300002//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence./3.8e-32:214:89//U14571  
20 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-136:637:98//  
AJ011972  
F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds./5.4e-05:571:60//L14320  
F-NT2RP3000047  
25 F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9./1.0e-67:626:74//  
M27877  
F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence./3.5e-10:394:64//AC001227  
F-NT2RP3000068  
F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence./1.0:301:61//AC004746  
30 F-NT2RP3000080//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING  
DRAFT SEQUENCE./1.9e-44:297:79//AL021391  
F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds./  
4.5e-33:528:65//U12536  
F-NT2RP3000092//RPCI11-22M5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22M5, genomic survey se-  
quence./3.3e-27:157:97//B84237  
35 F-NT2RP3000109//Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete  
cds./0.92:185:64//L29260  
F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence./1.2e-112:286:89//  
AC005189  
F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds./9.0e-181:849:98//AB011164  
40 F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence./4.2e-24:155:  
94//AC005884  
F-NT2RP3000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING  
DRAFT SEQUENCE./7.2e-43:269:81//AL023583  
45 F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9./0.098:405:57//L39063  
F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence./0.96:  
608:55//AC004716  
F-NT2RP3000220  
F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds./2.0e-18:509:58//  
AF059569  
50 F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence./3.5e-05:224:65//AC004101  
F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds./2.1e-109:691:86//D86972  
F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence./0.20:119:68//Z70213  
F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence./9.8e-78:174:88//AF065393  
F-NT2RP3000255  
55 F-NT2RP3000267  
F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds./5.9e-48:374:82//  
U48853  
F-NT2RP3000312//Fruit fly (D.melanogaster) Glued mRNA, complete cds./4.9e-22:583:63//J02932

F-NT2RP3000320//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107  
 F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//5.5e-26:283:79//U78090  
 5 F-NT2RP3000333//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533  
 F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//6.7e-42:465:74//Z97181  
 F-NT2RP3000348  
 10 F-NT2RP3000350//Homo sapiens cosmid 1F1, complete sequence.//3.4e-79:174:88//AF065393  
 F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//2.2e-127:816:85//M25757  
 F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds.//0.0075:288:  
 15 58//D83743  
 F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds.//7.1e-134:693:94//L04966  
 F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:308:60//AJ011318  
 F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//0.00012:441:58//Z72642  
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//5.0e-174:841:97//AF071185  
 F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053\_B\_8, complete sequence.//7.9e-53:817:  
 20 68//AC006083  
 F-NT2RP3000433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681  
 F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence.//4.0e-19:169:  
 25 81//AL026471  
 F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488  
 F-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650  
 30 F-NT2RP3000451//HS\_2024\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=1, genomic survey sequence.//0.011:367:57//AQ229420  
 F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548  
 F-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353  
 35 F-NT2RP3000487//H.sapiens CpG island DNA genomic Mse1 fragment, clone 11b11, forward read cpg11b11.ft1a.//1.7e-11:96:92//Z64440  
 F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667  
 F-NT2RP3000526//Homo sapiens full-length insert cDNA clone YZ38E04.//4.1e-30:283:76//AF086071  
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966  
 40 F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260  
 F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554  
 F-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//9.0e-171:827:98:  
 45 45 AC006012  
 F-NT2RP3000562  
 F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271  
 F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597  
 50 F-NT2RP3000584  
 F-NT2RP3000590//H.sapiens CpG island DNA genomic Mse1 fragment, clone 170d7, forward read cpg170d7.ft1a.//3.0e-22:128:100//Z59723  
 F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868  
 55 F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305  
 F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043

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- F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds./.0.37:520:57//L14320  
F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence./.8.8e-155:526:97//AC006128  
5 F-NT2RP3000622//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence./.4.1e-29:238:85//AQ175104  
F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence./.0.47:75:80//AC004890  
F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete 10 sequence./.0.078:393:58//AL031313  
F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds./.1.4e-96:541:79//U71363  
F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces./.5.2e-46:421:77//AC005089  
F-NT2RP3000661  
15 F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence./.1.7e-11:292:65//AL022237  
20 F-NT2RP3000685//H.sapiens mRNA for novel protein./.2.4e-80:460:92//X99961  
F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 Taql fragment, SC6pA10F6./.1.0:141:65//Z77872  
F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds./.6.1e-20:127:96//D50930  
F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds./.1.1e-46:622:67//AF015264  
25 F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds./.4.7e-37:429:70//U16655  
F-NT2RP3000753  
F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence./.2.8e-38:519:69//Z99281  
F-NT2RP3000815//HS\_2237\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence./.0.79:151:61//AQ067252  
30 F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds./.0.36:378:58//L39387  
F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds./.0.0025:291:62//U02513 F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete cds, clone 9C4./.0.69:563:57//M29009  
35 F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments./.2.1e-46:666:68//Z86062  
F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence./.3.4e-92:193:93//AC005581  
40 F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02./.3.4e-32:261:81//D16938  
F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces./.5.1e-44:358:81//AC005082  
F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LNHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectin precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast, plant and worm proteins. Contains ESTs and STSs, complete sequence./.4.4e-123:150:98//AL021940  
50 F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence./.0.016:185:65//B60831  
F-NT2RP3000865  
F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds./.2.0e-29:766:60//U53445  
55 F-NT2RP3000869//H.sapiens gene for plectin./.1.1e-12:700:60//Z54367  
F-NT2RP3000875//HS\_2236\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=N, genomic survey sequence./.0.98:153:68//AQ154007  
F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL27) gene, complete cds./.0.44:213:65//

AF021340  
 F-NT2RP3000904//Rat Na<sup>+</sup> channel mRNA, 3' end.//3.6e-106:505:99//M27223  
 F-NT2RP3000917//Mouse mRNA for Dhm1 protein, complete cds.//3.1e-132:691:93//D38517  
 F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//  
 5 3.2e-97:585:88//AF015264  
 F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:  
 89//U91326  
 F-NT2RP3000980//R.norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335  
 F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 10 Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529  
 F-NT2RP3001004//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39c1, reverse read cpg39c1.rt1a./  
 15.9e-27:150:99//Z60925  
 F-NT2RP3001007//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:  
 610:57//AC006039  
 15 F-NT2RP3001055//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORK-  
 ING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653  
 F-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927  
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//  
 AF060219  
 20 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325  
 F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 2305P8, genomic survey se-  
 quence.//3.4e-37:222:93//AQ021278  
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712:64//D86969  
 F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pdJ457j11 containing DNA polymerase gamma  
 25 (polg) gene, complete sequence.//2.7e-116:186:99//AC005317  
 F-NT2RP3001111  
 F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers DXS366 and DXS87 on chro-  
 mosome X.//2.4e-05:702:58//Z68871  
 F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.9e-170:821:98//  
 30 AC005189  
 F-NT2RP3001116//HS\_3075\_A1\_F01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581  
 F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
 35 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,  
 complete sequence.//1.4e-121:598:97//AL031864  
 F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U09367  
 F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:  
 64//Z49078  
 F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds.//0.00021:529:60//  
 40 AF027735  
 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851:98//AB018305  
 F-NT2RP3001147//RPCI11-3M16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-3M16, genomic survey se-  
 quence.//2.1e-15:106:96//B48859  
 F-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
 45 DRAFT SEQUENCE.//2.0e-159:418:95//AL034379  
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891:98//AJ006266  
 F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, com-  
 plete sequence.//1.1e-69:207:97//AL034351  
 F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 50 DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507  
 F-NT2RP3001216//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-  
 05:561:56//AC004845  
 F-NT2RP3001221  
 F-NT2RP3001232//Mouse mRNA for serine protease PC6, comlete cds.//1.0e-11:120:87//D12619  
 55 F-NT2RP3001236  
 F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501:61//X51396  
 F-NT2RP3001245//CITBI-E1-2505C1.TF.1 CITBI-E1 Homo sapiens genomic clone 2505C1, genomic survey se-  
 quence.//8.5e-70:337:100//AQ242007

F-NT2RP3001253//CITBI-E1-2505N14.TR CITBI-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence./0.83:235:60//AQ260430  
 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds./3.8e-47:761:64//AB018269  
 F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds./2.3e-64:618:72//  
 5 AF027513  
 F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein./2.6e-99:669:83/Y18101  
 F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds./0.99:400:58//U07561  
 10 F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence./5.9e-39:304:  
 70//AC005837  
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds./7.6e-47:544:69//D87457  
 F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds./2.4e-27:547:63//AF047465  
 15 F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces./0.00022:624:60//AC004709  
 F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12./0.25:523:59//AF078790  
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds./5.1e-29:345:73//D86966  
 F-NT2RP3001339//Rattus norvegicus mytonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds./1.2e-151:821:91//AF021935  
 20 F-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds./5.3e-27:247:81//AF083105  
 F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT  
 SEQUENCE, 7 unordered pieces./2.1e-16:130:76//AC000052  
 F-NT2RP3001356  
 F-NT2RP3001374  
 25 F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27./0.00082:365:  
 61//AL008628  
 F-NT2RP3001384//Homo sapiens HRIHFB2018 mRNA, partial cds./6.4e-157:743:98//AB015332  
 F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-qter. Contains STS, complete sequence./0.045:359:61//Z82198  
 30 F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence./1.3e-16:336:65//AC004296  
 F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds./3.1e-100:711:82//U49046  
 F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence./5.4e-20:245:73//  
 AC005521  
 35 F-NT2RP3001407//RPCI11-41A20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41A20, genomic survey sequence./0.051:306:59//AQ029031  
 F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs./0.90:170:65//AL021327  
 F-NT2RP3001426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING  
 40 DRAFT SEQUENCE./2.9e-89:138:98//AL031447  
 F-NT2RP3001427//CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence./8.1e-36:212:94//AQ020997  
 F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds./8.5e-73:  
 431:91//U69668  
 45 F-NT2RP3001432//HS\_3032\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence./0.00024:111:76//AQ096619  
 F-NT2RP3001447  
 F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence./2.1e-105:223:99//AL031282  
 50 F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds./0.75:  
 349:59//AF026065

F-NT2RP3001457  
 F-NT2RP3001459  
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//  
 AF072836  
 5 F-NT2RP3001490  
 F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//1.0e-26:191:90//U13395  
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//  
 8.5e-171:804:98//AF064801  
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete, cds.//8.9e-140:743:  
 10 91//U36499  
 F-NT2RP3001529//Streptomyces griseus DNA for ribosoma protein L21, ribosomal protein L27, Obg, complete  
 cds.//2.1e-14:517:59//D87916  
 F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence.//4.7e-05:217:  
 63//AF078176  
 15 F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1A MAP1A (Mtap-1) mRNA, complete cds.//  
 4.3e-17:332:67//M83196  
 F-NT2RP3001580//RPCI11-91E19.TV RPCI11 Homo sapiens genomic clone R-91E19, genomic survey se-  
 quence.//4.2e-15:110:91//AQ281332  
 F-NT2RP3001587//S.pombe chromosome II cosmid c16H5.//6.6e-28:491:64//AL022104  
 20 F-NT2RP3001589//RPCI11-68M15.TK RPCI11 Homo sapiens genomic clone R-68M15, genomic survey se-  
 quence.//8.7e-108:517:98//AQ237629  
 F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete  
 sequence.//1.0e-09:257:65//AC004674  
 25 F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component A alpha chain, methane mo-  
 nooxygenase A beta chain and methane monooxygenase component C genes, complete cds.//0.59:450:57//  
 M90050  
 F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger  
 protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST,  
 30 STS, GSS, complete sequence.//1.8e-42:278:79//AL021808  
 F-NT2RP3001629  
 F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97//AJ130978  
 F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.018:127:66//Z68117  
 F-NT2RP3001646  
 35 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4e-171:816:98//AJ012449  
 F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds.//1.6e-  
 38:542:66//U49793  
 F-NT2RP3001676//HS\_3090\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=3090 Col=7 Row=D, genomic survey sequence.//3.1e-07:333:64//AQ123250  
 F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3; P1 clone DS01859, WORK-  
 ING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539:57//AC004358  
 F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
 non-small cell lung cancer , segment 3/11.//2.8e-130:355:96//AB020860  
 F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//  
 2.1e-37:512:70//AF059273  
 45 F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey se-  
 quence.//2.8e-19:123:95//AQ012480  
 F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds.//9-4e-11:167:74//D31962  
 F-NT2RP3001708//H.sapiens CpG island DNA genomic Mse1 fragment, clone 4g7, reverse read cpg4g7.rt1d.//  
 1.3e-17:113:97//Z61312  
 50 F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein.//2.2e-95:601:88//X99642  
 F-NT2RP3001716  
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.4e-159:  
 565:97//AF054177  
 F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2)-mRNA, partial cds.//1.7e-132:786:  
 88//AF008554  
 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds.//3.9e-104:811:78//D50918  
 55 F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete se-  
 quence.//6.5e-07:178:69//AC000097

F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence./.5.2e-31:311:77//AL031311  
 F-NT2RP3001753//Sequence 29 from patent US 5658882./.0.11:513:58//I62381  
 F-NT2RP3001764//Sequence 6 from Patent WO9706245./.6.4e-47:673:66//A59888  
 5 F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10./.0.078:290:63//U39644  
 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds./.2.8e-151:710:98//AB007928  
 F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds./.1.2e-26:213:85//  
 U13262  
 F-NT2RP3001799//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING  
 10 DRAFT SEQUENCE./.8.4e-51:168:95//AL031284  
 F-NT2RP3001819//S.glaucescens genes strU, strX, strV and strW for 5'-hydroxystreptomycin pruduction and  
 transport polypeptides./.0.084:526:58//X89010  
 F-NT2RP3001844//HS\_3110\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3110 Col=19 Row=J, genomic survey sequence./.1.5e-40:232:82//AQ140433  
 15 F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces./.0.14:452:58//AC005505  
 F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknox1) mRNA, complete cds./.2.7e-39:575:67//  
 AF061270  
 F-NT2RP3001857//M.musculus tex292 mRNA (5'region)./.8.7e-07:106:81//X80434  
 20 F-NT2RP3001896  
 F-NT2RP3001898//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 163G9, WORKING  
 DRAFT SEQUENCE./.0.094:456:60//AL008733  
 F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence./.0.58:482:56//Z73969  
 F-NT2RP3001926//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
 25 DRAFT SEQUENCE./.0.42:401:58//AL034557  
 F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence./.3.1e-28:  
 263:77//AC004651  
 F-NT2RP3001931  
 F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey se-  
 30 quence./.3.6e-24:182:91//B95475  
 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds./.1.8e-165:815:96//AB014575  
 F-NT2RP3001944  
 F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPCI11-350L7, WORKING DRAFT SEQUENCE,  
 35 72 unordered pieces./.4.8e-62:304:89//AC005844  
 F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2),  
 CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein  
 (cg2), and CG7 (cg7) genes, complete cds./.8.2e-10:564:60//AF030694  
 F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs./.2.5e-57:361:80//  
 Z83822  
 40 F-NT2RP3002004//Sequence 3 from patent US 5798245./.1.6e-26:104:100//AR025386  
 F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syn-  
 drome region, complete sequence./.0.0053:633:58//AC004137  
 F-NT2RP3002014//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), com-  
 plete sequence./.1.3e-32:334:68//AC004640  
 45 F-NT2RP3002033//H.sapiens DNA sequence./.0.012:214:63//Z22493  
 F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin./.8.7e-  
 116:713:86//X53773  
 F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162./.1.6e-12:613:60//  
 AL021841  
 50 F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X./.0.17:566:59//Z77249  
 F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces./.  
 3.3e-24:167:82//AC005682  
 F-NT2RP3002062  
 55 F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4./.0.24:508:58//  
 AJ235272  
 F-NT2RP3002081//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2001 Col=11 Row=J, genomic survey sequence./.9.7e-22:155:90//AQ218494  
 F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-

plete sequence./.9.6e-66:562:77//AC006210  
 F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence./.5.9e-16:214:74//AQ018040  
 F-NT2RP3002108  
 5 F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence./.7.6e-29:414:68//AC004020  
 F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds./.0.96:434:60//AF003370  
 F-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING  
 10 DRAFT SEQUENCE./.1.3e-63:380:91//AL031710  
 F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence./.9.9e-60:  
 315:80//U95742  
 F-NT2RP3002163  
 F-NT2RP3002165//M.musculus HCNGP mRNA./.1.4e-142:867:87//X68061  
 15 F-NT2RP3002166//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence./.0.090:394:59//  
 AC006121  
 F-NT2RP3002173//HS\_3062\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3062 Col=9 Row=N, genomic survey sequence./.3.3e-101:509:96//AQ193219  
 F-NT2RP3002181//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger  
 20 protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST,  
 STS, GSS, complete sequence./.4.5e-106:432:84//AL021808  
 F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence./.0.63:353:60//  
 AC005321  
 F-NT2RP3002248//HS\_3029\_A1\_D10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3029 Col=19 Row=G, genomic survey sequence./.3.5e-10:125:79//AQ094880  
 F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5'  
 end./.5.6e-09:629:59//L14321  
 F-NT2RP3002273//cSRSL-165E12-u cSRSL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
 30 clone cSRSL-165E12, genomic survey sequence./.4.9e-35:366:74//B03004  
 F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex./.0.023:326:  
 60//X64898  
 F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of  
 the complete genome./.3.8e-12:643:57//AE000810  
 F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING  
 35 DRAFT SEQUENCE, 3 unordered pieces./.1.6e-09:490:60//AC005504  
 F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome  
 4p16.3, containing STS matches./.1.9e-93:572:88//Z49862  
 F-NT2RP3002343//HS\_3010\_A2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3010 Col=16 Row=C, genomic survey sequence./.9.0e-75:373:97//AQ119068  
 40 F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase  
 (EC 1.5.1.15).//4.9e-64:588:75//X16396  
 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form./.  
 1.3e-164:770:98//Y16355  
 F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds./.1.4e-190:911:98//AB018331  
 45 F-NT2RP3002399  
 F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds./.7.2e-25:249:79//D89340  
 F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds./.1.2e-138:649:99//AB014578  
 F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey se-  
 quence./.5.0e-18:115:96//B78927  
 50 F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence./.0.00020:170:65//Z49068  
 F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence./.1.6e-59:308:97//AF091088  
 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds./.1.4e-144:763:93//  
 U35246  
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds./.1.8e-178:833:98//AB018272  
 55 F-NT2RP3002549//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces./.4.7e-  
 26:123:72//AC004821  
 F-NT2RP3002566//Streptomyces viridifaciens sigma factor (hrdD) gene, complete cds./.0.76:459:59//U60418  
 F-NT2RP3002587//Homo sapiens chromosome Y, clone 264,M,20, complete sequence./.4.6e-13:199:76//

AC004617  
 F-NT2RP3002590//*Porphyra purpurea* chloroplast, complete genome./.0.88:284:60//U38804  
 F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK Homo sapiens genomic clone A-441H11, genomic survey sequence./.2.0e-22:140:95//B68331  
 5 F-NT2RP3002603  
 F-NT2RP3002628//*C.acetobutylicum* dnaJ and orfB genes./.2.0e-05:333:60//X69050  
 F-NT2RP3002631  
 F-NT2RP3002650//*Mus musculus* mRNA for cartilage-associated protein (CASP)./.1.5e-20:641:62//AJ006469  
 F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes./.5.2e-05:621:59//Z78205  
 10 F-NT2RP3002660//Homo sapiens PAC clone DJ1006K12 from 7q31.2-q31, complete sequence./.0.98:453:57//AC004946  
 F-NT2RP3002663//Homo sapiens chromosome 19, cosmid F6697, complete sequence./.3.3e-22:407:67//AC006129  
 F-NT2RP3002671//*S.pombe* chromosome III cosmid c553./.1.0e-12:336:66//AL023704  
 15 F-NT2RP3002682//*Caenorhabditis elegans* cosmid F17C11, complete sequence./.1.3e-21:448:64//Z72507  
 F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK Homo sapiens genomic clone A-789B1, genomic survey sequence./.2.5e-25:173:91//B51656  
 F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds./.1.2e-73:728:74//D17577  
 F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 Homo sapiens genomic clone 2507L14, genomic survey se-  
 20 quence./.0.0012:55:92//AQ263530  
 F-NT2RP3002713  
 F-NT2RP3002763//*Caenorhabditis elegans* cosmid T20F10, complete sequence./.0.98:209:63//Z81594  
 F-NT2RP3002770  
 25 F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short variant, partial cds./.0.78:515:57//AF029325  
 F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence./.1.9e-21:167:79//AL022718  
 30 F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence./.0.32:187:66//AC005549  
 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds./.6.9e-54:615:70//AF004715  
 F-NT2RP3002861//*Caenorhabditis elegans* cosmid M03F4./.4.2e-05:226:65//U64601  
 35 F-NT2RP3002869//*Mus musculus* semaphorin VIa mRNA, complete cds./.2.0e-93:638:83//AF030430  
 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds./.8.5e-89:557:88//AB001895  
 F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces./.7.9e-12:160:78//AC006087  
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds./.5.7e-180:853:98//AB018314  
 F-NT2RP3002911//RPCI11-24N15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-24N15, genomic survey  
 40 sequence./.2.3e-13:442:61//B88815  
 F-NT2RP3002948//, complete sequence./.2.2e-110:637:91//AC005500  
 F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence./.1.7e-166:  
 793:98//AC005754  
 F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5./.0.00011:61:95//D17024  
 45 F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds./.1.2e-128:808:85//D30666  
 F-NT2RP3002972//*H.sapiens* (xs168) mRNA, 381bp./.1.5e-43:312:85//Z36820  
 F-NT2RP3002978//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./.0.00044:527:57//AC005505  
 F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence./.0.92:341:60//AC001644  
 50 F-NT2RP3002988//HS\_3015\_A1\_B07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence./.4.4e-05:379:58//AQ091708  
 F-NT2RP3003008//*Mus musculus* major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes./.1.4e-72:  
 197:79//AF109905  
 55 F-NT2RP3003032//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-80, complete sequence./.1.6e-08:809:58//AL010153  
 F-NT2RP3003059//*Rattus norvegicus* potassium channel regulator 1 mRNA, complete cds./.4.1e-111:804:81//U78090

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F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1).//1.4e-12:633:59//X16609  
F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//0.034:282:60//AC002410  
F-NT2RP3003071//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read  
cpg13d12.r1c.//6.8e-15:95:100//Z64565  
5 F-NT2RP3003078  
F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//8.1e-72:732:71//D88315  
F-NT2RP3003121  
F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.5e-12:168:76//  
AC004510  
10 F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//4.0e-148:908:87//  
D12646  
F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//  
U17995  
F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.5e-22:430:63//AF017639  
15 F-NT2RP3003150  
F-NT2RP3003157//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-92:493:94//AQ155489  
F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete  
cds.//8.6e-06:228:65//AF064868  
20 F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:737:71//X78933  
F-NT2RP3003197  
F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//  
4.1e-48:640:67//AF015264  
F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:81//U31059  
25 F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799  
F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//6.3e-75:  
776:74//U20286  
F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-62:575:74//AJ006064  
F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//3.7e-128:617:98//AF055460  
30 F-NT2RP3003251//H.sapiens Staf50 mRNA.//3.5e-67:651:76//X82200  
F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC004153  
F-NT2RP3003278//H.sapiens CpG island DNA genomic Mse1.fragment, clone 28b4, forward read cpg28b4.ft1a.//  
4.0e-27:174:93//Z60555  
35 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//1.3e-131:694:93//L36983  
F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds.//1.7e-64:662:  
71//AF004162  
F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds.//4.9e-37:682:64//  
D85610  
40 F-NT2RP3003302//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.6e-95:680:82//AC006213  
F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete se-  
quence.//1.0:191:62//AC004527  
F-NT2RP3003313//Streptomyces coelicolor cosmid 5A7.//0.0084:403:61//AL031107  
F-NT2RP3003327//H.sapiens Staf50 mRNA.//2.5e-29:253:67//X82200  
45 F-NT2RP3003330  
F-NT2RP3003344  
F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//9.0e-41:296:  
84//AC005284  
F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a  
50 BAC end-sequence (GSS).//0.047:404:60//AL021069  
F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//  
8.3e-122:632:96//AC005519  
F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unor-  
dered pieces.//0.0036:127:74//AC000360  
55 F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//2.0e-110:843:79//U09874  
F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//AC002407  
F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//1.0e-20:430:  
63//U90653

F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds./.4.2e-139:524:90//AF071317

F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence./.8.8e-18:111:97//B40173

5 F-NT2RP3003433//HS\_2219\_B2\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence./.1.2e-57:410:83//AQ145866

F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds./.5.2e-181:853:98//AF004828

10 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds./.1.6e-173:826:98//AB018268

F-NT2RP3003491//CIT-HSP-2344O1.TR CIT-HSP Homo sapiens genomic clone 2344O1, genomic survey sequence./.1.2e-39:213:97//AQ057124

F-NT2RP3003500//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence./.0.025:253:60//AQ090347

15 F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL), complete sequence./.0.95:279:60//AC004234

F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequence./.1.8e-88:166:84//AC006049

F-NT2RP3003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE./.8.9e-17:245:72//AL031985

20 F-NT2RP3003564//HS\_3141\_B1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence./.2.7e-79:442:93//AQ187798

F-NT2RP3003572

F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces./.5.8e-55:275:84//AC005632

25 F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein./.1.1e-94:488:95//X56387

F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence./.6.0e-88:463:84//AC004235

F-NT2RP3003625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING DRAFT SEQUENCE./.0.98:307:60//AL031600

30 F-NT2RP3003656

F-NT2RP3003659//*F.rubripes* GSS sequence, clone 013G07cE7, genomic survey sequence./.1.7e-25:284:74//AL011271

F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence./.0.011:279:65//AC002096

35 F-NT2RP3003672

F-NT2RP3003680//*Drosophila melanogaster*; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, 9 unordered pieces./.3.4e-16:425:64//AC005811

F-NT2RP3003686//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence./.3.1e-27:153:98//AQ136993

40 F-NT2RP3003701

F-NT2RP3003716//*Rattus norvegicus* Shal-related potassium channel Kv4.3 mRNA, complete cds./.4.6e-107:788:82//U42975

F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds./.2.3e-148:700:98//AB018300

45 F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence./.0.39:212:61//AQ015785

F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYBGRIB, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete sequence./.4.2e-21:445:66//AL022326

F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence./.1.0:257:63//AF038458

50 F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds./.1.2e-63:484:81//M17031

F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence./.0.96:353:60//AC005321

F-NT2RP3003809//Bovine herpesvirus 1 complete genome./.7.2e-12:615:60//AJ004801

F-NT2RP3003819

- F-NT2RP3003825  
F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2).//6.2e-16:543:62//X17626  
F-NT2RP3003831//RPCI11-50N15.TJ RPCI11 Homo sapiens genomic clone R-50N15, genomic survey sequence.//1.1e-21:174:85//AQ082633
- 5 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e-47:242:98//AF070611  
F-NT2RP3003842//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//9.7e-25:143:97//AQ195884  
F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.2e-36:335:68//AB018268
- 10 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4.1e-174:805:99//AB018343  
F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:709:84//U19181  
F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.//8.9e-11:193:70//U20554  
F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//2.6e-47:404:77//AF057358
- 15 F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597:55//AC005504  
F-NT2RP3003989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404H4, WORKING DRAFT SEQUENCE.//0.37:548:56//AL031661  
F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG2) mRNA, complete cds.//0.021:433:58//U58837
- 20 F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//1.4e-164:838:94//X84692  
F-NT2RP3004016//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING DRAFT SEQUENCE.//0.00042:356:62//AL031726  
F-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 809F4, WORKING DRAFT SEQUENCE.//6.8e-112:627:82//AL022400
- 25 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774:67//AB002317  
F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//7.9e-17:484:62//AL021939
- 30 F-NT2RP3004078//M.musculus (BALB/c) MRFX2 mRNA.//1.9e-102:684:83//X76089  
F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence.//0.021:207:63//B09433  
F-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.5e-25:272:77//AC005038
- 35 F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.6e-28:223:73//AC003973  
F-NT2RP3004125//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds.//2.2e-28:637:63//AF000560  
F-NT2RP3004145  
F-NT2RP3004148
- 40 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds.//6.5e-120:578:98//AF032900  
F-NT2RP3004189//M.musculus tex292 mRNA (5'region).//1.1e-06:102:82//X80434  
F-NT2RP3004206//D.melanogaster crn mRNA.//7.3e-69:715:71//X58374  
F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//4.8e-42:650:66//D64009
- 45 F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//8.4e-55:184:84//D42052  
F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//0.22:458:60//AC006084  
F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence.//1.6e-29:409:69//Z22181
- 50 F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//3.6e-117:242:100//AC005385  
F-NT2RP3004253//H.sapiens 28S rRNA V8 region (LAN5-6).//2.6e-12:589:59//X69353  
F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//1.2e-88:489:91//AF013967  
F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//3.1e-153:733:98//AF088982  
F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//1.3e-24:597:61//AF007871
- 55 F-NT2RP3004332  
F-NT2RP3004334//L.esculentum gene for fruit ripening polygalacturonase.//0.23:501:57//X80908  
F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence.//0.0014:198:66//Z93020

F-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877  
 F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025  
 F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23 :352:67//AC005653  
 F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249  
 F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678  
 F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206  
 F-NT2RP3004451//RPCI11-51J15.TK RPCI11 Homo sapiens genomic clone R-51J15, genomic survey sequence.//8.8e-19:180:82//AQ052326  
 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917  
 F-NT2RP3004466//HS\_3038\_B2\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458  
 F-NT2RP3004470//H.sapiens CpG island DNA genomic Mse1 fragment, clone 81a11, reverse read cpg81a11.rt1a.//7.0e-25:148:96//Z56029  
 F-NT2RP3004472//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//1.6e-20:143:92//AQ052792  
 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925  
 F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//U47024  
 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851  
 F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//4.0e-67:265:84//AC006023  
 F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.2e-55:415:78//AC004673  
 F-NT2RP3004504//M.musculus mRNA for CPEB protein.//2.0e-110:618:91//Y08260  
 F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//AC005328  
 F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574  
 F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316  
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532  
 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126  
 F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Emzf1) mRNA, complete cds.//6.9e-18:433:64//AF031955  
 F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//5.3e-15:138:84//AQ280780  
 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//1.0e-179:860:97//AF026445  
 F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946  
 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266  
 F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1 unordered pieces.//9.3e-14:360:65//AC004977  
 F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.9e-52:539:73//AF005355  
 F-NT2RP3004669//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.046:437:57//S69350  
 F-NT2RP3004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.9e-05:625:59//Z98882  
 F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//1.5e-155:844:92//AC006121  
 F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.//0.012:417:59//AB012242  
 F-NT2RP4000035//Homo sapiens BAC clone NH035P23 from 2, complete sequence.//8.0e-18:242:74//AC005035  
 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds.//2.1e-81:556:85//AF029761  
 F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP).//1.6e-19:654:63//AJ006469  
 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5e-149:720:97//AJ012449  
 F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:336:57//AL034558

F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds./.4.4e-166:774:99//AB011538  
 F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor./.2.6e-137:678:91//X75931  
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds./.3.3e-114:548:98//AB007952  
 F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds./.1.2e-104:677:85//U35776  
 F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds./.7.2e-54:327:74//L20681  
 F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence./.2.2e-62:360:92//AF091088  
 F-NT2RP4000159//RPCI11-75N16.TJ RPCI11 Homo sapiens genomic clone R-75N16, genomic survey sequence./.2.6e-19:119:98//AQ267551  
 10 F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence./.3.3e-49:683:67//AC006210  
 F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region./.1.1e-99:543:93//U92989  
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds./.4.9e-174:825:98//AB014600  
 F-NT2RP4000212//, complete sequence./.4.0e-131:233:94//AC005300  
 15 F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence./.1.8e-161:751:99//AC005261  
 F-NT2RP4000218//RPCI11-69B7.TJ RPCI11 Homo sapiens genomic clone R-69B7, genomic survey sequence./.1.7e-84:413:98//AQ268504  
 20 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470  
 F-NT2RP4000246//Mus musculus neural variant mena+++ protein (Mena) mRNA, complete cds./.2.1e-120:707:  
 87//U72523  
 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence./.2.8e-128:604:99//AF091092  
 F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence./.0.27:124:69//AQ043515  
 25 F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w./.8.6e-32:619:63//Z71408  
 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds./.4.7e-41:685:63//D63481  
 F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds./.6.9e-05:756:59//  
 U59322  
 F-NT2RP4000323  
 30 F-NT2RP4000355  
 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds./.2.0e-140:654:99//AB018281  
 F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds./.2.6e-  
 135:649:97//AF044195  
 F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4./.2.0e-23:524:62//  
 AJ235272  
 F-NT2RP4000376//Sequence 1 from patent US 5580968./.1.6e-115:716:87//I30536  
 F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c./.4.3e-  
 05:450:58//D63850  
 F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence./.9.2e-  
 40 37:336:69//AC006116  
 F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8./.0.30:222:60//U56966  
 F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4./.1.8e-48:580:69//AL021086  
 F-NT2RP4000424//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence./.1.6e-42:265:81//  
 AC003101  
 45 F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey se-  
 quence./.2.0e-56:287:98//AQ110194  
 F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey se-  
 quence./.2.4e-42:236:95//AQ076183  
 F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence./.0.17:158:67//AC003982  
 50 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:  
 532:57//Z72499  
 F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds./.0.0094:616:58//U10483  
 F-NT2RP4000481  
 F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150./.5.7e-24:633:60//Z38125  
 55 F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor./.2.4e-62:667:73//X74904  
 F-NT2RP4000515  
 F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence./.1.6e-179:851:  
 98//AC006238

- F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial./.6.7e-33:203:93//AJ010840  
 F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyro3) gene, alternative 5' coding exon 2C./.0.26:162:61//U23720  
 5 F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds./.1.2e-139:809:89//U32498  
 F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12./.1.0e-06:404:59//AF003386  
 F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)), complete sequence./.1.3e-05:  
 10 498:58//AC002443  
 F-NT2RP4000556//Sequence 1 from Patent EP 0285405./.1.2e-18:586:61//I05465  
 F-NT2RP4000560//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence./.2.5e-53:183:82//AF059580  
 F-NT2RP4000588//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE./.0.00062:253:65//AL033543  
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds./.3.2e-138:666:98//  
 15 AF067730  
 F-NT2RP4000638//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence./.3.0e-06:78:89//AQ099333  
 F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds./.1.9e-11:104:85//AB017335  
 20 F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1./.0.34:350:62//AF100904  
 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856./.3.3e-167:785:  
 99//AB004852  
 F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds./.3.7e-07:261:65//U61149  
 F-NT2RP4000724//Human endogenous retrovirus env mRNA./.9.2e-136:474:89//X82272  
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds./.3.1e-41:350:71//AB011178  
 25 F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds./.1.0:504:58//  
 L19301  
 F-NT2RP4000739//CIT-HSP-2010O22.TR CIT-HSP Homo sapiens genomic clone 2010O22, genomic survey sequence./.1.1e-24:161:93//B57903  
 F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence./.0.052:493:58//AC004917  
 30 F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds./.9.6e-18:259:68//U22818  
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds./.1.5e-174:816:98//AB007939  
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence./.0.97:52:92//  
 35 AC005189  
 F-NT2RP4000837//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE./.2.1e-128:644:97//AL034420  
 F-NT2RP4000839//RPCI11-6D8.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6D8, genomic survey sequence./.1.5e-44:281:91//B48216  
 40 F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds./.9.5e-43:722:64//D87515  
 F-NT2RP4000865//Human zinc finger protein ZNF136./.6.8e-95:415:78//U09367  
 F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein./.7.0e-87:646:80//  
 AJ001616  
 F-NT2RP4000879//N.tabaccum mRNA for ubiquitin activating enzyme E1./.9.0e-17:806:58//Y10804  
 45 F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds./.6.8e-153:934:86//  
 D45913  
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein./.9.4e-79:584:78//AJ224901  
 F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence./.2.0e-08:609:58//AC004290  
 50 F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds./.3.5e-64:415:  
 87//U42975  
 F-NT2RP4000927//H.sapiens genomic DNA (chromosome 3; clone NRL062R).//.0.75:175:62//X87547  
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds./.3.5e-163:781:97//  
 AF069532  
 F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence WORKING DRAFT SEQUENCE, 4 unordered pieces./.0.94:763:56//AC004688  
 55 F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces./.1.0e-128:673:96//AC005519  
 F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence./.1.6e-15:255:69//AL032657

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F-NT2RP4000975//CIT-HSP-2307I6.TF CIT-HSP Homo sapiens genomic clone 2307I6, genomic survey sequence./.6.5e-31:317:79//AQ015742  
F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end./.0.88:54:90//M22942  
F-NT2RP4000984//Rhodobacter sphaeroides mRNA./.0.76:214:64//M83823  
5 F-NT2RP4000989//*F.rubripes* GSS sequence, clone 011A11aE12, genomic survey sequence./1.0:149:65//AL010911  
F-NT2RP4000996//Penaeus setiferus microsatellite Pse017 repeat region./.3.3e-08:139:74//AF047358  
F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds./.3.6e-126:824:  
10 84//AF025424  
F-NT2RP4001004  
F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds./.1.4e-110:861:  
78//U83176  
F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds./.2.0e-135:789:  
89//U67140  
15 F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds./.3.7e-120:718:88//  
U20086  
F-NT2RP4001041//*Schizosaccharomyces pombe* mRNA, partial cds, clone: SY 0717./.4.1e-22:452:64//D89170  
F-NT2RP4001057  
F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469  
20 F-NT2RP4001078//*Streptomyces coelicolor* cosmid 1C2./.0.0025:474:59//AL031124  
F-NT2RP4001079//Rat alternatively spliced mRNA./.1.4e-141:832:88//M93018  
F-NT2RP4001080//*H.sapiens* PTB-4 gene for polypyrimidine tract binding protein./.9.0e-64:628:70//X65372  
F-NT2RP4001086//*Homo sapiens* mRNA for KIAA0592 protein, partial cds./.4.7e-84:604:86//AB011164  
F-NT2RP4001095  
25 F-NT2RP4001100//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey se-  
quence./.9.4e-17:185:79//AQ263402  
F-NT2RP4001117//*Canis familiaris* sec61 homologue mRNA, complete cds./.1.0e-143:760:87//M96629  
F-NT2RP4001122  
30 F-NT2RP4001126//*Homo sapiens* shox gene, alternatively spliced products, complete cds./.4.2e-17:636:61//  
U82668  
F-NT2RP4001138//*Homo sapiens* PAC clone DJ1121E10 from 7q21.1-q2, complete sequence./.2.5e-23:408:60//  
AC004969  
F-NT2RP4001143//Sequence 5 from patent US 5753432./.1.8e-39:276:86//AR008079  
F-NT2RP4001148//*Homo sapiens* clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces./.2.7e-  
35 116:684:89//AC005095  
F-NT2RP4001149//*Mouse* mRNA for thymic epithelial cell surface antigen, complete cds./.3.0e-48:581:66//  
D67067  
F-NT2RP4001150//*Homo sapiens* alone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces./.9.4e-  
25:193:67//AC004952  
40 F-NT2RP4001159//Human FMR1 gene, 5' end./.0.28:130:66//L19476  
F-NT2RP4001174//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//.0.0014:187:67//  
S74494  
F-NT2RP4001206//*Dictyostelium discoideum* random slug cDNA19 protein (rscl9) mRNA, partial cds./.0.032:453:  
58//U82511  
45 F-NT2RP4001207//HS\_2248\_A1\_C03\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* ge-  
nomic clone Plate=2248 Col=5 Row=E, genomic survey sequence./.0.00018:58:94//AQ192358  
F-NT2RP4001210//*Homo sapiens* chromosome 10 clone CIT987SK-1019O18 map 10p11.2-10p12.1, complete  
sequence./.0.93:515:58//AC005877  
F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds./.3.6e-44:  
50 187:74//U37251  
F-NT2RP4001219//*Caenorhabditis elegans* cosmid Y47H9C, complete sequence./.1.3e-15:288:67//AL032657  
F-NT2RP4001228//*Homo sapiens* actin binding protein MAYVEN mRNA, complete cds./.2.2e-26:855:60//  
AF059569  
55 F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey  
sequence./.2.7e-15:101:98//B88081  
F-NT2RP4001256//*Amycolatopsis mediterranei* 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete  
cds./.1.0:459:59//U33061  
F-NT2RP4001260//Sequence 2 from Patent WO9601901./.0.0018:246:63//A48324

F-NT2RP4001274//Homo sapiens, complete sequence./.2.5e-05:201:67//AC005854  
 F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey se-  
 quence./.3.5e-18:138:92//AQ040728  
 5 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding  
 mitochondrial protein, complete cds./.7.4e-30:535:65//AF043250  
 F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5./.3.5e-145:795:91//AJ001119  
 F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey se-  
 quence./.8.4e-16:109:94//B89870  
 10 F-NT2RP4001339//HS\_3205\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3205 Col=15 Row=J, genomic survey sequence./.7.1e-24:305:73//AQ183725  
 F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence./.1.9e-17:106:91//  
 AC004918  
 F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase./.7.6e-40:631:66//X91011  
 15 F-NT2RP4001351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING  
 DRAFT SEQUENCE./.2.7e-30:608:64//AL031428  
 F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7./.0.23:540:57//AL031107  
 F-NT2RP4001372//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey se-  
 quence./.8.5e-23:129:100//AQ051701  
 20 F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1./.0.15:213:61//X78609  
 F-NT2RP4001375  
 F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311\_F\_12, complete sequence./.7.3e-28:153:  
 88//AC005722  
 F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence./.7.2e-47:518:73//  
 AC004691  
 25 F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds./.0.00079:686:57//J03998  
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds./.2.0e-76:818:71//D86957  
 F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein./.3.5e-87:839:73//X78933  
 F-NT2RP4001442  
 30 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds./.0.21:218:63//AB018326  
 F-NT2RP4001474//Human Nott linking clone 924A058R, genomic survey sequence./.7.6e-14:109:90//U49884  
 F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds./.2.5e-59:480:75//D10523  
 F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds./.9.7e-39:392:72//  
 AF049612  
 35 F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat./.2.7e-24:147:96//X61693  
 F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds./.0.  
 87:583:58//M32513  
 F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces./.0.93:394:58//AC005308  
 40 F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds./.3.1e-143:820:89//  
 U20086  
 F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w./.2.2e-05:319:61//Z71663  
 F-NT2RP4001551//S.pombe chromosome II p1 p8B7./.0.64:335:60//AL032684  
 F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Li-  
 brary) complete sequence./.1.0:309:58//AC004806  
 45 F-NT2RP4001567//HS\_2166\_B1\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2166 Col=13 Row=F, genomic survey sequence./.0.99:188:59//AQ086290  
 F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds./.7.0e-53:566:72//D79989  
 F-NT2RP4001571//RPCI11-21F20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F20, genomic survey  
 sequence./.2.8e-19:119:97//B85885  
 50 F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop./.5.8e-129:813:85//X92987  
 F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein./.3.4e-131:795:86//AJ223830  
 F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase./.1.3e-14:663:59//X74219  
 F-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore hu-  
 man cosmid library) complete sequence./.6.4e-10:135:73//AC002364  
 55 F-NT2RP4001614//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3042 Col=10 Row=H, genomic survey sequence./.3.4e-06:78:89//AQ099333  
 F-NT2RP4001634  
 F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic

clone cSRL-161Fl, genomic survey sequence./4.9e-12:144:76//B02870  
 F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2./3.8e-69:437:86//Y11092  
 F-NT2RP4001656//HS\_2013\_A1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=1 Row=G, genomic survey sequence./2.0e-30:207:89//AQ224793  
 5 F-NT2RP4001677//*Hylobates lar* huntingtin gene, partial exon./0.23:105:71//L49362  
 F-NT2RP4001679//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE./2.7e-45:351:84//AL031431  
 F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence./1.8e-30:163:88//U96629  
 10 F-NT2RP4001725//*Drosophila melanogaster* DNA sequence (P1 DS08860 (D181)), complete sequence./1.1e-13:402:63//AC004296  
 F-NT2RP4001730//RPCI11-37M21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-37M21, genomic survey sequence./0.88:177:67//AQ029840  
 F-NT2RP4001739  
 15 F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read 12QTELOO023.seq./4.9e-36:192:98//Z96232  
 F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds./2.3e-140:866:86//L11316  
 F-NT2RP4001790//Homo sapiens clone NH0569I24, complete sequence./1.4e-29:327:74//AC005678  
 F-NT2RP4001803  
 20 F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds./1.0e-16:576:60//AF054841  
 F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAPI2 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete sequence./2.1e-08:601:59//Z98743  
 25 F-NT2RP4001828  
 F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds./2.2e-53:555:73//D31888  
 F-NT2RP4001841  
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds./1.7e-55:813:65//AB014572  
 F-NT2RP4001861//Human simple repeat polymorphism./0.0014:145:66//M87691  
 30 F-NT2RP4001889//HS\_2052\_B1\_H06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=11 Row=P, genomic survey sequence./1.0e-23:187:86//AQ270425  
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence./7.3e-76:178:95//AC005014  
 F-NT2RP4001896//T3B4TFC TAMU *Arabidopsis thaliana* genomic clone T3B4, genomic survey sequence./0.99:  
 35 354:61//B26193  
 F-NT2RP4001901//*Streptomyces griseus* genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds./0.031:409:60//AB011413  
 F-NT2RP4001927//HS\_2216\_B1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=5 Row=H, genomic survey sequence./4.9e-32:216:89//AQ184677  
 40 F-NT2RP4001938//*Mus musculus* zinc finger protein (Zfp64) mRNA, complete cds./1.2e-83:709:79//U49046  
 F-NT2RP4001946//HS\_3021\_B2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=20 Row=P, genomic survey sequence./7.6e-09:120:76//AQ133185  
 F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence./2.1e-18:421:65//AL022577  
 F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 2294D14, genomic survey sequence./0.030:358:61//AQ005028  
 45 F-NT2RP4001966//*Mus musculus* DOC4 (Doc4) mRNA, complete cds./2.5e-68:812:68//AF059485  
 F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence./1.9e-57:555:75//AC003976  
 F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence./8.9e-21:123:98//B01950 F-NT2RP4002047//*Saccharomyces cerevisiae* chromosome XII cosmid 8003./1.6e-29:520:64//U17243  
 55 F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence./2.8e-22:137:96//B80243  
 F-NT2RP4002058//T20L11-T7 TAMU *Arabidopsis thaliana* genomic clone T20L11, genomic survey sequence./0.019:141:65//AQ248640

F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence.//0.99:163:63//AQ027223  
 F-NT2RP4002075//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841  
 5 F-NT2RP4002078//RPCI11-73M20.TJ RPCI11 Homo sapiens genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030  
 F-NT2RP4002081//F.rubripes GSS sequence, clone 190O22bB9, genomic survey sequence.//0.0024:350:60//Z92062  
 F-NT2RP4002083//M.musculus tex27 mRNA.//8.2e-77:456:89//X80437  
 10 F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LET-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515  
 F-NT2RP4002791  
 F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383  
 15 F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//6.5e-91:672:83//AC004662  
 F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197  
 F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901  
 20 F-NT2RP5003477//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380  
 F-NT2RP5003492  
 F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-111:623:93//Z81365  
 25 F-NT2RP5003506//H.sapiens CpG island DNA genomic Mse1 fragment, clone 71h2, reverse read cpg71h2.rt1a.//1.4e-49:283:93//Z62703  
 F-NT2RP5003512//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312  
 F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236  
 30 F-NT2RP5003524//Homo sapiens beta-spectrin (HS<sub>p</sub>TB1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178  
 F-NT2RP5003534//H.sapiens CpG island DNA genomic Mse1 fragment, clone 14c10, forward read cpg14c10.f11b.//0.00013:70:91//Z54631  
 35 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934  
 F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510  
 F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.//9.1e-56:392:84//U38933  
 F-OVARC1000013  
 40 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922  
 F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674  
 F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds.//6.8e-36:238:89//AF064603  
 F-OVARC1000058  
 F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625  
 45 F-OVARC1000068//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883  
 F-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387  
 F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259  
 F-OVARC1000087//HS\_2004\_B2\_E11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037  
 50 F-OVARC1000091//nbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020P17r, genomic survey sequence.//5.2e-05:238:64//AQ258489  
 F-OVARC1000092//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.1e-10:720:58//AC004617  
 F-OVARC1000106//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369  
 F-OVARC1000109  
 F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250

5 F-OVARC1000114//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574  
 F-OVARC1000133//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027  
 F-OVARC1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640

10 F-OVARC1000145//HS\_2257\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-30:203:90//AQ304854  
 F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703  
 F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//I64695

15 F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequence.//4.9e-19:381:63//AC005764  
 F-OVARC1000191//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557  
 F-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//6.4e-161:781:97//AC004604

20 F-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//9.2e-33:511:65//AF068332  
 F-OVARC1000212//F.rubripes GSS sequence, clone 185L11aC1, genomic survey sequence.//1.1e-13:139:79//AL019910  
 F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//I81226

25 F-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-112:697:87//AF060194  
 F-OVARC1000288 2.2e-22:181:83//J00345  
 F-OVARC1000302//A-192A9.TP CIT978SK Homo sapiens genomic clone A-192A9, genomic survey sequence.//4.8e-18:110:99//B18003  
 F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574  
 F-OVARC1000309  
 F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.1e-122:325:95//AC005236

30 F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.0e-46:339:84//U19614  
 F-OVARC1000335//Caenorhabditis elegans cosmid F15B10.//0.020:545:57//AF036696  
 F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:252:59//AC005007  
 F-OVARC1000384//Homo sapiens expanded SCA7 CAG repeat.//2.2e-09:276:64//AF020275

35 F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//0.61:343:59//AC003693  
 F-OVARC1000411//S.cerevisiae chromosome XI reading frame ORF YKL202w.//0.075:242:60//Z28201  
 F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete sequence.//0.00088:285:62//AC005166

40 F-OVARC1000420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718  
 F-OVARC1000427//Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete sequence.//4.9e-30:195:84//AC005826  
 F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-05:651:59//AL034558

45 F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M74165  
 F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99//U09284  
 F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANS-GLUTAMINASE 3), and another member of the Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.0e-138:566:99//AB014583

50 F-OVARC1000461  
 F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//4.7e-

124:650:93//AF023451  
 F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence./.1.0e-15:  
 5 510:59//AC004221  
 F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic survey sequence./.2.5e-06:272:62//  
 AJ227191  
 F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding  
 protein).//1.1e-117:652:90//E12829  
 F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a  
 10 Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloro-  
 plast 30S ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691  
 and STSs./.1.7e-13:709:60//Z99297  
 F-OVARC1000496//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING  
 DRAFT SEQUENCE./.6.0e-23:316:72//AL031733  
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds./.2.1e-113:539:99//AF051850  
 15 F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces./.  
 8.0e-149:716:98//AC005024  
 F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence./.5.8e-137:545:97//  
 AC004510  
 20 F-OVARC1000543//HS\_3055\_A2\_F10\_MF CIT Approved Human Genomic\_Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3055 Col=20 Row=K, genomic survey sequence./.0.19:104:71//AQ102820  
 F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3  
 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence./.4.4e-136:670:97//AL022069  
 F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete  
 25 sequence./.1.3e-15:262:69//AC002985  
 F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence./.1.9e-41:476:70//AF046733  
 F-OVARC1000573//HS\_3241\_B1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3241 Col=5 Row=P, genomic survey sequence./.2.2e-101:530:95//AQ211942  
 F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces./.9.7e-97:445:  
 30 90//AC002414  
 F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence./.9.1 e-27:354:  
 72//AC003973  
 F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-  
 domain containg transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and  
 35 GSSs, and a ca repeat polymorphism, complete sequence./.0.97:276:62//AL023775  
 F-OVARC1000605  
 F-OVARC1000622//Homo sapiens (subclone 2\_d8 from P1 H42) DNA sequence, complete sequence./.7.2e-60:  
 457:82//LB1648  
 F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence./.6.2e-58:499:80//AC002069  
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-  
 40 plete cds./.5.1e-77:424:93//D43772  
 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds./.4.8e-99:536:94//AB011162  
 F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone  
 cSRL-29c7, genomic survey sequence./.2.5e-57:336:91//B04244  
 F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7./.1.6e-81:291:84//AJ001713  
 45 F-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING  
 DRAFT SEQUENCE./.8.2e-158:782:96//AL034424  
 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds./.1.5e-151:549:99//AF027156  
 F-OVARC1000689//nxb0003aG01f CUGI Rice BAC Library Oryza sativa genomic clone nxb0003M01f, genomic  
 50 survey sequence./.0.17:499:60//AQ050003  
 F-OVARC1000700  
 F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene,  
 partial cds./.3.5e-26:425:65//U34925  
 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete  
 cds./.3.7e-109:451:91//AF038661  
 55 F-OVARC1000730  
 F-OVARC1000746  
 F-OVARC1000769//HS\_2056\_B2\_G06\_T7 CIT Approved Human Genomic Sperm-Library D Homo sapiens ge-  
 nomic clone Plate=2056 Col=12 Row=N, genomic survey sequence./.8.8e-19:147:86//AQ245905

- F-OVARC1000771//M.musculus mRNA for GTP-binding protein./.2.2e-62:305:78//X95403  
 F-OVARC1000781//Sequence 5 from Patent WO9722695./.1.9e-89:705:78//A63552  
 F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence./.3.0e-131:631:  
 98//AC004542
- 5 F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete sequence./.1.7e-32:295:80//  
 AC003691  
 F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered  
 pieces./.3.2e-55:356:88//AC004469  
 F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC./.9.5e-27:163:94//Y17711  
 10 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds./.6.0e-150:432:100//AB014543  
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds./.1.0e-135:632:99//AF045584  
 F-OVARC1000862//M.musculus mRNA for FT1./.2.6e-109:769:83//Z67963  
 F-OVARC1000876//S.cerevisiae chromosome IX cosmid 9150./.7.4e-21:541:61//Z38125  
 F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds./.2.2e-08:98:88//U20086  
 15 F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to katA).//.0.25:231:61//Z82044  
 F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey se-  
 quence./.0.00035:139:69//B89721  
 F-OVARC1000890  
 F-OVARC1000891  
 20 F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a  
 Homeobox domain containing gene and GSSs, complete sequence./.1.4e-18:473:64//AL024494  
 F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, com-  
 plete cds./.8.9e-08:378:63//L14320  
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds./.7.7e-85:440:95//AB011172  
 25 F-OVARC1000924//HS\_2022\_A1\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2022 Col=1 Row=E, genomic survey sequence./.5.7e-21:122:99//AQ269493  
 F-OVARC1000936//Human PAC clone DJ0093I03 from Xq23, complete sequence./.1.2e-113:476:91//AC003983  
 F-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING  
 DRAFT SEQUENCE./.0.00066:436:61//AL031848  
 30 F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds./.5.0e-89:  
 556:86//AB005549  
 F-OVARC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B).//.0.98:160:64//X95276  
 F-OVARC1000959//CIT-HSP-2348O16.TR CIT-HSP Homo sapiens genomic clone 2348O16, genomic survey se-  
 quence./.0.99:270:59//AQ062850  
 35 F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate  
 receptor, CpG island, CA repeat./.3.9e-41:577:72//AL009181  
 F-OVARC1000964//P.falciparum malaria antigen (M26-32-2) gene, partial cds./.0.19:83:73//M63270  
 F-OVARC1000971//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11,  
 WORKING DRAFT SEQUENCE./.0.013:670:57//Z92841  
 40 F-OVARC1000984//Leishmania major chromosome 1, complete sequence./.0.80:345:58//AE001274  
 F-OVARC1000996//MO25 gene [mice, embryos, mRNA, 2322 nt].//.2.6e-55:403:82//S51858  
 F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds./.0.33:105:69//  
 AF042785  
 F-OVARC1001000//HS\_2247\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 45 nomic clone Plate=2247 Col=9 Row=O, genomic survey sequence./.3.1e-60:315:96//AQ153910  
 F-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence./.3:1e-124:595:98//  
 AC004190  
 F-OVARC1001010//CIT-HSP-2034M3.TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey se-  
 quence./.1.0:151:60//B74290  
 50 F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87.on chro-  
 mosome X contains rad21 and T-cell cyclophilin pseudogenes, STS./.3.0e-08:149:79//Z78021  
 F-OVARC1001032//Yeast (S.cerevisiae) mitochondrial Tyr-tRNA gene./.3.2e-13:667:60//M12451  
 F-OVARC1001034//Mus musculus Fn54 mRNA, partial cds./.2.5e-119:737:86//AF001533  
 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds./.2.7e-150:733:97//AF099149  
 55 F-OVARC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces./.  
 9.8e-29:277:76//AC005081  
 F-OVARC1001044//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING  
 DRAFT SEQUENCE./.0.0017:387:6.1//AL031319

F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//0.012:112:74//AF053768  
 F-OVARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381:81//I30292  
 F-OVARC1001062//nbxb0026H08r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026H08r, genomic  
 5 survey sequence.//0.018:344:59//AQ271878  
 F-OVARC1001065//S.pombe chromosome I cosmid c29E6.//0.86:338:59//Z66525  
 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620:98//  
 AF082657  
 F-OVARC1001072//Homo sapiens glycan 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285:  
 10 65//AF003529  
 F-OVARC1001074//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS,  
 GSS, complete sequence.//2.0e-07:652:59//AL022153  
 F-OVARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187:99//M14333  
 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,  
 15 LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289:95//AJ005897  
 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds.//3.6e-72:351:86//AF015913  
 F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//6.4e-150:710:98//AF051782  
 F-OVARC1001117//Homo sapiens chromosome 5, P1 clone 328E3 (LBNL H53), complete sequence.//0.99:148:  
 20 67//AC005178  
 F-OVARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.6e-35:302:74//AC000382  
 F-OVARC1001129//CIT-HSP-647P20.TP CIT-HSP Homo sapiens genomic clone 647P20, genomic survey se-  
 quence.//0.94:106:66//B79052  
 F-OVARC1001154//R.norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462:79//X62322  
 25 F-OVARC1001161//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.9e-90:496:  
 84//AC004069  
 F-OVARC1001162  
 F-OVARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
 30 0.00090:219:64//AC004961  
 F-OVARC1001169//Borrelia burgdorferi (section 27 of 70) of the complete genome.//1.0:265:59//AE001141  
 F-OVARC1001170//H.sapiens (xs170) mRNA, 350bp.//4.6e-58:355:90//Z36823  
 F-OVARC1001171//CIT-HSP-2285E22.TP CIT-HSP Homo sapiens genomic clone 2285E22, genomic survey se-  
 quence.//1.5e-25:152:83//AQ002315  
 F-OVARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and  
 35 GSSs, complete sequence.//0.0024:94:80//AL022323  
 F-OVARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gene, complete cds.//1.0:356:60//  
 AF063001  
 F-OVARC1001180//G.gallus DNA for polyubiquitin gene Ub II.//0.0062:275:60//X58195  
 F-OVARC1001188//Homo sapiens full-length insert cDNA clone ZD93F03.//1.8e-32:180:97//AF086486  
 40 F-OVARC1001200  
 F-OVARC1001232//Caenorhabditis elegans cosmid F10B5, complete sequence.//0.013:128:67//Z48334  
 F-OVARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENCE, 44 unordered  
 pieces.//3.7e-131:811:87//AC001235  
 F-OVARC1001243//Human BAC clone GS117O10 from 7q21-q22, complete sequence.//0.044:457:59//AC003078  
 45 F-OVARC1001244//Human homolog of Drosophila female sterile homeotic mRNA, complete cds.//8.4e-18:118:  
 95//M80613  
 F-OVARC1001261//Mus musculus putative membrane-associated guanylate kinase 1 (Magi-1) mRNA, alterna-  
 tively spliced c form, partial cds.//1.4e-95:649:84//AF027505  
 F-OVARC1001268//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, com-  
 50 plete cds.//0.00051:72:83//U35776  
 F-OVARC1001270  
 F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds.//2.1e-142:644:96//AB014543  
 F-OVARC1001282//RPC11-60K8.TP RPC11 Homo sapiens genomic clone R-60K8, genomic survey sequence.//  
 55 0.0089:285:58//AQ195857  
 F-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, com-  
 plete cds.//3.0e-20:263:73//U97018  
 F-OVARC1001306//nbxb0002M13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002M13r, genomic  
 survey sequence.//0.98:170:66//AQ156061

F-OVARC1001329//Homo sapiens BAC clone RG370M10 from 7p15, complete sequence.//1.3e-05:432:61//  
AC003986  
F-OVARC1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING  
DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//AC005504  
5 F-OVARC1001339//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, complete sequence.//0.76:89:74//  
AC006071  
F-OVARC1001341//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey se-  
quence.//0.99:45:86//AQ263402  
F-OVARC1001342  
10 F-OVARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
Plate=CT 781 Col=4 Row=O, genomic survey sequence.//1.5e-07:254:67//B44456  
F-OVARC1001357//Homo sapiens Xp22-149 BAC RPCI11-466O4 (Roswell Park Cancer Institute Human BAC  
Library) complete sequence.//0.83:376:61//AC005297  
F-OVARC1001360  
15 F-OVARC1001369//Homo sapiens clone 162B15, complete sequence.//0.0066:99:76//AC004811  
F-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801  
F-OVARC1001376//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING  
DRAFT SEQUENCE.//1.9e-52:382:73//AL031680  
F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//  
20 AJ224819  
F-OVARC1001391//S.coelicolor whiB gene.//0.018:454:59//X62287  
F-OVARC1001399//CIT-HSP-2291I8.TR CIT-HSP Homo sapiens genomic clone 2291I8, genomic survey se-  
quence.//1.7e-11 :104:87//AQ007611  
F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651  
25 F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.9e-48:586:69//U52426  
F-OVARC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudo-  
gene similar to ribosomal protein S3A and part of a gene similar to C.elegans protein CE02118, ESTs, STS, GSS,  
complete sequence.//0.0019:96:78//Z99714  
F-OVARC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein  
30 (mix-1) mRNA, complete cds.//0.77:519:59//U96387  
F-OVARC1001442//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING  
DRAFT SEQUENCE.//1.0:167:64//AL031687  
F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS.//4.4e-64:376:79//  
Z84482  
35 F-OVARC1001476//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y24F12,  
WORKING DRAFT SEQUENCE.//0.20:107:71//AL022277  
F-OVARC1001480  
F-OVARC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//0.20:281:63//AC005140  
40 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//8.1e-85:479:92//AF016507  
F-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence,  
complete sequence.//1.2e-98:503:83//AC002039  
F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1.//1.7e-13:87:100//M16411  
F-OVARC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5.//  
45 0.43:190:68//X69219  
F-OVARC1001547//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//0.017:533:56//AC005140  
F-OVARC1001555//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//  
7.4e-159:416:99//AC005037  
50 F-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//2.4e-115:540:99//  
AF031165  
F-OVARC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//5.5e-13:529:62//  
AF043945  
F-OVARC1001610//, complete sequence.//1.4e-12:152:77//AC005409  
55 F-OVARC1001611  
F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12 Contains STS, GSS,  
complete sequence.//0.022:146:70//AL031682  
F-OVARC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.5e-109:358:96//AB005543

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds./.1.8e-47:393:81//AB006867  
 F-OVARC1001703/CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence./.0.94:85:69//B92840  
 F-OVARC1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317C6, WORKING DRAFT SEQUENCE./.1.9e-06:489:61//Z97651  
 5 F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds./.1.0:262:59//U41662  
 F-OVARC1001726//Human telomere associated repeat sequence, complete sequence./.7.5e-08:283:65//M57752  
 F-OVARC1001731//Mus musculus gene for beta-tropomyosin./.2.6e-83:606:81//X12650  
 F-OVARC1001745//HS\_3007\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey sequence./.0.00020:269:60//AQ164522  
 10 F-OVARC1001762//S.pombe chromosome III cosmid c338./.3.0e-17:624:61//AL023781  
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds./.4.2e-149:706:98//U97670  
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds./.3.0e-115:580:96//AB014575  
 15 F-OVARC1001768  
 F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence./.5.7e-64:477:78//AC005066  
 F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence./.6.5e-11:171:76//AC004704  
 20 F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone 2502A17, genomic survey sequence./.0.98:214:61//AQ264481  
 F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence./.9.5e-151:712:99//AL023694  
 25 F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds./.2.7e-56:522:75//AF068748  
 F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete sequence./.1.7e-63:526:81//AC003662  
 F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chromosome X contains STS./.0.17:214:65//Z70224  
 30 F-OVARC1001820//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 445N2, WORKING DRAFT SEQUENCE./.3.2e-55:379:82//AL031779  
 F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence./.2.8e-17:509:62//AC005609  
 35 F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X./.0.35:403:58//Z73361  
 F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence./.2.4e-25:148:96//B94622  
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence./.1.2e-18:122:95//AF070611  
 40 F-OVARC1001879//HS\_3026\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey sequence./.4.9e-29:204:87//AQ207748  
 F-OVARC1001880//Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds./.3.5e-05:489:60//U51127  
 F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces./.1.9e-29:350:74//AC005020  
 45 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds./.8.6e-56:300:96//AF061749  
 F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs, complete sequence./.2.3e-10:253:66//AL031904  
 50 F-OVARC1001911//HS\_2196\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence./.3.4e-09:123:78//AQ294069  
 F-OVARC1001916//HS\_3054\_B1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence./.1.2e-31:126:97//AQ099979  
 F-OVARC1001928  
 55 F-OVARC1001942//H.sapiens CpG island DNA genomic Mse1 fragment, clone 21d7, forward read cpg21d7.ft1a./.7.2e-12:83:98//Z60390  
 F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds./.3.5e-50:535:69//AF059179

F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds.//1.7e-16:294:67//U37263  
 F-OVARC1001950//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.5e-  
 20:261:68//AJ011929  
 F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4.//0.99:447:57//Z19021  
 5 F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//  
 2.9e-19:178:83//AC005995  
 F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence.//0.17:232:62//AL034559  
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//2.1e-158:739:98//AB007934  
 F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15,  
 10 WORKING DRAFT SEQUENCE.//3.0e-17:781:59//AP000011  
 F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 5.4e-136:683:96//AC006015  
 F-OVARC1002107//Homo sapiens BAC clone RG276003 from 7q22-q31.1, complete sequence.//1.0:220:61//  
 AC004668  
 15 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//6.1e-115:557:98//AF041483  
 F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//0.013:461:57//  
 AC006241  
 F-OVARC1002138//Caenorhabditis elegans cosmid F32D1.//1.0e-29:545:64//AF016427  
 F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey se-  
 20 quence.//2.3e-11:258:67//AQ055576  
 F-OVARC1002156  
 F-OVARC1002158//F17O7-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic survey sequence.//1.8e-  
 16:383:66//B11616  
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosinephosphatase.//0.0041:300:64//X79568  
 25 F-OVARC1002182//F.rubripes GSS sequence, clone 123I23aA7, genomic survey sequence.//1.4e-10:240:66//  
 AL017241  
 F-PLACE100004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey se-  
 quence.//8.2e-10:158:75//AQ003859  
 F-PLACE100005//Mouse alpha-1 antitrypsin gene, segment 1.//4.8e-15:89:93//M12585  
 30 F-PLACE100007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//3.8e-51:550:72//  
 AF022789  
 F-PLACE1000014  
 F-PLACE1000031//Homo sapiens alone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.91:  
 333:61//AC004821  
 35 F-PLACE1000040//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains  
 ESTs STS and CpG island.//2.6e-20:279:67//Z93023  
 F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.6e-63:488:82//  
 AC005177  
 F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:  
 40 141:75//U31508  
 F-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//1.9e-30:190:94//L22154  
 F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//6.0e-63:597:74//  
 AC005521  
 F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6  
 45 unordered pieces.//5.2e-09:143:73//AC005848  
 F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete se-  
 quence.//0.52:390:60//AC002389  
 F-PLACE1000094  
 F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and  
 50 CpG Island, complete sequence.//4.4e-129:731:92//AL023580  
 F-PLACE1000142//H.sapiens AUH mRNA.//6.4e-09:328:62//X79888  
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//7.7e-150:737:97//  
 AF058291  
 F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//I76211 F-PLACE1000213  
 55 F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57//AC005504  
 F-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING  
 DRAFT SEQUENCE.//2.6e-39:191:83//AL032818

F-PLACE1000246//HS\_2008\_A2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=8 Row=G, genomic survey sequence./.0.96:153:61//AQ269813  
 F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region./.5.1e-12:571:60//U11584  
 F-PLACE1000308//D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & amp; tRNA-Val./.0.00013:  
 5 369:59//X54011  
 F-PLACE1000332//HS\_2016\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence./.7.5e-83:424:96//AQ232106  
 F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 2326A16, genomic survey sequence./.0.13:46:100//AQ047350  
 10 F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript mCBF1, complete cds./.0.00048:84:83//U19891  
 F-PLACE1000380//F.rubripes GSS sequence, clone 047P21aA10, genomic survey sequence./.0.43:198:62//  
 Z88163  
 F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTMR1) mRNA, partial cds./.8.7e-149:740:96//  
 15 U58032  
 F-PLACE1000401//Pinctada fucata mRNA for insoluble protein, complete cds./.0.22:484:56//D86074  
 F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds./.3.3e-19:372:65//U89867  
 F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence./.1.6e-85:421:  
 87//AC005899  
 20 F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17./.0.88:145:68//U61515  
 F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence./.0.076:196:66//  
 AC005189  
 F-PLACE1000435//HS\_3217\_A2\_A12\_MR CIT Approved Human Genomic-Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence./.2.2e-47:438:76//AQ181698  
 25 F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence./.6.9e-  
 61:616:71//AC004382  
 F-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence./.5.8e-18:314:69//AF059580  
 F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a In DGCR Region, complete sequence./.1.1e-33:349:76//AC002491  
 30 F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds./.1.1e-34:256:83//  
 U35245  
 F-PLACE1000540//P.falciparum complete gene map of plastid-like DNA (IR-B)./.0.099:336:58//X95276  
 F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds./.5.4e-  
 35 11:279:63//AF076484  
 F-PLACE1000562//, complete sequence./.1.7e-97:559:88//AC005409  
 F-PLACE1000564  
 F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9./.3.3e-46:631:68//  
 M27877  
 40 F-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds./.7.3e-84:503:88//  
 M55542  
 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)./.3.8e-164:798:97//AJ012449  
 F-PLACE1000599//P.falciparum complete gene map of plastid-like DNA (IR-B)./.0.018:295:61//X95276  
 45 F-PLACE1000610//HS\_2056\_A1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence./.5.3e-24:188:87//AQ235967  
 F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds./.2.4e-47:687:66//  
 AF044201  
 F-PLACE1000636  
 50 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds./.1.5e-152:747:  
 96//AF102265  
 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and  
 LLNLc110F1857Q7 (RZPD Berlin))./.2.3e-156:775:97//AJ005896  
 F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt]./.8.0e-60:675:70//S78219  
 F-PLACE1000712  
 55 F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 Plate=CT 779 Col=5 Row=A, genomic survey sequence./.2.7e-42:266:82//B43026  
 F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 2372J8, genomic survey se-  
 quence./.0.023:157:68//AQ113109

F-PLACE1000749//Plasmodium falciparum MAL3P7, complete sequence./.0.099:664:57//AL034559  
 F-PLACE1000755//H.sapiens DNA 3' flanking simple sequence region clone wg2c3./.0.00068:206:62//X76589  
 F-PLACE1000769//RPCI11-3J18.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-3J18, genomic survey sequence./6.5e-08:93:89//B63806  
 5 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds./3.5e-138:663:98//AB014548  
 F-PLACE1000786//Drosophila melanogaster cosmid 80H7./1.4e-43:589:68//AL031027  
 F-PLACE1000793//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.rt1c./4.6e-09:71:100//Z64565  
 10 F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence./5.0e-14:235:72//AC002310  
 F-PLACE1000841//Homo sapiens clone NH0441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces./.0.013:404:60//AC006158  
 F-PLACE1000849//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72a10, reverse read cpg72a10.rt1a./3.3e-09:82:92//Z62712  
 15 F-PLACE1000856//Hydra vulgaris HT4 mRNA for collagen-like protein, partial cds./1.0:317:59//AB008935  
 F-PLACE1000863//H.sapiens CpG island DNA genomic Mse1 fragment, clone 53d2, forward read cpg53d2.ft1b./.7.3e-37:199:98//Z55621  
 F-PLACE1000909//H.sapiens CpG island DNA genomic Mse1 fragment, clone 173f8, reverse read cpg173f8.rt1a./1.5e-17:128:92//Z57391  
 20 F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat./.8.1e-55:647:72//AL009181  
 F-PLACE1000948  
 F-PLACE1000972//RPCI11-61B1.TJ RPCI11 Homo sapiens genomic clone R-61B1, genomic survey sequence./.1.0e-26:148:99//AQ194348  
 25 F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds./.6.1e-08:413:61//AB014572  
 F-PLACE1000979//H.sapiens CpG island DNA genomic Mse1 fragment, clone 76e8, reverse read cpg76e8.rt1a./.2.7e-10:84:94//Z55963  
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds./.8.0e-140:694:96//AB018267  
 F-PLACE1001000//Herpetomonas muscarum muscarum kinetoplast 12S rRNA gene./.0.0056:443:58//U01011  
 30 F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 2013L15, genomic survey sequence./.0.99:277:58//B58681  
 F-PLACE1001010//Human cosmid g1572c101, complete sequence./.3.6e-55:294:88//AC000357  
 F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence./.7.2e-33:333:73//AC004741  
 35 F-PLACE1001024  
 F-PLACE1001036//CIT-HSP-2373I10.TF CIT-HSP Homo sapiens genomic clone 2373I10, genomic survey sequence./.1.1e-80:393:98//AQ108662  
 F-PLACE1001054//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence./.8.8e-40:483:66//AB013390  
 40 F-PLACE1001062//Mus musculus mRNA encoding lysine-ketoglutarate reductase/saccharopine dehydrogenase./.1.2e-23:224:80//AJ224761  
 F-PLACE1001076//HS\_2195\_B1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=9 Row=H, genomic survey sequence./.0.0014:168:66//AQ066659  
 F-PLACE1001088  
 45 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds./.3.1e-95:489:96//AF065485  
 F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds./.0.0073:253:62//U81400  
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds./.2.5e-64:676:71//AF022158  
 50 F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).//.3.8e-26:174:93//M30702  
 F-PLACE1001168  
 F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence./.7.6e-23:245:68//AC005603  
 F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker-CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence./.0.010:102:70//AL031177  
 55 F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds./.9.3e-82:684:

77//D14336  
 F-PLACE1001241  
 F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF067219  
 F-PLACE1001272//H.sapiens subunit of coatomer complex.//0.31:50:96//X70476  
 5 F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.054:352:60//AC005507  
 F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320  
 F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-107:826:80//X71642  
 10 F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-67:510:77//X17617  
 F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-47:491:73//AC005282  
 F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey sequence.//9.6e-26:142:100//B31181  
 15 F-PLACE1001351  
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.6e-25:155:95//AB018342  
 F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48614  
 F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324  
 20 F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08:117:84//AJ001319  
 F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I57340  
 F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11:620:60//X52177  
 25 F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412  
 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//2.0e-69:365:96//AF091087  
 F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//8.2e-121:608:97//AC006241  
 30 F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.3e-06:437:61//AC000384  
 F-PLACE1001456//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//0.98:348:60//AC003106  
 F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148  
 35 F-PLACE1001484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660  
 F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene, exon L//0.00015:333:59//L78720  
 F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//0.00016:  
 40 161:66//AC004373  
 F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//3.7e-22:260:76//AL021786  
 F-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667  
 45 F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//2.7e-139:482:96//AC005669  
 F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.9e-116:681:89//AC005261  
 F-PLACE1001570//HS\_3105\_A1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817  
 50 F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//1.8e-102:217:99//AB020860  
 F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984  
 55 F-PLACE1001608//HS\_2189\_A1\_G07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey sequence.//2.9e-60:429:84//AQ221959  
 F-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.4e-114:552:98//AC005037

F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence./.0.93:131:71//AL031587  
 5 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds./.1.1e-74:702:75//AB018341  
 F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds./.1.2e-18:114:100//U17032  
 F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence./.7.7e-159:788:  
 97//AC005971  
 F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen Ki-  
 10 67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DDX1003 and DDX1055, complete sequence./.7.8e-36:365:73//AL022165  
 F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence./.9.1e-149:760:  
 96//AC005921  
 15 F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds./.2.9e-57:643:71//M16200  
 F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958\_E\_11, WORKING DRAFT SEQUENCE, 2 ordered pieces./.3.9e-18:284:71//AC005883  
 F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds./.6.6e-68:369:73//D83776  
 20 F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGLC Region, complete sequence./.1.0:274:59//AC000051  
 F-PLACE1001729//Streptomyces coelicolor cosmid 1C2./.0.22:433:57//AL031124  
 F-PLACE1001739//Caenorhabditis elegans cosmid C18H7./.0.049:341:61//AF067607  
 F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence./.4.8e-26:  
 25 372:68//AC005221  
 F-PLACE1001745  
 F-PLACE1001746//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE./.0.018:472:57//AL031744  
 F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds./.8.8e-159:773:97//AF061243  
 30 F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPCI11-303E5, WORKING DRAFT SEQUENCE, 65 unordered pieces./.1.9e-54:274:81//AC005842  
 F-PLACE1001761//HS\_3027\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence./.0.095:49:93//AQ130972  
 F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds./.1.0e-146:709:97//  
 35 AF080394  
 F-PLACE1001781 1.3e-08:238:65//AC005637  
 F-PLACE1001799//HS\_3075\_B1\_H03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence./.1.7e-09:166:69//AQ138474  
 F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence./.40 0.00035:196:66//AB020749  
 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds./.1.1e-108:546:96//AF058953  
 F-PLACE1001821//RPCI11-35D17.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35D17, genomic survey sequence./.2.1e-55:300:97//AQ045286  
 45 F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence./.2.8e-67:443:86//AC005177  
 F-PLACE1001845//Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence./.0.34:219:64//AC005850  
 F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds./.50 7.1e-11:505:57//AF045244  
 F-PLACE1001897//RPCI11-46D15.TJ RPCI11 Homo sapiens genomic clone R-46D15, genomic survey sequence./.9.3e-08:383:63//AQ194408  
 F-PLACE1001912  
 F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds./.7.3e-156:753:98//AF099935  
 55 F-PLACE1001928//HS\_2220\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence./.2.8e-43:233:97//AQ152361  
 F-PLACE1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE./.1.6e-07:396:62//AL031596

F-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE./.1.0e-109:602:93//AL023755  
F-PLACE1002004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317E23, WORKING DRAFT SEQUENCE./.1.0e-69:475:87//AL020996  
5 F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds./.7.2e-97:623:85//U58337  
F-PLACE1002052//HS\_2178\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence./.4.8e-22:140:95//AQ307908  
F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds./.0.0063:371:60//U72284  
10 F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A./.0.97:248:60//AF043195  
F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds./.1.3e-37:635:64//AB011178  
F-PLACE1002090//Homo sapiens full-length insert cDNA clone ZA85C09./.7.0e-122:583:98//AF086131  
15 F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0038A20r, genomic survey sequence./.0.039:210:69//AQ291086  
F-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds./.7.1e-61:540:77//AF079527  
F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence./.2.1e-125:491:98//AL022162  
20 F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence./.0.12:408:61//AL034556  
F-PLACE1002157//Homo sapiens BAC clone NH0335J18 from 2, complete sequence./.1.1e-44:515:71//AC005539  
F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence./.0.98:210:65//AE000662  
25 F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence./.1.2e-06:283:60//AC004805  
F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds./.1.0e-24:313:71//U06244  
30 F-PLACE1002205//Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces./.1.6e-05:428:60//AC005720  
F-PLACE1002213//HS\_3238\_B1\_G03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence./.2.2e-74:371:98//AQ206965  
F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence./.2.1e-07:174:71//B42800  
35 F-PLACE1002256//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-72, complete sequence./.0.022:458:59//AL010142  
F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence./.3.5e-91:637:84//AL022324  
40 F-PLACE1002319  
F-PLACE1002342//Caenorhabditis elegans cosmid M03A1./.0.47:403:58//U49956  
F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence./.1.9e-127:487:93//AC004623  
F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence./.5.6e-05:474:59//  
45 AC005922  
F-PLACE1002433//Drosophila melanogaster fidipidine gene, exons 1-7./.1.7e-11:613:58//AJ011928  
F-PLACE1002437//M.musculus abc1 mRNA./.5.5e-62:452:85//X75926  
F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (DG1098) gene, partial cds./.0.013:  
372:59//AF081801  
50 F-PLACE1002450//HS\_3233\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence./.3.1e-07:449:59//AQ204769  
F-PLACE1002465  
F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds./.1.5e-110:720:85//U69262  
55 F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence./.3.9e-05:195:71//AC005926  
F-PLACE1002493//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence./.0.020:301:60//AC006060  
F-PLACE1002499

- F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927  
 F-PLACE1002514//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//3.7e-08:139:76//Z93930  
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256  
 5 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//0.00019:193:65//AC004774  
 F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575  
 10 F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds.//2.0e-13:400:60//L25314  
 F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//AC002523  
 F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443  
 F-PLACE1002591//H.sapiens mRNA for coronin.//7.2e-26:279:74//X89109  
 15 F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.0013:375:64//AC005537  
 F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785  
 F-PLACE1002625  
 F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:  
 20 92//AC005281  
 F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//AF079765  
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-186:804:97//AF068180  
 25 F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:64//AF051726  
 F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723  
 F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//0.0076:161:70//AL031273  
 30 F-PLACE1002772//HS\_3058\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567  
 F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//AF084259  
 F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927  
 35 F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey sequence.//1.3e-71:368:96//AQ075879  
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994  
 F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295  
 F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691  
 40 F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//9.3e-41:240:93//M27877  
 F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045  
 F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140  
 45 F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.//0.032:275:62//M10126  
 F-PLACE1002881//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.//4.7e-38:355:76//Z98200  
 F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CKII) mRNA, complete cds.//0.00012:200:64//  
 50 U19889  
 F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120  
 F-PLACE1002962  
 F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558  
 F-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.8e-121:605 :93//AL023755  
 55 F-PLACE1002993//CIT-HSP-2338I16.TF CIT-HSP Homo sapiens genomic clone 2338I16, genomic survey sequence.//1.9e-13:100:95//AQ054760  
 F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980

F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence./.0.84:374:58//Z98551  
 F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds./.6.1e-130:632:97//AB011088  
 F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829  
 5 F-PLACE1003045//H.sapiens CpG island DNA genomic Mse1 fragment, clone 47g6, forward read cpg47g6.ft1a./.0.0064:52:96//Z61200  
 F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence./.0.0031:249:63//B60158  
 10 F-PLACE1003100//Human Hep27 protein mRNA, complete cds./.8.9e-65:650:73//U31875  
 F-PLACE1003108  
 F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence./.6.3e-46:  
 606:68//AC004219  
 F-PLACE1003145  
 15 F-PLACE1003153//RPCI11-13P16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13P16, genomic survey sequence./.2.7e-63:478:82//B76206  
 F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence./.0.61:147:65//Z99495  
 20 F-PLACE1003176//HS\_2255\_A2\_B01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence./.6.3e-09:137:76//AQ131934  
 F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces./.2.4e-  
 138:791:901//AC005095  
 F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.7e-06:728:57//X95276  
 F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence./.7.5e-05:249:63//AC002466  
 25 F-PLACE1003238//HS\_3239\_A2\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence./.0.36:64:87//AQ209954  
 F-PLACE1003249  
 F-PLACE1003256,  
 F-PLACE1003258//HS\_3223\_A1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence./.1.4e-07:227:65//AQ190317  
 30 F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 2337F11, genomic survey sequence./.1.1e-13:97:95//AQ057429  
 F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9./.2.3e-92:485:95//  
 M27877  
 F-PLACE1003334  
 35 F-PLACE1003342  
 F-PLACE1003343//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces./.1.0e-  
 20:179:84//AC004951  
 F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete  
 40 cds./.8.0e-143:773:92//U92715  
 F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence./.1.9e-30:402:70//AC004095  
 F-PLACE1003366  
 F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence./.7.6e-07:378:60//AL034558  
 F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence./.6.0e-18:471:61//  
 45 AC005247  
 F-PLACE1003375  
 F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer , segment  
 10/10./.2.3e-157:779:96//AB020878  
 F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds./.1.2e-104:596:91//M83680  
 50 F-PLACE1003401//RPCI11-71J5.TJ RPCI11 Homo sapiens genomic clone R-71J5, genomic survey sequence./.  
 0.85:140:65//AQ268588  
 F-PLACE1003420//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORK-  
 55 ING DRAFT SEQUENCE./.0.0015:286:60//AL021388  
 F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence./.0.0084:219:61//AF015470  
 F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) gene, complete cds./.1.3e-  
 11:746:60//AF039401  
 F-PLACE1003493  
 F-PLACE1003516//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence./.8.2e-41:379:78//  
 AC002994

F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a./.6.2e-21:247:76//AF064859  
 F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSs and a GSS./.4.4e-68:502:79//AL008729  
 5 F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence./.1.0:323:58//AL022336  
 F-PLACE1003537//Homo sapiens multispanning membrane protein mRNA, complete cds./.0.0054:322:59//U94831  
 10 F-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE./.2.9e-78:267:88//AL031297  
 F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence./.0.00026:514:58//Z98547  
 F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces./.0.079:755:54//AC004688  
 15 F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence./.1.1e-41:212:74//AL022324  
 F-PLACE1003584//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-56, complete sequence./.0.0038:465:57//AL010230  
 20 F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces./.0.72:111:71//AC002557  
 F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence./.0.096:162:66//AC002476  
 F-PLACE1003596//Mus musculus integral membrane protein 1 (itm1) mRNA, complete cds./.1.4e-54:685:68//L34260  
 25 F-PLACE1003602//Homo sapiens mRNA expressed in placenta./.1.1e-138:679:97//D83200  
 F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence./.0.0074:265:63//AC005356  
 F-PLACE1003611//HS\_2198\_B1\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence./.2.1e-23:137:97//AQ184475  
 30 F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence./.3.0e-122:725:89//AC006226  
 F-PLACE1003625//HS\_2238\_B2\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence./.4.8e-12:92:94//AQ065662  
 35 F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence./.0.043:264:63//AB011478  
 F-PLACE1003669  
 F-PLACE1003704//RPCI11-23H21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-23H21, genomic survey sequence./.7.1e-31:199:91//AQ013830  
 F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds./.4.3e-132:669:95//AF053305  
 40 F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence./.1.5e-31:166:99//AL021920  
 F-PLACE1003723//HS\_2231\_A2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence./.1.2e-12:114:90//AQ235672  
 F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds./.5.9e-33:592:67//M58297  
 F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds./.3.6e-11:92:93//AF054840  
 F-PLACE1003762  
 F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE./.4.8e-77:737:76//AP000014  
 50 F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence./.2.1e-164:793:98//AC004160  
 F-PLACE1003783//HS\_2190\_A2\_C02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence./.1.1e-26:147:100//AQ218757  
 55 F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence./.4.5e-57:706:68//AC006210  
 F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyl-

transferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.015:296:60//U52112  
 F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

5 F-PLACE1003850//*P.falciparum* histidine-rich protein genes.//0.39:330:60//M17028  
 F-PLACE1003858//Human DNA sequence from PAC 332O11 on chromosome 1q24-1q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043  
 F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139

10 F-PLACE1003870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304  
 F-PLACE1003885//*Mus musculus* poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//U58134  
 F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030

15 F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//D42108  
 F-PLACE1003892//RPCI11-24P17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759  
 F-PLACE1003900//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

20 F-PLACE1003903//*Mus musculus* CTP synthetase homolog (CTPsH) mRNA, complete cds.//2.7e-86:533:87//U49385  
 F-PLACE1003915//*Mus musculus* clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591  
 F-PLACE1003923//Homo sapiens full-length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251  

25 F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505  
 F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone 2387C11, genomic survey sequence.//1.0:223:62//AQ239494  
 F-PLACE1003968//*Rattus norvegicus* 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413

30 F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954  
 F-PLACE1004104//*Rattus norvegicus* rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666  
 F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052

35 F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences.//0.87:209:64//M34651  
 F-PLACE1004128//*M.musculus* G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658  
 F-PLACE1004149//*Oryctolagus cuniculus* translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355

40 F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099  
 F-PLACE1004161  
 F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ010071  
 F-PLACE1004197  

45 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493  
 F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

50 F-PLACE1004256//HS\_2010\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434  
 F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//0.00011:349:63//AC005034

55 F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806  
 F-PLACE1004270//Human IgA C alpha 1 switch region (Sa1).//1.7e-08:622:61//L19121  
 F-PLACE1004274//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 18g6, forward read cpg18g6.ft1b.//8.6e-37:196:98//Z57691  
 F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//6.0e-156:756:

97//AF084830  
 F-PLACE1004284//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MP17, complete sequence.//  
 0.0060:635:57//AB011480  
 F-PLACE1004289//HS\_3023\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 5 nomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451  
 F-PLACE1004302//Streptomyces coelicolor cosmid 7H1.//0.26:297:64//AL021411  
 F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//2.9e-150:797:94//Y11588  
 F-PLACE1004336//Drosophila melanogaster DNA sequence (P1 DS07968 (D117)), complete sequence.//0.87:  
 10 206:59//AC004267  
 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//5.9e-139:  
 688:97//AF100153  
 F-PLACE1004376//Mus musculus clone OST20307, genomic survey sequence.//4.1e-81:498:89//AF046631  
 F-PLACE1004384//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1121J18, WORKING  
 15 DRAFT SEQUENCE.//3.6e-41:482:73//AL031653  
 F-PLACE1004388//Caenorhabditis elegans cosmid K08F11.//8.6e-26:615:62//U70855  
 F-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.2e-  
 150:749:96//AC005027  
 F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//2.4e-08:129:76//  
 AC005532  
 20 F-PLACE1004428//R.norvegicus mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188  
 F-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene  
 encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283  
 F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 con-  
 tains BRCA2 exons 1-24, Interferon Induced 56Kd pseudogene and ESTs.//4.8e-23:231:71//Z74739  
 25 F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56//  
 AC004954  
 F-PLACE1004467//HS\_2058\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700  
 30 F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-74:665:70//  
 M27877  
 F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15; genomic survey se-  
 quence.//3.3e-20:140:92//B80243  
 F-PLACE1004491//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 35 DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709  
 F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150  
 F-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.2e-  
 146:699:98//AF040701  
 F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.//  
 40 1.4e-33:367:71//Z86001  
 F-PLACE1004518  
 F-PLACE1004548//Dictyostelium discoideum MigA (migA) gene, complete cds.//2.6e-05:318:62//U86962  
 F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476  
 F-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931  
 45 F-PLACE1004629//Anolis carolinensis Brain-1 gene, complete cds.//0.00013:188:67//AB001868  
 F-PLACE1004645//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//0.66:337:60//  
 Z95120  
 F-PLACE1004646//Rattus norvegicus retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds.//  
 1.1e-19:326:63//AF035673  
 50 F-PLACE1004658//H.sapiens CpG island DNA genomic Mse1 fragment, clone 55h1, forward read cpg55h1.ft1a./  
 12.4e-34:188:98//Z61632  
 F-PLACE1004664//Caenorhabditis elegans cosmid W10G6, complete sequence.//1.0:148:65//Z81140  
 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene,  
 complete cds.//1.9e-101:182:95//U07561  
 F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//4.3e-109:625:91//  
 55 AF035606  
 F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
 non-small cell lung cancer , segment 3/11.//1.9e-152:759:96//AB020860  
 F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the

- SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//1.2e-34:320:71//Z95152
- 5 F-PLACE1004691//HS\_3044\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323
- F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577
- 10 F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.00081:428:59//Z98551
- F-PLACE1004722//HS\_3052\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence.//2.3e-05:104:75//AQ134959
- F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498
- 15 F-PLACE1004740//RPCI11-58A7.TJ RPCI11 Homo sapiens genomic clone R-58A7, genomic survey sequence.//8.6e-26:522:65//AQ195766
- F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//1.1e-112:711:86//AF061555
- F-PLACE1004751
- 20 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-171:828:97//AF084367
- F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//4.2e-134:763:90//AJ001713
- F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34), hypothetical protein EST, STS, GSS, complete sequence.//9.3e-132:759:90//AL022157
- 25 F-PLACE1004804
- F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//AC004710
- F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//9.8e-39:207:99//AC005921
- 30 F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73//AC004613
- F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849
- F-PLACE1004827//HS\_2230\_A2\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-38:330:81//AQ299313
- 35 F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825
- F-PLACE1004838//HS\_3241\_A2\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740
- F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//I92819
- F-PLACE1004868
- 40 F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.//0.14:465:59//Z97344
- F-PLACE1004900
- F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184
- F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91//AC005058
- 45 F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571
- F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//4.4e-106:545:95//AF070671
- F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989
- 50 F-PLACE1004937
- F-PLACE1004969
- F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.//0.012:316:61//AC004843
- 55 F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.7e-39:394:77//AL031073
- F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U64833

F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:  
 590:61//AE001373  
 F-PLACE1005026  
 F-PLACE1005027  
 5 F-PLACE1005046  
 F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SE-  
 QUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867  
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761:98//AB011148  
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//  
 10 AF059569  
 F-PLACE1005077  
 F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)  
 complete sequence.//6.9e-29:253:77//AC004673  
 F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//  
 15 AC002316  
 F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-  
 146:734:96//AC005225  
 F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//  
 AC004476  
 20 F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//0.46:179:64//AC003081  
 F-PLACE1005111  
 F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, com-  
 plete cds.//0.00051:287:63//L14320  
 25 F-PLACE1005146//HS\_3071\_A1\_E03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3071 Col=5 Row=I, genomic survey sequence.//7.4e-38:299:82//AQ103361  
 F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence.//2.6e-44:346:82//  
 AC002451  
 F-PLACE1005176  
 30 F-PLACE1005181//CIT-HSP-2340O5.TR CIT-HSP Homo sapiens genomic clone 2340O5, genomic survey se-  
 quence.//0.99:211:63//AQ054651  
 F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey se-  
 quence.//2.7e-07:80:90//AQ074445  
 F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//0.98:216:61//AC000061  
 35 F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//  
 0.70:245:63//AC004965  
 F-PLACE1005243  
 F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.//0.00041:254:61//Z47812  
 F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4\_2g).//9.6e-33:177:98//Z70695  
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.6e-148:706:98//AB011182  
 40 F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737:60//M69183  
 F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728:84//  
 M25757  
 F-PLACE1005308//Clethrionomys glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole  
 Cg14.//1.0:128:67//AJ233621  
 45 F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U88167  
 F-PLACE1005327//HS\_3080\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116  
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//  
 AC004794  
 50 F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
 5.5e-114:237:92//AC000380  
 F-PLACE1005373  
 F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305:58//  
 AF017104  
 55 F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//2.5e-148:760:95//AC003991  
 F-PLACE1005453//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y48A6,  
 WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854  
 F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859

- F-PLACE1005471//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence./.3.0e-23:530:67//AL023581  
 F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE./.3.3e-131:814:88/Z82191
- 5 F-PLACE1005480//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS./.7.0e-34:246:73//AL021878  
 F-PLACE1005481//RPCI11-74L17.TJ RPCI11 Homo sapiens genomic clone R-74L17, genomic survey sequence./.0.37:403:57//AQ266885
- 10 F-PLACE1005494//Homo sapiens transient receptor potential protein 6 mRNA, complete cds./.2.1e-67:325:99//AF080394  
 F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence./.0.015:403:61//AC005589  
 F-PLACE1005526//H.sapiens CpG island DNA genomic Mse1 fragment, clone 9f1, reverse read cpg9f1.rt1a./.15 3.6e-27:159:96//Z66485  
 F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE./.2.6e-28:449:67//AP000038  
 F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence./.6.5e-18:234:72//AC004860  
 F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic survey sequence./.20 1.2e-14:123:75//AL025925  
 F-PLACE1005554//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene./.0.43:209:66//X02354  
 F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence./.9.3e-113:536:97//AC004707  
 F-PLACE1005574//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces./.1.1e-10:514:59//AC005504  
 F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds./.0.00056:289:63//AB014517  
 F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence./.1.2e-111:262:89//AC004126  
 F-PLACE1005603  
 30 F-PLACE1005611//F16O5TFC IGF Arabidopsis thaliana genomic clone F16O5, genomic survey sequence./.2.0e-10:209:66//B98589  
 F-PLACE1005623  
 F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces./.1.2e-93:230:98//AC005840  
 35 F-PLACE1005639//HS\_3095\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence./.1.2e-05:220:63//AQ123022  
 F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds./.6.4e-150:721:98//AF083255  
 F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase./.1.3e-51:480:74//X59618  
 40 F-PLACE1005666//RPCI11-78O15.TV RPCI11 Homo sapiens genomic clone R-78O15, genomic survey sequence./.8.7e-05:243:62//AQ284667  
 F-PLACE1005698//Human membrane-associated lectin type-C mRNA./.1.9e-63:374:85//M98457  
 F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence./.0.69:633:57//AE001422  
 45 F-PLACE1005730//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence./.2.0e-24:286:74//AQ231147  
 F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds./.2.8e-55:621:71//U15635  
 F-PLACE1005755//HS\_2213\_A2\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=O, genomic survey sequence./.1.4e-25:290:75//AQ136844  
 50 F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds./.4.5e-40:297:70//M16200  
 F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5./.0.91:287:63//Y12517  
 F-PLACE10058021//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence./.5.0e-109:530:98//AC004827  
 55 F-PLACE1005803//HS\_3092\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey sequence./.2.4e-08:76:96//AQ103695  
 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds./.1.4e-126:636:96//AF027156  
 F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./.2.6e-154:739:98//AF065482

- F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces./.2.2e-37:355:77//AC004150
- F-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-105, complete sequence./.0.00080:663:58//AL010283
- 5 F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./.0.00015:340:58//AC004153
- F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence./.1.8e-46:278:85//AL031432
- F-PLACE1005851
- 10 F-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor./.5.0e-120:701:89//X75931
- F-PLACE1005884//CIT-HSP-2333O12.TR CIT-HSP Homo sapiens genomic clone 2333O12, genomic survey sequence./.4.6e-78:385:98//AQ039226
- F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Bem46+) mRNA, partial cds./.9.3e-16:638:57//U29892
- 15 F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds./.1.0:178:65//U67136
- F-PLACE1005921//M.musculus mRNA for immunity associated protein 38./.6.6e-17:614:59//Y08026
- F-PLACE1005923//RPCI11-33G19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-33G19, genomic survey sequence./.4.0e-10:535:57//AQ046151
- 20 F-PLACE1005925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE./.0.17:159:65//AL034405
- F-PLACE1005932
- F-PLACE1005934//H.sapiens CpG island DNA genomic Mse1 fragment, clone 165g2, forward read cpg165g2.ft1a./.8.3e-43:247:93//Z57153
- 25 F-PLACE1005936//F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence./.0.91:116:68//AL014719
- F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds./.0.0022:495:59//AF016236
- 30 F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence./.2.9e-05:442:61//AC004081
- F-PLACE1005955//Caenorhabditis elegans cosmid F01F1./.4.3e-20:409:64//U13070
- F-PLACE1005966//P.falciparum aarp3 gene, exon./.0.0083:270:64//Y08925
- F-PLACE1005968
- 35 F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces./.1.0e-100:513:96//AC005866
- F-PLACE1006002//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE./.2.5e-54:444:77//Z86090
- 40 F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=2 Row=M, genomic survey sequence./.3.4e-05:214:64//B44442
- F-PLACE1006011//Mus musculus poly-(ADPribosyl)-transferase homolog PARP mRNA, complete cds./.4.3e-71:580:79//AF072521
- F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 -complete genomic sequence, complete sequence./.8.6e-32:177:83//AC002299
- 45 F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA./.1.8e-34:269:83//U01139
- F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine./.3.4e-147:719:97//X99906
- F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence./.0.37:332:62//Z97200
- 50 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds./.1.3e-145:679:99//AF039023
- F-PLACE1006129
- F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965./.4.8e-27:693:60//D44597
- F-PLACE1006143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE./.4.7e-46:435:77//Z93015
- 55 F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone:B2./.0.048:290:60//D85750
- F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-1054O2 map 10q25, complete sequence./.3.2e-129:466:96//AC005661

F-PLACE1006164//HS\_3003\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence./.1.4e-70:388:93//AQ118200  
F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence./.4.3e-78:385:86//AC005239  
5 F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630:84//X14972  
F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds./.3.9e-149:694:99//AF091433  
F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence./.2.5e-16:283:70//AC003658  
10 F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds./.2.2e-94:648:84//L25125  
F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence./.0.15:533:58//U75931  
F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence./.0.0068:175:64//B19803  
15 F-PLACE1006225//CIT-HSP-2335I23.TF CIT-HSP Homo sapiens genomic clone 2335I23, genomic survey sequence./.2.1e-19:149:90//AQ039880  
F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence./.0.51:290:58//U91327  
F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence./.7.4e-158:452:96//AC004142  
20 F-PLACE1006246//RPCI11-36I23.TK RPCI-11 Homo sapiens genomic clone RPCI-11-36I23, genomic survey sequence./.2.6e-31:176:97//AQ045400  
F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds./.2.3e-166:791:98//AB014548  
F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence./.1.0:228:63//B16447  
25 F-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING DRAFT SEQUENCE./.6.6e-172:809:99//AL031320  
F-PLACE1006318  
F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence./.0.079:396:59//AC004454  
30 F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region./.1.0:90:67//M55721  
F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unorderd pieces./.0.16:445:56//AC005504  
F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence./.6.1e-05:625:57//AL034559  
35 F-PLACE1006368//X.laevis mRNA for KLP2 protein./.3.0e-25:376:68//X94082  
F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence./.2.0e-146:711:97//AC004232  
F-PLACE1006382  
F-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds./.5.1e-110:539:97//AF062085  
40 F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence./.1.3e-23:463:68//AC005029  
F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds./.1.3e-109:525:98//AF069735  
F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds./.6.9e-23:531:65//AB011129  
45 F-PLACE1006445//HS\_3071\_A1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence./.4.7e-74:392:95//AQ 103347  
F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome./.1.1e-40:686:65//AF010496  
F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA./.0.99:250:59//Z15118  
50 F-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE./.4.3e-120:328:98//AL021977  
F-PLACE1006488//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//6.5e-86:478:91//X53744  
F-PLACE1006492  
F-PLACE1006506  
55 F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence./.0.0010:547:58//AC005083  
F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds./.2.6e-84:625:80//AF005355

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F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence./.0.00031:671:58//AL033510  
F-PLACE1006540  
F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete cds./.6.0e-10:636:59//J03998  
F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence./.9.8e-25:170:  
5 77//AC006044  
F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds./.6.7e-167:781:99//U97670  
F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete  
10 sequence./.0.98:514:59//AC004470  
F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone wg2c3./.0.00079:206:62//X76589  
F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence./.0.0012:576:57//  
AC004015  
F-PLACE1006640//P.falciparum complete gene map of plastid-like DNA (IR-B).//.0.0018:588:59//X95276  
F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
15 DRAFT SEQUENCE, 4 unordered pieces./.0.0028:469:58//AC004688  
F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-I (b3GT1) gene, complete  
cds./.0.00011:184:64//AF029790  
F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds./.0.0013:  
380:62//U67916  
20 F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-IN-  
TERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS./.1.5e-  
78:520:86//Z98048  
F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequencer/1.9e-135:378:99//  
AC005626  
25 F-PLACE1006760//CIT-HSP-2336O13.TR CIT-HSP Homo sapiens genomic clone 2336O13, genomic survey se-  
quence./.0.018:147:66//AQ039246  
F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence./.2.6e-08:  
823:58//AE001426  
F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces./.  
30 0.043:252:65//AC005487  
F-PLACE1006792//HS\_3165\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3165 Col=1 Row=P, genomic survey sequence./.1.4e-11:249:67//AQ149559  
F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds./.1.3e-12:155:80//  
M68513  
35 F-PLACE1006800//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-92, complete  
sequence./.6.7e-05:391:62//AL010272  
F-PLACE1006805//paramecium species 1,168 mt dna dimer: replication init. region./.9.1e-09:369:62//K00915  
F-PLACE1006815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING  
40 DRAFT SEQUENCE./.0.89:465:58//AL031033  
F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence./.1.5e-121:618:91//AC005230  
F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160  
nt].//0.011:145:68//S69350  
F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence./.2.2e-07:691:58//AL034559  
45 F-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING  
DRAFT SEQUENCE./.1.5e-132:643:98//AL033378  
F-PLACE1006878  
F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162./.1.0:236:62//  
Z95120  
50 F-PLACE1006901//Mus musculus t complex testis-specific protein (Tctex2) gene, t haplotype, promoter se-  
quence./.2.7e-19:171:81//U21672  
F-PLACE1006904  
F-PLACE1006917//H.sapiens CpG island DNA genomic Mse1 fragment, clone 79g10, forward read  
cpg79g10.ft1a./.1.3e-21:131:98//Z63175  
F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds./.0.99:248:61//L07063  
55 F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen  
gene families./.0.85:161:63//AF029308  
F-PLACE1006956//Hylobates lar involucrin gene, complete cds./.0.077:355:61//M35447  
F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds./.2.9e-89:483:86//

U23921  
F-PLACE1006961//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//  
1.6e-06:651:58//AJ223323  
F-PLACE1006962//H.sapiens ir1B mRNA.//7.1e-15:202:71//X63417  
5 F-PLACE1006966//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8,  
WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594  
F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
clone cSRL-172A4, genomic survey sequence.//1.0:97:67//B03188  
F-PLACE1007014//Rattus norvegicus equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mR-  
10 NA, complete cds.//4.2e-07:592:58//AF015305  
F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403; complete sequence.//5.1e-17:285:70//  
AC005777  
F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic  
CA repeat\*.//6.2e-131:775 :89//Z82899  
15 F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-  
143:675:99//AC004895  
F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence.//1.3e-131:652:  
97//AC005224  
F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular  
20 Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein  
LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted  
tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//  
8.3e-158:768:97//AL021368  
F-PLACE1007105//Mus musculus muskelin mRNA, complete cds.//4.1e-124:687:91//U72194  
25 F-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING  
DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//AC005139  
F-PLACE1007112//HS\_2234\_B2\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2234 Col=20 Row=N, genomic survey sequence.//0.26:200:62//AQ087801  
F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic clone A-211C6, genomic survey  
30 sequence.//1.3e-40:255:92//BT2112  
F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal cells, mRNA Partial, 3884 nt].//4.9e-15:  
386:62//S68151  
F-PLACE1007178//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61//AC005140  
35 F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:180:63//M62899  
F-PLACE1007238//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//2.8e-08:269:  
63//S74494  
F-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.3e-57:  
40 405:87//D50495  
F-PLACE1007242//HS\_3006\_A1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3006 Col=21 Row=C, genomic survey sequence.//0.088:191:59//AQ089443  
F-PLACE1007243//Human transporter protein (g17) mRNA, complete cds.//7.9e-12:245:66//U49082  
F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:677:98//Y15908  
45 F-PLACE1007274//HS\_3003\_A1\_D08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154  
F-PLACE1007276//Fugu rubripes GSS sequence, clone 014O10aG11, genomic survey sequence.//0.0052:228:  
62//AL024982  
F-PLACE1007282//F.rubripes GSS sequence, clone 019O07aB3, genomic survey sequence.//0.024:289:58//  
AL011743  
50 F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence.//0.0048:185:  
69//AC002492  
F-PLACE1007301//Dictyostelium discoideum gene for TRFA, complete cds.//0.069:761:57//AB009080  
F-PLACE1007317  
F-PLACE1007342  
55 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//5.4e-120:  
567:98//AF096870  
F-PLACE1007367//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-  
59:613:75//AC005077

F-PLACE1007375//Caenorhabditis elegans cosmid D2092//1.8e-12:193:70//U88167  
F-PLACE1007386  
F-PLACE1007402//HS\_2170\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, genomic survey sequence././/5.6e-06:162:67//AQ125590  
5 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence././/1.6e-25:165:93//AF093772  
F-PLACE1007416  
F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence././/4.9e-34:764:62//AC003973  
10 F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds././/4.1e-17:374:64//AF041433  
F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment././/8.1e-52:317:93//L40391  
F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence././/0.0019:280:64//AL031117  
15 F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -complete genomic sequence, complete sequence././/2.5e-24:362:71//AC002302  
F-PLACE1007484  
F-PLACE1007488//Danio rerio faciosexual dysplasia protein (fgd) mRNA, complete cds././/3.8e-14:293:63//AF017370  
20 F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence././/4.6e-10:152:75//AL031311  
F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence././/3.6e-139:477:98//AC004231  
25 F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence././/0.0055:395:59//AF015461  
F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxidase subunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and apocytochrome b (cytb) genes, complete cds, and complete 9S rRNA gene and partial 12S rRNA gene././/0.0013:550:58//U11682 F-PLACE1007537//H.sapiens CpG island DNA genomic Mse1 fragment, clone 198g6, reverse read cpg198g6.rt1a././/0.98:121:67//Z60280  
F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence././/2.3e-10:141:75//U31508  
30 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds././/3.1e-69:733:71//AB014561  
F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule././/0.022:393:61//X03240  
F-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING DRAFT SEQUENCE././/3.6e-114:565:97//AL031665  
35 F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic clone 2371G14, genomic survey sequence././/2.0e-22:304:70//AQ111183  
F-PLACE1007618//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence././/1.0:386:59//AC005245  
F-PLACE1007621  
F-PLACE1007632//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence././/1.0e-88:276:96//AC006064  
40 F-PLACE1007645//Bovine elastin mRNA, partial cds././/2.1e-07:110:79//M26132  
F-PLACE1007649  
F-PLACE1007677//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE././/1.2e-21:567:64//AL023755  
45 F-PLACE1007688//Pseudorabies virus immediate-early gene././/2.2e-05:287:66//X15120  
F-PLACE1007690//Caenorhabditis elegans cosmid R07G3././/0.40:122:70//U23452  
F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment././/0.85:117:71//L40483  
F-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE././/0.0035:75:88//AL031662  
50 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds././/1.3e-147:709:97//AF061243  
F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence././/1.0:510:58//AB005231  
F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro and pol pseudogenes././/4.8e-136:516:89//U86698  
55 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds././/7.9e-155:728:98//AB014585  
F-PLACE1007737//Homo sapiens clone DJ0847O08, WORKING DRAFT SEQUENCE, 3 unordered pieces././/5.8e-22:806:60//AC005484  
F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING

DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504  
 F-PLACE1007746//HS\_2268\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=19 Row=N, genomic survey sequence.//0.10:171:63//AQ124780  
 F-PLACE1007791//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//0.63:241:58//AL031749  
 5 F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879\_D\_6, complete sequence.//1.0e-120:743:87//AC005273  
 F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.0e-113:739:86//AC003658  
 10 F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey sequence.//1.0e-47:254:97//AQ196438  
 F-PLACE1007843//F.rubripes GSS sequence, clone 162K02bC12, genomic survey sequence.//1.6e-10:148:72//AL006903  
 15 F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AP000010  
 F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174  
 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3.9e-189:894:98//AB018309  
 F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone 2353D11, genomic survey sequence.//0.015:279:61//AQ263271  
 20 F-PLACE1007877  
 F-PLACE1007897  
 F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//2.3e-154:755:97//AB007956  
 25 F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING DRAFT SEQUENCE.//1.1e-59:310:81//AC003097  
 F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//2.1e-61:522:79//AC006157  
 F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//2.7e-171:813:98//AF084530  
 30 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.5e-153:730:98//AF079529  
 F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//3.4e-32:383:74//U13262  
 F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198:96//Z94758  
 35 F-PLACE1008000//Mus musculus veli 3 mRNA, complete cds.//1.5e-118:706:88//AF087695  
 F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.4e-163:786:98//AC005628  
 F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625:  
 40 84//L31840  
 F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165:65//Z35719  
 F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16.3.//4.0e-07:251:64//Z68883  
 F-PLACE1008095//RPCI11-21F19.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F19, genomic survey sequence.//1.5e-30:166:99//B85883  
 45 F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//7.5e-06:414:60//AF069163  
 F-PLACE1008122//S.cerevisiae chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867  
 F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase II genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586  
 50 F-PLACE1008132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//3.6e-20:111:93//Z82199  
 F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-88:866:73//D14849  
 F-PLACE1008181//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//0.0033:727:56//AL034397  
 55 F-PLACE1008198//HS\_3073\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=11 Row=E, genomic survey sequence.//2.3e-12:94:92//AQ171450  
 F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.5e-

162:791:97//AC005069  
 F-PLACE1008209  
 F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:174:66//M26332  
 F-PLACE1008244//CIT-HSP-2337B4.TR CIT-HSP Homo sapiens genomic clone 2337B4, genomic survey sequence.//6.7e-28:165:95//AQ039317  
 F-PLACE1008273//B.primigenius mRNA for coat protein gamma-cop.//2.8e-71:709:71//X92987  
 F-PLACE1008275//D.discoideum actin A-13 gene, 5' flank.//0.12:131:64//M29123  
 F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.011:96:73//AC005913  
 10 F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//8.2e-86:672:77//AF078779  
 F-PLACE1008329//HS\_2027\_A1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey sequence.//8.7e-09:116:81//AQ244432  
 15 F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//2.2e-141:670:98//AC005176  
 F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-27:157:78//AC005000  
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.1e-137:659:98//AB014579  
 20 F-PLACE1008368//CIT-HSP-2311C9.TR CIT-HSP Homo sapiens genomic clone 2311C9, genomic survey sequence.//7.1e-08:398:60//AQ016352  
 F-PLACE1008369//HS\_2251\_B1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey sequence.//2.1e-35:217:93//AQ066512  
 F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.4e-11:403:64//AC005856  
 25 F-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//3.7e-144:681:99//AL034417  
 F-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//2.8e-45:257:96//AC004604  
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711:98//D86326  
 30 F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.089:672:56//AC004688  
 F-PLACE1008424  
 F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 7/11.//1.0e-88:331:84//AB020864  
 35 F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//0.55:530:58//U62317  
 F-PLACE1008437//CIT-HSP-2376H4.TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence.//3.3e-78:349:94//AQ112479  
 F-PLACE1008455//HS\_2064\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471:81//AQ246589  
 40 F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307:73//AC004526  
 F-PLACE1008465//CIT-HSP-2163F24.TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence.//8.9e-41:210:99//B90014  
 45 F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516:58//AB003494  
 F-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//1.3e-161:778:98//AL031778  
 F-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//1.1e-78:191:100//AF045555  
 50 F-PLACE1008532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//3.8e-24:257:70//Z93097  
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215:71//AC004997  
 55 F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//0.66:263:64//Z99571  
 F-PLACE1008584//Homo sapiens cosmid clone U39B3 from Xp22.1-22.2, complete sequence.//1.1e-19:315:68//U73023  
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-173:812:98//AB018334

F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces./.3.9e-09:198:71//AC005077  
 F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBNL H91), complete sequence./.0.68:568:59//AC005373  
 5 F-PLACE1008626//HS\_3221\_A2\_F03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence./.1.7e-13:147:82//AQ180967  
 F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor./.9.7e-98:586:88//Y12836  
 F-PLACE1008629//CIT-HSP-2012I4.TR CIT-HSP Homo sapiens genomic clone 2012I4, genomic survey sequence./.0.00085:203:66//B53732  
 10 F-PLACE1008630//Sequence 26 from Patent WO9517522./.9.7e-05:97:80//A45356  
 F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds./.1.4e-23:299:64//D38595  
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds./.1.1e-133:622:99//AF044333  
 15 F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence./.0.24:89:76//AQ060732  
 F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds./.1.4e-94:420:97//AF038406  
 20 F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence./.2.1e-70:349:98//AQ007199  
 F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence./.0.14:347:59//AC004260  
 F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence./.7.9e-25:244:71//AC003037  
 25 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds./.4.5e-120:503:97//AF060543  
 F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence./.0.00026:370:61//AF001549  
 F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence./.3.3e-08:220:65//AQ036643  
 30 F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds./.1.7e-120:470:97//AF030933  
 F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds./.2.8e-87:504:89//AF032668  
 F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence./.4.0e-21:212:74//AL021920  
 35 F-PLACE1008854  
 F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE./.4.7e-77:477:84//Z82209  
 F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence./.3.4e-53:699:70//AC005539  
 40 F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds./.2.1e-06:164:68//M63660  
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds./.6.4e-158:753:98//AB018308  
 F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces./.0.00013:400:63//AC002042  
 45 F-PLACE1008934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE./.7.4e-05:145:71//AL022312  
 F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds./.4.3e-41:282:87//L15309  
 F-PLACE1008947//Pseudorabies virus with upstream and downstream sequences./.5.9e-15:710:60//M34651  
 50 F-PLACE1009020//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence./.1.9e-21:167:86//AQ253727  
 F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence./.4.1e-152:763:97//AL031117  
 F-PLACE1009039//HS\_2034\_A2\_F08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey sequence./.0.17:252:59//AQ230137  
 55 F-PLACE1009045//HS\_3185\_B2\_B03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey sequence./.1.9e-34:260:86//AQ172861  
 F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit gene, 5'flank and exon 1./.4.7e-70:463:80//D00766

F-PLACE1009050//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence./.0.63:280:61//AC004241  
 F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X), complete CDS./.5.9e-113:725:85//AJ005073  
 5 F-PLACE1009090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1045J21, WORKING DRAFT SEQUENCE./.9.1e-27:222:84//AL021919  
 F-PLACE1009091//Homo sapiens clone DJ0968I16, complete sequence./.0.027:630:58//AC006016  
 F-PLACE1009094  
 10 F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds./.2.1e-85:726:76//M36515  
 F-PLACE1009110  
 F-PLACE1009111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 138B7, WORKING DRAFT SEQUENCE./.6.0e-12:362:64//Z98752  
 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds./.3.4e-138:671:97//AF035586  
 15 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds./.3.6e-23:718:59//D25215  
 F-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE./.6.1e-142:684:98//AJ011929  
 F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SE-  
 QUENCE./.4.3e-36:227:77//AP000031  
 20 F-PLACE1009158//H.sapiens genomic sequence for ERCC2 gene 3'region involved in DNA excision repair./.1.0:  
 173:60//X52222  
 F-PLACE1009166  
 F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence./.4.0e-35:257:85//AC002070  
 F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library)  
 25 complete sequence./.2.9e-19:288:72//AC004805  
 F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence./.0.053:388:60//AB008266  
 F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, complete cds./.1.8e-50:317:89//AF061242  
 F-PLACE1009190//RPCI11-81N5.TJ RPCI11 Homo sapiens genomic clone R-81N5, genomic survey sequence./.  
 30 0.91:114:67//AQ281881  
 F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone 2509J16, genomic survey se-  
 quence./.2.8e-44:175:83//AQ262198  
 F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glycoprotein./.1.1e-106:495:88//X63203  
 F-PLACE1009246//HS\_3058\_B1\_A06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 35 nomic clone Plate=3058 Col=11 Row=B, genomic survey sequence./.0.10:175:68//AQ185945  
 F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds./.1.8e-94:575:89//U47024  
 F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region./.0.0017:350:62//U23862  
 F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds./.3.0e-06:411:  
 59//U83192  
 40 F-PLACE1009328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191P20, WORKING DRAFT SEQUENCE./.5.7e-138:830:86//AL034399  
 F-PLACE1009335//Human (lambda) DNA for immunoglobin light chain./.0.071:253:62//D87015  
 F-PLACE1009338//RPCI11-74N24 TV RPCI11 Homo sapiens genomic clone R-74N24, genomic survey se-  
 45 quence./.2.4e-34:180:100//AQ268811  
 F-PLACE1009368  
 F-PLACE1009375  
 F-PLACE1009388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1014D13, WORKING DRAFT SEQUENCE./.2.0e-37:288:84//AL022311  
 F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds./.4.3e-78:730:74//M27878  
 50 F-PLACE1009404//SmD homolog [mice, liver, mRNA Partial, 199 nt].//0.16:95:71//S71494  
 F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence./.1.6e-150:701:  
 99//AC005919  
 F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence./.2.9e-73:442:88//AF046700  
 F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162./.0.012:582:56//  
 55 AL022022  
 F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds./.4.6e-21:  
 146:93//AF012872  
 F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequence./.2.9e-31:264:81//AF046660

F-PLACE1009468//Sequence 1 from patent US 5580968.//1.9e-83:567:84//I30536  
 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//1.9e-142:704:97//AC004531  
 F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence.//2.2e-09:235:68//AC004601  
 5 F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.9e-83:171:92//U91321  
 F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part  
 of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown  
 10 gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-  
 69:175:92//Z94160  
 F-PLACE1009539//Mus musculus synaptjanin 2 isoform alpha mRNA, complete cds.//7.0e-26:237:78//  
 AF041862  
 F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene sim-  
 15 ilar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS  
 and a CpG island, complete sequence.//3.1e-10:126:79//AL031587  
 F-PLACE1009571//RPCI11-60K12.TK RPCI11 Homo sapiens genomic clone R-60K12, genomic survey se-  
 quence.//1.4e-05:68:91//AQ195869  
 F-PLACE1009581  
 20 F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), complete sequence.//6.6e-19:  
 309:70//AC003959  
 F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) gene,  
 complete cds.//9.0e-09:485:59//AF016049  
 F-PLACE1009607//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING  
 DRAFT SEQUENCE.//4.9e-43:714:66//Z83824  
 25 F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.017:655:57//AC004157  
 F-PLACE1009621  
 F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 Plate=CT 791 Col=16 Row=J, genomic survey sequence.//2.7e-15:100:98//B33248  
 30 F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces.//0.63:130:67//AC005308  
 F-PLACE1009639//S.pombe chromosome II cosmid c24E9.//0.86:509:58//AL021816  
 F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.4e-171:816:98//AB011159  
 35 F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.4e-67:437:87//  
 AC005177  
 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5e-147:701:98//AF062534  
 F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//1.5e-98:228:100//AC006011  
 F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//2.2e-130:736:91//AC000109  
 40 F-PLACE1009731//M.musculus mRNA for immunity associated protein 38.//1.1e-13:311:64//Y08026  
 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//4.2e-125:602:98//AF046024  
 F-PLACE1009794  
 F-PLACE1009798//Hnman DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-  
 45 quone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene  
 Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER; TYK3) pseudogenes, and part of a novel gene  
 similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs,  
 complete sequence.//1.3e-73:271:84//AL030996  
 F-PLACE1009845  
 F-PLACE1009861//B.tauris cathepsin B mRNA, 3' end.//0.00023:147:65//M64620  
 50 F-PLACE1009879//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING  
 DRAFT SEQUENCE.//4.9e-27:725:63//AL034397  
 F-PLACE1009886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING  
 DRAFT SEQUENCE.//8.2e-12:135:82//AL031427  
 F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence.//  
 0.0044:232:60//AQ251431  
 55 F-PLACE1009908//S.pombe chromosome I cosmid c3F10.//1.5e-19:559:59//Z69369  
 F-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//5.9e-48:304:87//  
 M63005  
 F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SE-

QUENCE, 4 unordered pieces.//2.4e-51:481:78//AC004529  
 F-PLACE1009925//nxb0027C22r CUGI Rice BAC Library Oryza sativa genomic clone nxb0027C22r, genomic survey sequence.//0.98:220:67//AQ272066  
 F-PLACE1009935//Sequence 16 from patent US 5552281.//0.030:152:67//I25655  
 5 F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-12:322:67//AC006026  
 F-PLACE1009971  
 F-PLACE100992//HS\_3178\_B1\_F04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence.//4.9e-23:142:95//AQ150311  
 10 F-PLACE100995//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00019:231:64//Z81029  
 F-PLACE100997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//7.9e-87:552:80//U48288  
 F-PLACE1010023  
 F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//6.9e-101:181:98//AL031775  
 15 F-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//2.3e-136:689:95//X84692  
 F-PLACE1010069//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING  
 20 DRAFT SEQUENCE.//0.0090:383:60//Z95114  
 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//1.8e-166:792:98//AF065482  
 F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//7.5e-13:203:77//D25540  
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-152:727:98//AB007925  
 25 F-PLACE1010089//HS\_3111\_A1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3111 Col=15 Row=l, genomic survey sequence.//4.8e-07:124:78//AQ101268  
 F-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//1.2e-108:700:85//X64411  
 F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//AC005506  
 30 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//3.8e-25:728:60//AF059569  
 F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22.//6.5e-25:488:63//Z93928  
 F-PLACE1010134//S.pombe chromosome I cosmid c29B12.//1.9e-13:238:67//Z99164  
 F-PLACE1010148//Homo sapiens partial human cDNA (660 bp).//4.8e-83:409:98//AJ222636  
 35 F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 2381F24, genomic survey sequence.//1.5e-28:163:98//AQ196757  
 F-PLACE1010181//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence.//2.4e-15:197:72//AC004973  
 F-PLACE1010194//Ictalurus punctatus tumor suppressor p53 mRNA, complete cds.//3.0e-14:181:74//AF074967  
 40 F-PLACE1010202//Homo sapiens mRNA for MBNL protein.//1.2e-27:509:66//Y13829  
 F-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033377  
 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds.//5.8e-145:693:97//AB007917  
 F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence; WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//AC004710  
 45 F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00040:231:64//Z81029  
 F-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70//AC004464  
 F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//3.5e-1 0:185:67//AL031005  
 50 F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.010:524:58//Z84468  
 F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence.//9.1e-90:448:97//AQ041837  
 F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome.//2.8e-08:384:64//L06178  
 55 F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence.//4.1e-21:141:92//B38252  
 F-PLACE1010362//Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.//0.94:398:57//AL022121

F-PLACE1010364//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y102G3,  
WORKING DRAFT SEQUENCE./.0.11:404:56//AL020985  
F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence./.0.066:88:76//  
AC004675

5 F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey se-  
quence./.2.4e-71:454:88//AQ076825  
F-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds./.7.5e-134:722:93//AF003927  
F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds./.2.2e-150:702:99//AF039081  
F-PLACE1010492

10 F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28./.0.022:405:60//U82695  
F-PLACE1010529//Sequence 1 from patent US 5776717./.2.9e-145:684:98//AR016417  
F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and  
GSSs, complete sequence./.1.0:283:61//AL031677  
F-PLACE1010562//RPCI11-65I16.TK RPCI11 Homo sapiens genomic clone R-65I16, genomic survey sequence./.  
15 0.017:216:67//AQ200831  
F-PLACE1010579//Homo sapiens full-length insert cDNA YI23D12./.3.9e-19:147:89//AF075014  
F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete  
cds./.6.4e-96:559:89//L25125  
F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete  
20 cds./.3.1e-146:707:97//AF045186  
F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
DRAFT SEQUENCE, 5 unordered pieces./.0.045:454:59//AC005308  
F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence./.9.1e-07:378:60//AL034558  
F-PLACE1010624//Streptomyces coelicolor cosmid 5A7./.1.4e-05:518:61//AL031107

25 F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces./.  
5.0e-137:675:97//AC004846  
F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence./.2.5e-  
17:187:80//AC004682  
F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence./.  
30 0.21:159:64//AB016872  
F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces./.1.2e-  
144:720:97//AC005069  
F-PLACE1010661

35 F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)./.0.90:257:61//  
AL021960  
F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds./.3.3e-73:697:74//  
U35376  
F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence./.0.010:447:59//  
AC004583

40 F-PLACE1010720//Mouse TPA-induced TIS11 mRNA./.2.0e-86:535:88//X14678  
F-PLACE1010739//HS\_2013\_B2\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2013 Col=20 Row=D, genomic survey sequence./.5.7e-87:435:97//AQ235864  
F-PLACE1010743//R.norvegicus mRNA for myr5./.1.7e-87:582:85//X77609  
F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence./.4.7e-45:235:  
45 99//AC005921  
F-PLACE1010771//M.musculus HCNGP mRNA./.1.6e-135:801:88//X68061  
F-PLACE1010786//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-15, complete  
sequence./.0.35:334:60//AL010221  
F-PLACE1010800//RPCI11-79H17.TV RPCI11 Homo sapiens genomic clone R-79H17, genomic survey se-  
quence./.5.8e-18:168:82//AQ284252

50 F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence./.1.6e-30:693:63//AC004384  
F-PLACE1010811//RPCI11-51N5.TK RPCI11 Homo sapiens genomic clone R-51N5, genomic survey sequence./.  
8.3e-11:142:78//AQ052380  
F-PLACE1010833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING  
55 DRAFT SEQUENCE./.7.3e-40:147:88//AL031283  
F-PLACE1010856//M.musculus mRNA for utrophin./.7.3e-17:150:86//Y12229  
F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
non-small cell lung cancer, segment 11/11./.1.4e-94:422:95//AB020868

- F-PLACE1010870//*M.musculus* mRNA for ZT3 zinc finger factor./.1.3e-93:530:90//Z67747  
 F-PLACE1010877//*Homo sapiens* mRNA for KIAA0610 protein, partial cds./.1.1e-147:694:98//AB011182  
 F-PLACE1010891  
 F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence./.3.9e-26:394:68//AC003997  
 F-PLACE1010900  
 F-PLACE1010916//HS\_2242\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2242 Col=7 Row=E, genomic survey sequence./.1.0e-78:391:97//AQ146687  
 F-PLACE1010917  
 5 F-PLACE1010925//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces./.0.11:629:56//AC004688  
 F-PLACE1010926//*Homo sapiens* mRNA for KIAA0554 protein, partial cds./.9.5e-138:653:98//AB011126  
 F-PLACE1010942//*Homo sapiens* intersectin short form mRNA, complete cds./.5.6e-90:437:98//AF064243  
 F-PLACE1010944//*Homo sapiens* full-length insert cDNA clone ZD38E12./.1.4e-09:208:68//AF086247  
 10 F-PLACE1010947  
 F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP *Homo sapiens* genomic clone 2283D9, genomic survey sequence./.2.1e-29:190:91//B98965  
 F-PLACE1010960//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence./.0.00074:421:60//AL010226  
 15 20 F-PLACE1010965//CIT-HSP-2386K24:TF.1 CIT-HSP *Homo sapiens* genomic clone 2386K24, genomic survey sequence./.1.8e-84:412:99//AQ240696  
 F-PLACE1011026//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence./.0.00037:257:64//AL008972  
 F-PLACE1011032//*Homo sapiens* chromosome 5, BAC clone 118L13 (LBNL H176), complete sequence./.3.8e-06:315:65//AC005348  
 25 F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds./.1.5e-56:286:98//U70669  
 F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds./.1.3e-24:278:76//M20636  
 F-PLACE1011054//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 981L23, WORKING DRAFT SEQUENCE./.3.8e-27:196:84//AL031686  
 30 F-PLACE1011056//*Ovis aries* bactinecin 11 (Bac11) gene, exon 4, and complete cds./.5.4e-06:182:67//U77049  
 F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt]./.3.2e-31:169:100//S75548  
 F-PLACE1011090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE./.5.1e-80:479:89//AL031687  
 35 F-PLACE1011109//*Rattus norvegicus* nuclear-encoded mitochondrial elongation factor G mRNA, complete cds./.2.3e-24:192:84//L14684  
 F-PLACE101114//*S.cerevisiae* chromosome XI reading frame ORF YKR024c./.1.4e-14:346:60//Z28249  
 F-PLACE1011133//T7E9-T7.1 TAMU *Arabidopsis thaliana* genomic clone T7E9, genomic survey sequence./.0.010:345:60/B19698  
 40 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP *Homo sapiens* genomic clone 2375J10, genomic survey sequence./.0.00013:95:76//AQ109305  
 F-PLACE1011160//*Homo sapiens* PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence./.3.7e-111:692:87//AC004893  
 F-PLACE1011165//*H.sapiens* galactokinase (GK2) mRNA, complete cds./.8.4e-31:194:92//M84443  
 45 F-PLACE1011185//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-249B10, complete sequence./.3.1e-43:447:72//AC002288  
 F-PLACE1011203//*Homo sapiens* chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds./.3.3e-124:584:99//AF038664  
 F-PLACE1011214//HS\_2046\_A2\_B01\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2046 Col=2 Row=C, genomic survey sequence./.2.0e-39:346:81//AQ305965  
 50 F-PLACE1011219  
 F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 *Homo sapiens* genomic clone 2513F18, genomic survey sequence./.2.4e-20:119:100//AQ279801  
 F-PLACE1011229//*Homo sapiens* mRNA for KIAA0529 protein, partial cds./.4.4e-146:675:99//AB011101  
 55 F-PLACE1011263//*Homo sapiens* BAC clone GS166A23 from 7p21, complete sequence./.1.7e-42:212:84//AC005014  
 F-PLACE1011273//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y37D8, WORKING DRAFT SEQUENCE./.1.0:214:60//Z92819

F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-16P9, genomic survey sequence./.8.0e-08:66:98//B81770  
 F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), complete sequence./.0.027:135:  
 67//AC004647

5 F-PLACE1011310//H.sapiens CpG island DNA genomic Mse1 fragment, clone 53c10, reverse read  
 cpg53c10.rt1b./.1.4e-05:57:100//Z61496  
 F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial  
 cds./.0.077:193:60//L02290

10 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds./.3.1e-150:699:  
 99//AF102265  
 F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388\_F\_14, complete sequence./.2.4e-38:186:  
 83//AC005375  
 F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds./.6.0e-35:689:63//AF023919  
 F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4./.6.0e-88:584:86//AJ010310

15 F-PLACE1011399//paramecium species 7,325 mt dna dimer: replication init. region./.0.00011:255:63//K00919  
 F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13./.0.067:337:62//AJ006996  
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds./.4.6e-157:743:98//AB011102  
 F-PLACE1011452//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE./.1.1e-  
 53:557:73//AJ011929

20 F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence./.3.5e-  
 71:498:80//AC004605  
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds./.4.8e-151:703:99//AB018255  
 F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./.5.2e-145:675:99//AF065482  
 F-PLACE1011492//Ray (T.californica) acetylcholine receptor beta-subunit mRNA./.1.0:448:59//J00964

25 F-PLACE1011503  
 F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence./.3.8e-147:692:99//AC004968  
 F-PLACE1011563//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//.0.00036:296:  
 61//X83546  
 F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete sequence./.1.1e-38:315:82//  
 30 AC004984  
 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds./.1.3e-65:  
 268:86//AF054180  
 F-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence./.2.0e-82:188:96//  
 AC004477

35 F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence./.1.8e-153:752:  
 97//AC005224  
 F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5)  
 of the Complete Nucleotide Sequence./.4.8e-05:190:67//AE000660  
 F-PLACE1011643//Alcaligenes eutrophus phaP gene./.0.16:466:59//X85729

40 F-PLACE1011646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING  
 DRAFT SEQUENCE./.9.1e-19:156:76//AL033383  
 F-PLACE1011649  
 F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds./.6.4e-09:172:74//AF037062  
 F-PLACE1011664//D.melanogaster crn mRNA./.1.1e-52:650:68//X58374

45 F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces./.0.11:443:58//AC005507  
 F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and  
 a GSS, complete sequence./.0.31:127:71//AL008719  
 F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence./.4.6e-52:461:77//AC002487

50 F-PLACE1011725  
 F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome  
 region, WORKING DRAFT SEQUENCE, 3 unordered pieces./.0.011:320:62//AC004737  
 F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces./.0.00031:544:59//AC004157  
 F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence./.2.4e-115:682:90//  
 AC004003  
 F-PLACE1011778//RPCI11-22D17.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22D17, genomic survey  
 sequence./.2.7e-114:611:93//AQ008944

F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey sequence.//2.3e-17:120:94//AQ042330  
 F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds.//4.1e-24:565:64//U00147  
 F-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.5e-141:678:98//AC004478  
 5 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds.//1.6e-108:526:98//AB011152  
 F-PLACE1011891//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392  
 F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969  
 10 F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:61//U81400  
 F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617  
 F-PLACE1011962//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//2.4e-07:154:74//AQ175369  
 15 F-PLACE1011964//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799  
 F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529  
 F-PLACE1011995//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library)  
 20 complete sequence.//8.8e-53:687:71//AC006054  
 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.2e-146:690:98//AB018256  
 F-PLACE2000003//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//1.7e-62:293:  
 25 88//AC005837  
 F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unorderd pieces.//1.4e-116:261:91//AC006057  
 F-PLACE2000007  
 F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//5.2e-102:489:99//  
 AC005578  
 F-PLACE2000014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING  
 30 DRAFT SEQUENCE.//0.0095:307:62//AL022574  
 F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unorderd pieces.//2.0e-  
 36:316:81//AC005069  
 F-PLACE2000017//HS\_3042\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074  
 35 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//4.6e-84:844:72//AF082556  
 F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638  
 F-PLACE2000033//C.capitata mRNA for chorion protein s18.//0.0019:342:62//Y08913  
 F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA, complete cds.//2.8e-13:335:63//  
 40 AF041082  
 F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:  
 489:90//L08505  
 F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626  
 45 F-PLACE2000050//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.1e-32:527:68//  
 AC003101  
 F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20, genomic survey sequence.//1.1e-05:89:83//AQ059010  
 F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457  
 50 F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219  
 F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SE-  
 QUENCE, 39 unorderd pieces.//1.6e-16:119:93//AC005910  
 F-PLACE2000100//HS\_3184\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004  
 55 F-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL031848  
 F-PLACE2000111//Homo sapiens DNA, trinucleotide repeats region.//1.0:200:64//AB018491  
 F-PLACE2000115

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F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//6.2e-43:  
362:80//AC004531  
F-PLACE2000132//RPCI11-79F15.TV RPCI11 Homo sapiens genomic clone R-79F15, genomic survey se-  
quence.//5.4e-35:206:94//AQ284166  
5 F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence.//2.7e-12:814:59//AC002070  
F-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING  
DRAFT SEQUENCE.//3.6e-165:799:97//AL020995  
F-PLACE2000164//Canine histamine H2 receptor gene, complete cds.//0.10:392:56//M32701  
F-PLACE2000170  
10 F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence.//3.9e-91:552:88//  
AC006005  
F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete  
sequence.//0.98:201:64//AC004032  
F-PLACE2000187  
15 F-PLACE2000216  
F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12L17, genomic survey  
sequence.//0.00039:325:58/B75888  
F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence.//7.5e-55:237:78//  
AC003003  
20 F-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58  
unordered pieces.//2.4e-92:236:94//AC005902  
F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudo-  
genes similar to ribosomal protein, ESTs, GSSs, complete sequence.//1.4e-32:331:78//AL031577  
F-PLACE2000274//Anthocidaris crassispina mRNA for B2HC, partial cds.//8.5e-48:765:66//AB012308  
25 F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//8.3e-  
08:662:58//US2064  
F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.4e-  
08:95:81//AC006021  
F-PLACE2000317//HS\_3183\_B2\_F05\_MR CIT Approved Human Genomic Sperm-Library D Homo sapiens ge-  
30 nomic clone Plate=3183 Col=10 Row=L, genomic survey sequence.//2.5e-71:346:99//AQ172747  
F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.7e-  
14:402:65//AC004952  
F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete  
cds.//4.5e-77:555:82//AF026554  
35 F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial  
cds.//1.8e-14:259:71//U66829  
F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmids R32543., and F15613 con-  
taining ZNF gene family member, genomic sequence, complete sequence.//6.0e-34:376:74//AC003006  
F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23J20, genomic survey  
40 sequence.//8.4e-21:288:69//AQ013849  
F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence.//5.0e-114:692:80//  
U49973  
F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cancer Institute Human PAC Library)  
complete sequence.//0.38:356:58//AC005182  
45 F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C18, genomic survey se-  
quence.//0.064:132:68//AQ051776  
F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete se-  
quence.//1.6e-130:776:88//AC003658  
F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human  
50 BAC Library) complete sequence.//5.4e-113:808:83//AC005909  
F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene.//0.87:286:  
63//X06967  
F-PLACE2000399  
F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence.//2.9e-59:532:68//Z36238  
55 F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.//  
0.44:553:56//U89984  
F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds.//1.4e-56:303:86//M13792  
F-PLACE2000425//HS\_3047\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3047 Col=9 Row=O, genomic survey sequence.//2.8e-42:224:97//AQ126949  
F-PLACE2000427  
F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//1.1e-19:363:  
67//AC005821  
5 F-PLACE2000435//HS\_3036\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999  
F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence.//4.6e-23:550:62//AL021492  
F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//1.0e-78:604:  
80//AC006025  
10 F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//8.2e-  
05:330:63//AC002300  
F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.7e-  
168:816:97//AC005740  
15 F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete se-  
quence.//4.3e-33:296:79//AC002037  
F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//  
3.4e-59:598:74//AC005057  
F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602  
F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187  
20 F-PLACE3000020//R.norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075  
F-PLACE3000029  
F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267  
F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.8e-  
17:250:74//AC005368  
25 F-PLACE3000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006  
F-PLACE3000119/\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670  
F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668  
F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//1.8e-48:330:79/  
30 AC005695  
F-PLACE3000136  
F-PLACE3000142//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING  
DRAFT SEQUENCE.//0.011:294:62//AL033520  
F-PLACE3000145//Gallus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662  
35 F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the  
DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//5.1e-37:305:81//AL031053  
F-PLACE3000148//Homo sapiens chromosome Y, clone 47511, complete sequence.//4.7e-32:766:63//AC004474  
F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//7.4e-173:822:  
98//AC005277  
40 F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and  
R32804, complete sequence.//2.2e-81:783:74//AC003682  
F-PLACE3000157  
F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500  
F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey se-  
45 quence.//0.080:259:59//B50878  
F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//9.8e-158:749:98//  
AC006130  
F-PLACE3000194  
50 F-PLACE3000197//F.rubripes GSS sequence, clone 075N04bB7, genomic survey sequence.//1.4e-08:164:68//  
AL003352  
F-PLACE3000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING  
DRAFT SEQUENCE.//0.0019:277:58//Z82207  
F-PLACE3000207//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//6.6e-21:312:67//  
AC005013  
55 F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII inter-  
genic region and (COL7A1) gene, complete cds.//1.0:279:61//L23982  
F-PLACE3000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//9.3e-43:383:79//  
AC004086

F-PLACE3000220//RPCI11-54B4.TV RPCI11 Homo sapiens genomic clone R-54B4, genomic survey sequence.//  
2.4e-36:381:76//AQ082056

F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces//7.2e-  
135:721:91//AC005231

5 F-PLACE3000226  
F-PLACE3000230//Homo sapiens c1cr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds,  
and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//3.3e-80:498:78//U95626

10 F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-  
Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene  
and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and ge-  
nomic marker DXS8032, complete sequence.//2.6e-54:254:92//Z98046

15 F-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.4e-139:850:86//X80169

F-PLACE3000254//Ateline herpesvirus 3 complete genome.//1.3e-10:399:61//AF083424

F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//1.8e-21:350:  
68//AF001548

20 F-PLACE3000276//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//5.7e-45:376:81//AQ231147

F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//1.6e-138:650:99//  
AC005328

25 F-PLACE3000310  
F-PLACE3000320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
DRAFT SEQUENCE.//1.9e-41:379:77//AL034379

F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//3.3e-35:419:  
68//AC005822

30 F-PLACE3000331//CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey se-  
quence.//2.7e-20:119:99//AQ061543

F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits Bchl (bchl) and BchD (bchD) genes,  
complete cds; and BchO (bchO) gene, partial cds.//0.99:310:58//AF017642

35 F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC  
Library) complete sequence.//7.5e-159:752:98//AC006055

F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds.//2.3e-107:592:  
92//AF084205

F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//2.1e-37:  
480:70//Z83732

40 F-PLACE3000353  
F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.//0.00011:373:  
60//AC005969

F-PLACE3000363  
F-PLACE3000365//Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chro-  
mosome X contains CpG island, EST.//0.074:279:61//Z81007

45 F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE  
LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.  
Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545

F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.2e-25:288:71//  
AC005154

50 F-PLACE3000399//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING  
DRAFT SEQUENCE.//2.3e-69:303:86//Z97630

F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239

55 F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//  
5.8e-25 :292:73//AC006023

F-PLACE3000402//RPCI11-20D6.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey  
sequence.//1.1e-10:154:74//AQ008761

F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.9e-41:515:  
72//AC005701

F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic  
clone cSRL-179E11, genomic survey sequence.//2.8e-91:540:89//B03443

F-PLACE3000413

F-PLACE3000416//F19L8-Sp6 IGF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence.//

0.0018:664:55//B11305  
F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence./.1.1e-16:284:70//AL022719  
5 F-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE./.3.6e-146:732:96//AL031284  
F-PLACE3000475//HS\_2164\_A2\_H10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=O, genomic survey sequence./.1.5e-07:159:71//AQ132983  
F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs./.2.9e-11:213:70//Z83843  
10 F-PLACE400009//Sequence 93 from patent US 5616500./.9.9e-08:692:60//I39845  
F-PLACE400014//Homo sapiens mRNA for KIAA0809 protein, partial cds./.1.1e-116:331:100//AB018352  
F-PLACE400034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence./.5.0e-05:244:63//AC004131  
15 F-PLACE400049//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence./.1.2e-37:385:74//AC005926  
F-PLACE400052//M.musculus abcl mRNA./.1.5e-110:671:88//X75926  
F-PLACE400063  
F-PLACE400089//M.musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation./.3.7e-12:114:85//X74311  
20 F-PLACE400093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence./.0.11:245:60//AQ108342  
F-PLACE4000100//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE./.2.9e-19:384:65//AL031848  
F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds./.1.2e-145:684:99//AB007931  
25 F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds./.3.7e-62:541:78//AF091234  
F-PLACE4000129  
F-PLACE4000131//HS\_3139\_B2\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence./.2.3e-14:221:70//AQ183207  
F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(IV) Chain Precursor. Contains GSSs, complete sequence./.0.28:412:58//  
30 AL031622  
F-PLACE4000156//Human zinc finger protein ZNF136./.7.2e-88:764:76//U09367  
F-PLACE4000192  
F-PLACE4000211  
35 F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence./.1.2e-14:177:76//B17158  
F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds./.9.8e-116:662:89//AF030430  
F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence./.5.2e-54:363:70//  
AC003973  
40 F-PLACE4000247  
F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence./.0.0053:229:65//AC004673  
F-PLACE4000252  
F-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein./.2.0e-25:191:87//Z70200  
45 F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds./.2.6e-23:314:71//  
AF084259  
F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds./.5.5e-122:734:88//AF032667  
F-PLACE4000270  
F-PLACE4000300  
50 F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds./.1.4e-21:135:96//  
L34075  
F-PLACE4000323//HS\_2165\_B1\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence./.4.3e-08:170:71//AQ125036  
F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2./.2.8e-06:311:63//  
55 M10296  
F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence./.0.014:  
252:60//AE001401  
F-PLACE4000367

F-PLACE4000369  
F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661  
F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649  
5 F-PLACE4000392//Rattus norvegicus polymorphic marker D20UIA1 sequence.//1.2e-05:222:68//AF054088  
F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540  
F-PLACE4000411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984  
10 F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200  
F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:100//B41346  
F-PLACE4000450  
15 F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//2.3e-07:273:65//AC005065  
F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//4.1e-34:351:70//AC005821  
F-PLACE4000489//HS\_3012\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-36:220:92//AQ095537  
20 20 F-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865  
F-PLACE4000521//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929  
25 F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial cds.//4.0e-124:686:90//U47645  
F-PLACE4000548  
F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747  
F-PLACE4000581  
30 F-PLACE4000590//Homo sapiens chromosome Y, clone 47S1, complete sequence.//3.6e-20:747:59//AC004474  
F-PLACE4000593//Caenorhabditis elegans cosmid F25D7, complete sequence.//5.6e-16:326:65//Z78418  
F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281  
F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039  
35 F-PLACE4000650  
F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267  
F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816  
F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577  
F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312  
40 40 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554  
F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616  
F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797  
F-THYRO1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561  
45 F-THYRO1000026//Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637  
F-THYRO1000034//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353  
50 50 F-THYRO1000035//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:303:83//AC004383  
F-THYRO1000040  
F-THYRO1000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383  
F-THYRO1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557  
55 55 F-THYRO1000085  
F-THYRO1000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2013L16, genomic survey sequence.//0.31:186:61//B60606  
F-THYRO1000107

F-THYRO1000111//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403  
F-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055  
5 F-THYRO1000124//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72a7, forward read cpg72a7.ft1a.//9.5e-26:169:94//Z62724  
F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142  
F-THYRO1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096  
10 F-THYRO1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574  
F-THYRO1000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331  
F-THYRO1000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419  
15 F-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207  
F-THYRO1000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214  
F-THYRO1000190//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//0.38:184:64//AC005746  
20 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698  
F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552  
F-THYRO1000206//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134  
F-THYRO1000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
25 DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157  
F-THYRO1000241//Gallus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186  
F-THYRO1000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156  
F-THYRO1000253//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055  
30 F-THYRO1000270  
F-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664  
F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068  
F-THYRO1000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//  
35 AF036894  
F-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:  
91//L35233  
F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333  
F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//U29091  
40 F-THYRO1000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080  
F-THYRO1000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668  
F-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:  
98//AC006019  
F-THYRO1000394//HS\_2061\_A2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672  
45 F-THYRO1000395//Drosophila melanogaster ring canel protein and ORF2 mRNA, complete cds.//4.3e-15:512:  
59//L08483  
F-THYRO1000401 3.2e-116:504:80//AF051908  
F-THYRO1000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
50 DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308  
F-THYRO1000452//RPCI11-1C19.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1C19, genomic survey sequence.//0.27:132:64//B49573  
F-THYRO1000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//  
AC005229  
55 F-THYRO1000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196  
F-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//6.3e-130:327:97//AC005740  
F-THYRO1000501//H.sapiens Staf50 mRNA.//9.8e-74:615:77//X82200

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F-THYRO1000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence./.0.076:380:59//Z94056  
F-THYRO 1000505  
5 F-THYRO1000558//Human PAC clone 127H14 from 12q, complete sequence./.2.4e-27:412:69//AC002563  
F-THYRO1000569//HS\_2178\_B2\_E03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence./.1.9e-27:326:74//AQ307499  
F-THYRO1000570  
10 F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds./.7.4e-167:808:97//AF075587  
F-THYRO1000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence./.0.99:280:61//U91323  
F-THYRO1000602//HS\_3037\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence./.1.2e-05:109:75//AQ097057  
15 F-THYRO1000605//Homo sapiens map 2p11.2; 83cM from GATA85A06 repeat region, complete sequence./.1.0:84:70//AF067777  
F-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence./.3.4e-174:820:98//AC005546  
20 F-THYRO1000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence./.3.6e-38:289:84//AL024474  
F-THYRO1000641//Plasmodium falciparum MAL3P7, complete sequence./.6.8e-07:540:56//AL034559  
F-THYRO1000658//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence./.1.1e-68:468:84//AC005696  
25 F-THYRO1000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence./.0.0072:141:70//AB016874  
F-THYRO1000666//Mus musculus mRNA for motor domain of KIF9, partial cds./.4.7e-58:367:87//AB001437  
F-THYRO1000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence./.1.2e-36:396:71//AC005778  
30 F-THYRO1000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes./.6.6e-13:236:69//AJ010317  
F-THYRO1000699//RPCI11-50D4.TK RPCI11 Homo sapiens genomic clone R-50D4, genomic survey sequence./.2.7e-09:135:78//AQ052641  
F-THYRO1000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence./.5.2e-17:290:67//AC005053  
35 F-THYRO1000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds./.8.6e-08:517:60//L14320  
F-THYRO1000734//HS\_3233\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D-Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence./.6.0e-72:463:89//AQ182143  
F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds./.9.7e-34:339:74//AB007871  
40 F-THYRO1000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase./.0.00034:349:60//X73523  
F-THYRO1000777//S.griseus strO gene and sts gene cluster./.8.2e-05:625:59//Y08763  
F-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds./.4.0e-70:860:69//U37373  
45 F-THYRO1000787//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366D1, WORKING DRAFT SEQUENCE./.5.3e-09:221:66//Z97986  
F-THYRO1000793  
F-THYRO1000796//Cristatella mucedo clone 5.9 microsatellite sequence./.0.34:173:63//AF085422  
50 F-THYRO1000805//Homo sapiens Xp21 PAC RPCI1-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence./.7.8e-43:677:66//AC004468  
F-THYRO1000815//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence./.5.5e-43:405:77//AC005914  
F-THYRO1000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence./.2.0e-20:159:88//AQ240053  
55 F-THYRO1000843  
F-THYRO1000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence./.1.8e-33:445:72//AC005782  
F-THYRO1000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA, complete cds./.0.038:208:

64//AF008573  
 F-THYRO1000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477  
 5 F-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720  
 F-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015  
 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529  
 10 F-THYRO1000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836  
 F-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229  
 F-THYRO1000952  
 15 F-THYRO1000974//HS\_3238\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//12.4e-26:154:96//AQ219846  
 F-THYRO1000975//Plasmodium falciparum Topoll gene.//0.32:491:58//X79345  
 F-THYRO1000983//Mvwf9A3 exon amplification products from BACs in Mvwf region Mus musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457  
 20 F-THYRO1000984//CIT-HSP-2167O17.TR CIT-HSP Homo sapiens genomic clone 2167O17, genomic survey sequence.//0.00015:186:66//B91313  
 F-THYRO1000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588  
 F-THYRO1001003  
 25 F-THYRO1001031//Homo sapiens chromosome 17, clone hRPC.859\_O\_20, complete sequence.//1.1e-55:543:72//AC003695  
 F-THYRO1001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799  
 F-THYRO1001062//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320  
 30 F-THYRO1001093//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//4.9e-34:353:76//AC006241  
 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end.//1.1e-72:742:74//L14787  
 F-THYRO1001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522  
 35 F-THYRO1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 671O14, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595  
 F-THYRO1001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996  
 F-THYRO1001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486  
 40 F-THYRO1001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178  
 F-THYRO1001173  
 F-THYRO1001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953  
 45 F-THYRO1001189//HS\_3171\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330  
 F-THYRO1001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925  
 F-THYRO1001213//, complete sequence.//1.7e-45:257:84//AC005300  
 50 F-THYRO1001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036  
 F-THYRO1001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496  
 F-THYRO1001287//Drosophila melanogaster cosmid clone 86E4.119.6e-49:586:69//AL021086  
 55 F-THYRO1001290//HS\_2045\_B1\_H09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237  
 F-THYRO1001313//S. lavandulae bla gene for beta-lactamase, complete cds.//1.0:229:64//D12693  
 F-THYRO1001320//Homo sapiens Chromosome 22q11.2 PAC Clone p\_n5 In BCRL2-GGT Region, complete sequence.//1.1e-88:672:82//AC002472

F-THYRO1001321//Human PAC clone DJ527C21 from Xq23, complete sequence./.1.2e-115:740:87//AC000114  
 F-THYRO1001322//HS\_3205\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=24 Row=F, genomic survey sequence./.0.00031:285:61//AQ304025  
 F-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds./.2.2e-43:638:64//AB018288  
 5 F-THYRO1001363//Homo sapiens PAC clone DJ0845I21 from 7q11.21-q11.23, complete sequence./.1.0e-09:189:74//AC004905  
 F-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map-10q25, complete sequence./.7.6e-168:821:97//AC005660  
 10 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds./.2.3e-155:740:97//AB014607  
 F-THYRO1001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence./.3.2e-07:138:73//AC005239  
 15 F-THYRO1001403//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces./.3.6e-70:360:86//AC005845  
 F-THYRO1001405//Bos taurus mRNA for NDP52, complete cds./.2.6e-14:559:63//AB008852  
 20 F-THYRO1001406//Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds./.1.0e-91:631:82//AF064635  
 F-THYRO1001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence./.5.5e-42:509:71//AC006126  
 25 F-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE./.2.7e-31:172:81//AJ002553  
 F-THYRO1001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces./.1.0:98:70//AC000384  
 F-THYRO1001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds./.1.9e-58:653:71//U87265  
 30 F-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces./.7.5e-42:357:80//AC006001  
 F-THYRO1001487//H.sapiens DNA sequence./.0.92:160:64//Z22449  
 F-THYRO1001534//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces./.4.8e-47:266:80//AC004666  
 35 F-THYRO1001537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE./.1.3e-79:479:89//AL031687  
 F-THYRO1001541//Human DNA sequence from clone 399M14 on chromosome Xq26.1-26.3. Contains ESTs, an STS and GSSs, complete sequence./.0.0034:106:77//Z96074  
 F-THYRO1001559//Rattus norvegicus simple sequence repeat D18Mco6./.1.6e-09:351:63//AF006056  
 40 F-THYRO1001570//RPCI11-49B23.TJ RPCI11 Homo sapiens genomic clone R-49B23, genomic survey sequence./.1.4e-65:384:91//AQ052105  
 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA./.8.2e-104:546:95//AF070572  
 F-THYRO1001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence./.1.3e-24:180:88//AQ080498  
 45 F-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE./.8.7e-145:779:93//AL023808  
 F-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.786\_O\_4, complete sequence./.2.9e-26:393:68//AC005863  
 F-THYRO1001605//Dictyostelium discoideum filopodin (talA) gene, complete cds./.0.0012:436:58//U14576  
 50 F-THYRO1001617//Homo sapiens full-length insert cDNA clone ZD69D05./.8.6e-43:342:82//AF086381  
 F-THYRO1001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces./.6.2e-15:318:66//AC004950  
 F-THYRO1001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence./.1.5e-05:147:68//AC004827  
 F-THYRO1001661  
 55 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform./.2.5e-164:780:98//AJ225089  
 F-THYRO1001673//Homo sapiens clone RG161A02, complete sequence./.4.4e-40:770:64//AC005071  
 F-THYRO1001703//S.coelicolor plasmid SCP2 transfer region DNA./.0.14:414:59//X72857  
 F-THYRO1001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, complete sequence./.2.6e-43:308:75//AC004745  
 F-THYRO1001721//, complete sequence./.9.9e-134:770:91//AC005500  
 F-THYRO1001738//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 355C18, WORKING DRAFT SEQUENCE./.0.99:163:61//AL022327

F-THYRO1001745  
 F-THYRO1001746  
 F-THYRO1001772//HS\_3069\_B1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence./.1.5e-61:360:91//AQ171021  
 5 F-THYRO1001793//B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel./.0.028:446:58//X89626  
 F-THYRO 1001809  
 F-THYRO1001828//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 110F11, WORKING DRAFT SEQUENCE./.1.3e-175:841:98//AL033526  
 10 F-THYRO1001854//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence./.7.9e-07:445:59//AC003664  
 F-THYRO1001895  
 4.4e-13:248:68//AB012576  
 F-THYRO1001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence./.2.9e-15:144:77//AC005058  
 15 F-VESEN1000122//HS\_3075\_B1\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence./.1.1e-16:130:90//AQ143749  
 F-Y79AA1000013  
 F-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence./.2.9e-95:300:94//AC006027  
 20 F-Y79AA1000037//Human prot-oncogene (BMI-1) mRNA, complete cds./.2.4e-19:230:66//L13689  
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds./.2.2e-38:629:64//U78521  
 F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on chromosome X contains EST./.5.3e-10:117:83//Z72005  
 F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1./.7.6e-10:381:64//U92893  
 25 F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence./.1.4e-165:732:99//AL031864  
 F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence./.9.1e-20:339:65//AC005115  
 30 F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces./.3.7e-72:397:93//AC004854  
 F-Y79AA1000230  
 F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds./.8.5e-151:833:90//AF053232  
 35 F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SAcP-1) gene, complete cds./.0.0099:547:58//U78522  
 F-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds./.4.0e-11:424:62//AF035207  
 F-Y79AA1000313  
 F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence./.5.9e-07:173:69//B55085  
 40 F-Y79AA1000342//RPCI11-57J6.TK.1 RPCI11 Homo sapiens genomic clone R-57J6, genomic survey sequence./.5.2e-27:151:99//AQ115511  
 F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop./.5.7e-69:694:71//X92987  
 F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein./.1.8e-98:535:92//X84692  
 45 F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces./.1.6e-21:129:85//AC005484  
 F-Y79AA1000368//H.sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpg12f1.rt1c./.0.00016:53:98//Z56610  
 F-Y79AA1000405//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING DRAFT SEQUENCE./.0.069:366:59//AL031747  
 50 F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X./.1.0e-25:235:80//Z86061  
 F-Y79AA1000420//H.sapiens CpG island DNA genomic Mse1 fragment, clone 82c3, forward read cpg82c3.ft1a./.2.0e-36:194:98//Z63378  
 F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds./.8.5e-121:696:89//U41736  
 55 F-Y79AA1000480//HS\_2175\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175 Col=22 Row=O, genomic survey sequence./.2.5e-26:178:89//AQ307693  
 F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces./.0.67:111:72//AC004980

F-Y79AA1000539//HS\_2237\_B2\_F10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey sequence.//1.2e-14:168:77//AQ153503  
 F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.94:127:67//AC005193  
 5 F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//1.7e-114:776:84//X14972  
 F-Y79AA1000574//M.musculus tex23 mRNA (5'region).//1.8e-23:291:75//X80424  
 F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//8.6e-153:755:97//AF091080  
 F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//5.2e-135:644:98//AF060503  
 F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//6.9e-148:902:86//X69942  
 10 F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds.//4.8e-180:850:98//AB018080  
 F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5.//0.00019:308:60//U23172  
 F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein.//1.7e-40:513:68//AJ003023  
 15 F-Y79AA1000774  
 F-Y79AA1000782  
 F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//3.5e-177:847:97//AF098799  
 F-Y79AA1000794//H.sapiens CpG island DNA genomic Mse1 fragment, clone 45a4, forward read cpg45a4.ft1a.//2.5e-13:104:92//Z61120  
 F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds.//0.98:244:60//AF056085  
 20 F-Y79AA1000802  
 F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//9.3e-76:528:85//U73642  
 F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence.//4.4e-14:99:95//B84538  
 F-Y79AA1000827//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING  
 25 DRAFT SEQUENCE.//1.5e-08:249:69//AL022315  
 F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin.//1.8e-103:603:89//X04757  
 F-Y79AA1000850  
 F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//0.038:468:59//Z82203  
 30 F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.7e-150:865:89//AF071314  
 F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//6.4e-122:717:88//U38253  
 F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence.//1.0:155:63//AC002397  
 35 F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1.//4.3e-06:130:73//U88165  
 F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//2.4e-44:428:77//U05823  
 F-Y79AA1001023  
 F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds.//2.3e-13:90:100//U63329  
 40 F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds.//2.6e-28:772:60//D43682  
 F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence.//9.4e-36:292:82//AC004701  
 F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt].//0.17:537:59//  
 45 S64314  
 F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cds.//0.17:231:64//D88452  
 F-Y79AA1001078  
 F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds.//3.1e-63:529:77//D26173  
 F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.3e-  
 50 23:228:76//AC005015  
 F-Y79AA1001167  
 F-Y79AA1001177//M.musculus mRNA for NfiX1-protein.//4.0e-10:398:64//Y07688  
 F-Y79AA1001185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING  
 DRAFT SEQUENCE.//1.1e-113:666:90//Z93015  
 55 F-Y79AA1001211//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//5.5e-12:87:96//AQ187492  
 F-Y79AA1001216  
 F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//0.028:188:67//

AL021841  
 F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds./.3.5e-24:731:  
 60//M36263

5 F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and  
 IMAGE 45355 and LLNLc110133Q7 (RZPD Berlin)).//1.2e-133:441:97//AJ005892

F-Y79AA1001281//HS\_2241\_B2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2241 Col=18 Row=L, genomic survey sequence./.5.0e-27:169:94//AQ217497

F-Y79AA1001299//Human Ini1 mRNA, complete cds./.6.7e-115:323:93//U04847

10 F-Y79AA1001312  
 F-Y79AA1001323  
 F-Y79AA1001384  
 F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds./.5.8e-42:245:74//  
 U59322

15 F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence./.7.8e-18:636:58//Z48583  
 F-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library)  
 complete sequence./.1.2e-110:738:85//AC005924

F-Y79AA1001493//H.sapiens DNA sequence./.2.0e-27:254:82//Z22497  
 F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,  
 complete sequence./.1.1e-158:804:95//AL034430

20 F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds./.1.7e-100:820:  
 78//D14336

F-Y79AA1001541//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3197 Col=22 Row=M, genomic survey sequence./.5.1e-28:218:86//AQ150183

25 F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complete sequence./.5.4e-21:167:86//  
 AC004151

F-Y79AA1001555//R.norvegicus mRNA for drebrin A./.0.88:463:59//X59267  
 F-Y79AA1001581//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//0.00051:252:  
 65//S74494

30 F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds./.7.2e-33:375:  
 76//M26434

F-Y79AA1001594  
 F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and  
 CHD5 genes, complete cds, complete sequence./.4.2e-06:338:66//AF064861

35 F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds./.0.024:520:57//AB014583  
 F-Y79AA1001647//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4, WORK-  
 ING DRAFT SEQUENCE./.0.014:331:61//Z92860

F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence./.0.99:  
 273:63//Z84468

40 F-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds./.1.2e-97:682:81//M22743  
 F-Y79AA1001692//insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of  
 4].//5.6e-05:426:59//S37712

F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyprotein (containing putative helicase and  
 putative RNA-dependent RNA polymerase domains), complete cds./.1.0:437:60//D32136

45 F-Y79AA1001705//M.musculus fkh-5 gene./.0.18:153:64//X71943  
 F-Y79AA1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING  
 DRAFT SEQUENCE./.5.4e-76:191:98//AL022240

F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15,  
 WORKING DRAFT SEQUENCE./.0.99:227:63//AP000017

50 F-Y79AA1001805//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read  
 cpg13d12.rt1c./.2.6e-13:88:100//Z64565  
 F-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds./.3.7e-130:775:88//U74297

F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey se-  
 quence./.8.3e-17:218:76//AQ012369

55 F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds./.4.2e-10:378:62//AB002388  
 F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds./.6.9e-41:441:71//  
 U41164

F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, com-  
 plete cds./.0.00017:412:62//AF029779

F-Y79AA1001875//CTT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence./1.9e-09:271:67//AQ042654  
 F-Y79AA1001923//H.sapiens CpG island DNA genomic Mse1 fragment, clone 193c12, forward read cpg193c12.ft1a./0.0031:108:75//Z60186  
 5 F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence./1.8e-05:56:100//AQ261184  
 F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds./3.3e-13:451:62//AF028340  
 10 F-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 526I14, WORKING DRAFT SEQUENCE./0.91:134:65//Z82214  
 F-Y79AA1002089  
 F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds./1.2e-112:678:88//U43548  
 15 F-Y79AA1002103//HS\_3052\_B1\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence./6.5e-18:238:72//AQ135014  
 F-Y79AA1002115  
 F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat./1.5e-14:99:96//X61693  
 F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds./2.5e-07:208:64//U19358  
 20 F-Y79AA1002204//HS\_2235\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence./2.9e-13:89:98//AQ154260  
 F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence./3.7e-27:154:98//B56397  
 F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase./2.8e-05:143:70//J01719  
 25 F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence./8.3e-22:229:78//AC005615  
 F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence./1.0e-06:241:67//AC003043  
 30 F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence./1.3e-68:375:95//AQ109738  
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds./0.12:203:63//D42045  
 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds./1.3e-174:821:98//AB014592  
 F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces./0.50:  
 45 470:60//AC005015  
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds./6.8e-159:748:98//AB014555  
 F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds./0.036:278:62//U10886  
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds./6.4e-129:622:97//AB014534  
 F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein./2.0e-116:693:82//X67877  
 F-Y79AA1002351//S.clavuligerus pah and cas genes./1.0:369:58//X84101  
 40 F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit)./5.4e-105:762:80//Y18208  
 F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence./1.0e-159:411:  
 100//AC005920  
 F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence./1.1e-118:609:  
 84//AC004662  
 45 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds./4.4e-90:529:88//  
 U49385  
 F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds./1.0:166:66//U36196  
 F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence./0.24:85:72//B51917  
 50 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence./1.9e-13:242:69//AC006116  
 F-Y79AA1002482//Homo sapiens full-length insert cDNA clone ZC18H06./1.2e-35:462:71//AF088022  
 F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

## 55 Homology Search Result Data 3.

- [0303] The result of the homology search of the GenBank using the clone sequence of 3'-end except EST and STS.  
 [0304] Data include

the name of clone,  
 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

5

[0305] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0306] Data are not shown for the clones in which the P-value was higher than 1.

- 10 R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953  
 R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//  
 Z88864  
 R-HEMBA1000042//RPCI11-77G23.TV RPCI11 Homo sapiens genomic clone R-77G23, genomic survey se-  
 quence.//1.3e-56:292:97//AQ268240  
 R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//U82696  
 15 R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948  
 R-HEMBA1000076//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-  
 41:364:79//AC005520  
 R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete  
 sequence.//4.7e-30:229:84//AC003684  
 20 R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//2.4e-93:503:93//  
 AC003104  
 R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340  
 R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-  
 37:289:83//AC005060  
 25 R-nnnnnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//  
 L43631  
 R-HEMBA1000158  
 R-nnnnnnnnnnnnn  
 R-HEMBA1000180//Plasmodium falciparum encoding Pfg27/25.//0.073:292:56//X84904  
 30 R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//  
 5.3e-40:286:85//AC006146  
 R-HEMBA1000193  
 R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126  
 R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655  
 35 R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:  
 79//AF001548  
 R-nnnnnnnnnnnnn  
 R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate  
 receptor, CpG island, CA repeat.//4.3e-24:400:68//AL009181  
 40 R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:  
 319:69//AC004526  
 R-HEMBA1000244  
 R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ri-  
 bosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262  
 45 R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15,  
 WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012  
 R-nnnnnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete  
 sequence.//3.5e-10:238:70//AC003037  
 R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF007270  
 50 R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:  
 267:82//AC003046  
 R-HEMBA1000290//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//  
 AC004223  
 R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey se-  
 quence.//1.0:215:61//B95105  
 R-nnnnnnnnnnnnnn//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131  
 R-nnnnnnnnnnnnnn//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:  
 546:90//U16802

R-HEMBA1000307//*Mus musculus* mRNA for CDV-1 protein./.3.8e-36:315:68//Y10496  
R-nnnnnnnnnnnn//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
DRAFT SEQUENCE, 8 unordered pieces./.0.078:379:59//AC005505  
R-HEMBA1000338//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING  
5 DRAFT SEQUENCE./.2.0e-33:399:72//AL031667  
R-HEMBA1000351//*Homo sapiens* complete genomic sequence between D16S3070 and D16S3275, containing  
Familial Mediterranean Fever gene disease./.1.7e-39:272:87//AJ003147  
R-HEMBA1000355//Human primary Alu transcript./.0.0045:67:85//U67829  
R-HEMBA1000357//*Homo sapiens* (subclone 9\_h8 from PI H16) DNA sequence./.8.7e-93:426:88//L42086  
10 R-HEMBA1000366//*Homo sapiens* PAC clone DJ0942I16 from 7q11, complete sequence./.1.7e-12:130:83//  
AC006012  
R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene sim-  
ilar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS  
15 and a CpG island, complete sequence./.1.9e-69:355:97//AL031587  
R-HEMBA1000376//*Homo sapiens* chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence./.3.7e-  
66:410:89//AC006116  
R-HEMBA1000387//*Homo sapiens* chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 un-  
ordered pieces./.2.0e-43:363:81//AC002993  
20 R-HEMBA1000390//*Homo sapiens* BAC clone RG041D11 from 7q21, complete sequence./.4.6e-23:417:69//  
AC005053  
R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence./.6.2e-05:174:68//  
AC004582  
R-HEMBA1000396//*Homo sapiens* DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains  
inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein./.1.4e-62:564:77//AL022575  
25 R-HEMBA1000411  
R-HEMBA1000418//Liverwort *Marchantia polymorpha* chloroplast genome DNA./.0.94:210:60//X04465  
R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP *Homo sapiens* genomic clone 2382A6, genomic survey se-  
quence./.4.4e-12:98:92//AQ078233  
R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs,  
30 complete sequence./.2.0e-93 :526:90//Z95400  
R-HEMBA1000434//*Homo sapiens* clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces./.  
2.7e-07:452:60//AC004826  
R-HEMBA1000442//*E.caballus* microsatellite DNA, clone HMB4./.0.39:135:62//Y07733  
R-HEMBA1000456//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, com-  
35 plete sequence./.2.6e-05:174:70//AL010226  
R-HEMBA1000459//*Arabidopsis thaliana* putative transmembrane protein G1p (AtG1), putative nuclear DNA-bind-  
ing protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane  
protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, com-  
plete cds; and unknown genes./.0.013:212:63//AF049236  
40 R-HEMBA1000460//*Homo sapiens* PAC clone DJ0593H12 from 7p31, complete sequence./.8.6e-114:556:98//  
AC004839  
R-HEMBA1000464//*Caenorhabditis elegans* cosmid C34B7, complete sequence./.0.086:334:61//Z83220  
R-HEMBA1000469//*Homō sapiens* BAC clone RG442F18 from 2, complete sequence./.1.8e-52:472:79//  
AC005104  
45 R-HEMBA1000488//, complete sequence./.3.3e-68:200:99//AC005500  
R-HEMBA1000490//*Caenorhabditis elegans* cosmid Y53C12B, complete sequence./.0.97:233:61//Z99278  
R-HEMBA1000491  
R-HEMBA1000504//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, com-  
50 plete sequence./.1.7e-08:440:60//AL009014  
R-HEMBA1000505//*Homo sapiens* genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
non-small cell lung cancer, segment 1/11./.0.37:189:62//AB020858  
R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chro-  
mosome X./.1.1e-25:248:80//Z70280  
55 R-HEMBA1000518//RPCI11-6022.TV RPCI-11 *Homo sapiens* genomic clone RPCI-11-6022, genomic survey se-  
quence./.0.0035:293:61//B49544  
R-HEMBA1000519  
R-HEMBA1000520//*Arabidopsis thaliana* chromosome II BAC F10A12 genomic sequence, complete sequence./.  
0.30:255:63//AC006232

R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds./.1.2e-53:203:92//U15782

R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence./.2.7e-24:137:99//B55638

5 R-HEMBA1000540//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE./.0.00014:329:60//Z98044

R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence./.6.9e-87:552:87//AC004103

10 R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE./.8.9e-121:584:98//AL034555

R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence./.5.7e-45:307:87//AC004381

R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence./.1.3e-43:279:90//AF046762

15 R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence./.3.8e-05:506:56//AE001368

R-HEMBA1000568//RPCI11-49P8.TK.1 RPCI11 Homo sapiens genomic clone R-49P8, genomic survey sequence./.1.7e-101:498:97//AQ116293

R-nnnnnnnnnnnn

20 R-HEMBA1000575//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 754E20, WORKING DRAFT SEQUENCE./.1.3e-47:458:75//AL022335

R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds./.2.9e-62:447:81//AF045573

R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein./.1.2e-111:591:9411AJ007509

25 R-HEMBA1000592//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence./.3.5e-09:421:60//AL010216

R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE, 5 unordered pieces./.1.1e-15:421:66//AC005044

30 R-HEMBA1000604//HS\_2220\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence./.1.0e-51:306:92//AQ151991

R-HEMBA1000608

R-HEMBA1000622//H.sapiens CpG island DNA genomic Mse1 fragment, clone 155e4, reverse read cpg155e4.rt1a./.4.5e-16:105:98//Z56962

R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE./.4.8e-62:421:86//AP000008

35 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds./.1.2e-97:443:97//AB014590

R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete sequence./.9.8e-61:311:90//AC005953

R-HEMBA1000657

R-HEMBA1000662

40 R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS./.1.0e-13:351:63//Z97196

R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces./.1.2e-50:298:79//AC005377

45 R-HEMBA1000686//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence./.0.00048:210:62//AQ093513

R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces./.9.7e-54:317:88//AC005000

R-HEMBA1000705//Glossonotus uhivittatus 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence./.0.080:138:65//U77850

50 R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds./.0.96:291:58//D50864

R-HEMBA1000722

R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from 7q33-q36, complete sequence./.4.4e-26:284:77//AC005531

55 R-HEMBA1000727//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence./.9.1e-05:351:60//AL010266

R-HEMBA1000747//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence./.2.5e-16:123:93//AL021326

R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence./2.8e-32:298:  
79//AC003108

R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE  
LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.  
Contains polymorphic CA repeat./2.8e-90:542:90//Z92545

R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence./2.7e-36:405:75//  
AC005031

R-HEMBA1000773//HS\_3050\_A2\_B08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3050 Col=16 Row=C, genomic survey sequence./0.00053:268:60//AQ105619

R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence./4.7e-46:338:85//  
AC004690

R-HEMBA1000791//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence./5.3e-47:279:91//U14571

R-HEMBA10008177//Sequence 1 from Patent WO 8904839./0.86:148:67//I09339

R-HEMBA1000822//T.brucei kinetoplast maxicircle variable region DNA./0.00061:246:61//Z15118

R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds./6.9e-  
43:228:98//AF048977

R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the  
TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase  
Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a  
probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted  
CpG island, ESTs, STSs and GSSs, complete sequence./1.7e-41:319:84//AL022394

R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence./  
0.40:168:67//AC004260

R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC  
Library) containing Arylsulfatase D and E genes, complete sequence./1.5e-112:572:96//AC005295

R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces./  
0.11:121:71//AC004938

R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SE-  
QUENCE, 5 unordered pieces./3.2e-22:186:76//AC002042

R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence./0.0060:283:63//  
AC002528

R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements./3.8e-05:269:61//M98801

R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPCI1-96H19, WORKING DRAFT SEQUENCE,  
66 unordered pieces./6.5e-38:327:77//AC006057

R-HEMBA1000908//CIT-HSP-2373I4.TR CIT-HSP Homo sapiens genomic clone 2373I4, genomic survey se-  
quence./5.0e-34:221:90//AQ108658

R-HEMBA1000910//T.pigmentosa UM1060 macronuclear rDNA telomeric region 3' term./0.19:280:61//X04205

R-HEMBA1000918//RPCI11-68E14.TK RPCI11 Homo sapiens genomic clone R-68E14, genomic survey se-  
quence./1.3e-32:172:100//AQ267293

R-HEMBA1000919

R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a  
Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP  
pseudogene. Contains ESTs, STSs and GSSs, complete sequence./2.6e-18:284:71//AL021997

R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE, 15 unordered pieces./  
1.4e-17:217:76//AC005098

R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence./9.0e-113:586:  
95//AC005324

R-HEMBA1000946//T5N8TFB TAMU Arabidopsis thaliana genomic clone T5N8, genomic survey sequence./  
0.030:369:59//B26224

R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces./  
2.5e-52:494:77//AC005096

R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class  
II DC-alpha (HLA-DCA) genes, complete cds./3.5e-77:568:83//U92032

R-HEMBA1000971//RPCI11-54D1.TJ RPCI11 Homo sapiens genomic clone R-54D1, genomic survey sequence./  
2.3e-27:153:98//AQ081552

R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete  
sequence./7.3e-43:375:79//AL023876

R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence./2.8e-104:521:97//AC004817

R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence./.8.0e-22:352:68//AL031311  
R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence./.8.5e-05:306:63//AC004888  
5 R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces./.5.7e-37:296:83//AC005632  
R-HEMBA1000991//RPCI11-22017.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22017, genomic survey sequence./.6.5e-44:162:90//AQ008952  
R-HEMBA1001007  
10 R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence./.0.082:313:60//AC005365  
R-HEMBA1001009//O.sativa osr40g2 gene./.0.99:203:62//Y08987  
R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds./.1.0e-113:587:95//AB007937  
15 R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds./.7.4e-24:215:82//L26547  
R-HEMBA1001020//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE./.2.8e-18:449:64//AL008722  
R-HEMBA1001022  
20 R-HEMBA1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence./.6.6e-48:536:74//AF070717  
R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence./.0.013:180:66//B97363  
R-nnnnnnnnnnnn//Caenorhabditis elegans cosmid R10H10, complete sequence./.1.2e-25:438:65//Z70686  
25 R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence./.7.3e-38:188:89//AC004217  
R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region./.2.4e-24:279:74//X04751  
R-HEMBA1001060//HS\_2056\_B1\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence./.4.1e-14:137:83//AQ245004  
R-HEMBA1001071//M.musculus COL3A1 gene for collagen alpha-I./.6.9e-38:513:70//X52046  
30 R-HEMBA1001077//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE./.1.9e-22:507:61//AL022318  
R-HEMBA1001080  
R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces./.2.2e-43:317:83//AC004586  
35 R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7./.0.46:301:60//AF067607  
R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence./.5.3e-98:501:96//AC005105  
R-HEMBA1001099  
R-HEMBA1001109//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE./.3.1e-39:335:80//AL033527  
40 R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2./.9.8e-11:122:81//U81833  
R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence./.0.0024:284:63//Z98551  
R-HEMBA1001123//Human NFE genomic fragment./.3.6e-26:318:72//M98511  
R-HEMBA1001133  
R-HEMBA1001137//Homo sapiens full-length insert cDNA clone ZD29F04./.4.2e-88:426:98//AF086241  
45 R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces./.4.0e-41:304:84//AC005077  
R-HEMBA1001172//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE./.3.7e-36:261:85//Z98304  
R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence./.1.0:219:  
50 58//AE001398  
R-HEMBA1001197  
R-HEMBA1001208//HS\_2233\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence./.0.083:174:68//AQ170789  
R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces./.5.1e-59:553:75//AC005377  
55 R-HEMBA1001235//RPCI11-50E6.TJ RPCI11 Homo sapiens genomic clone R-50E6, genomic survey sequence./.2.6e-08:97:76//AQ052666  
R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1./.2.4e-05:319:63//U58761

R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.//1.5e-24:439:66//U89905  
 R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//9.9e-21:537:63//AC004491  
 5 R-nnnnnnnnnnnn//Homo sapiens chromosome 17, clone HCIT75G16, complete sequence.//0.022:169:65//AC003042  
 R-HEMBA1001286  
 R-HEMBA1001289  
 10 R-HEMBA1001294//HS\_3219\_A2\_G01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence.//0.24:251:63//AQ189882  
 R-HEMBA1001299//Homo sapiens, clone hRPK.12\_A\_1, complete sequence.//1.3e-38:381:76//AC006222  
 R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//4.1e-28:114:92//E12258  
 15 R-HEMBA1001303//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00011:382:58//AL031744  
 R-HEMBA1001310  
 R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-09:491:58//AC005504  
 20 R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule.//8.3e-06:485:60//X03240  
 R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//2.2e-14:277:69//AL021368  
 25 R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.15:360:6I//AL024509  
 R-HEMBA1001330//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216  
 30 R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//7.1e-45:252:94//AC006238  
 R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//1.4e-113:569:97//AC006241  
 R-HEMBA1001375//Homo sapiens full-length insert cDNA clone ZE09H03.//2.8e-89:428:99//AF086542  
 35 R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865  
 R-HEMBA1001383  
 R-HEMBA1001387  
 R-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//8.9e-06:108:83//AC005073  
 40 R-HEMBA1001391//Yeast mitochondrial aapl gene for ATPase subunit 8.//7.3e-08:500:59//X00960  
 R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050  
 R-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//5.5e-35 :464:68//AL034380  
 45 R-HEMBA1001407  
 R-HEMBA1001411//Yeast (*S.cerevisiae*) mitochondria Ser-tRNA-UCN gene and flanks.//0.00029:301:62//K01981  
 R-HEMBA1001413  
 R-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732  
 50 R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.3e-37:302:81//AC006146  
 R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of *S.cerevisiae*, DNA binding protein similar to URE-B1, ESTs and STS.//1.9e-32:242:79//Z97054  
 55 R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//5.7e-59:457:82//AC004527  
 R-HEMBA1001442//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//0.051:276:63//Z98950

R-HEMBA1001446//HS\_3207\_A1\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence./.8.9e-06:119:73//AQ175385  
R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence./.0.0043:266:63//AC005065  
5 R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete sequence./.7.1e-25:210:82//AC004855  
R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence./.2.7e-08:316:62//AC005324  
10 R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence./.0.57:219:60//AC005208  
R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces./.9.3e-50:252:80//AC004840  
R-HEMBA1001478  
R-HEMBA1001497  
15 R-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence./.3.5e-41:282:86//U89337  
R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS./.1.9e-79:529:86//Z98753  
R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence./.4.3e-18:335:71//  
20 AC004549  
R-HEMBA1001522  
R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands./.5.6e-08:265:67//Z98258  
R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-13.1. Contains adenosine deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS./.7.8e-16:235:72//Z97053  
25 R-HEMBA1001557  
R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence./.2.2e-44:416:78//AC004383  
R-HEMBA1001569//Sequence 15 from patent US 5693476./.1.8e-59:389:88//I77040  
R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence./.1.e-44:316:87//  
30 AC004453  
R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces./.0.0047:437:60//AC005506  
R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B).//2.3e-07:491:58//X95276  
R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6./.0.68:224:62//U41012  
35 R-HEMBA1001589  
R-HEMBA1001595//CIT-HSP-2349G19.TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence./.8.0e-69:337:99//AQ060483  
R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence./.9.5e-59:514:78//AC005177  
40 R-HEMBA1001620//S.polyyrrhiza mRNA for D-myo-inositol-3-phosphate synthase./.4.5e-12:289:65//Z11693  
R-nnnnnnnnnnnn//HS\_2195\_A1\_E09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence./.5.8e-09:358:58//AQ292688  
R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds./.0.77:225:59//U04270  
45 R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and GS2 like genes, ESTs and an STS./.6.0e-49:404:79//Z84484  
R-nnnnnnnnnnnn  
R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence./.1.1e-103:532:95//AC005368  
50 R-HEMBA1001658//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE./.1.0:197:64//AL023808  
R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence./.1.5e-100:457:93//AC005740  
R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds./.1.2e-90:  
55 496:91//AF072247  
R-HEMBA1001675  
R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds./.1.3e-101:534:  
94//AF038962

R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124:68//AQ056593  
 R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801  
 5 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds.//1.9e-96:483:96//AB014598  
 R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:100//D16886  
 R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence.//0.0025:200:65/B32577  
 10 R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//6.6e-27:316:75//U12250  
 R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//3.1e-41:167:87//B89781  
 R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//0.53:275:61//AF018261  
 15 R-HEMBA1001731//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799  
 R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959  
 20 R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067  
 R-HEMBA1001745//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//0.00019:312:59//AC005084  
 25 R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC004153  
 R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//3.8e-39:331:80//AC006121  
 R-HEMBA1001781//Homo sapiens Xp22 BAC GS HB-590J6 (Genome Systems Human BAC library) complete sequence.//0.0062:245:60//AC004554  
 30 R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.1e-22:370:63//AC005740  
 R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-50:408:80//AL023575  
 35 R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//9.0e-37:335:77//AQ009222  
 R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.86:536:56//AC005506  
 R-nnnnnnnnnnnnnn//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//2.9e-93:553:89//M21977  
 40 R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//2.8e-112:548:98//AB007969  
 R-HEMBA1001809  
 R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//2.6e-48:363:84//AC004025  
 45 R-HEMBA1001819//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//1.1e-15:275:68//AJ009612  
 R-HEMBA1001820//HS\_3022\_B1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey sequence.//0.00054:335:59//AQ165107  
 R-nnnnnnnnnnnnnn//Xenopus laevis intersectin mRNA, complete cds.//1.4e-19:533:63//AF032118  
 50 R-HEMBA1001824//S.clavuligerus linear plasmid pSCL (complete sequence).//0.62:189:65//X54107  
 R-HEMBA1001835//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//1.0:450:60//AL024507  
 R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds.//1.6e-07:170:68//U50871  
 R-HEMBA1001847  
 R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//3.3e-108:553:96//AB014517  
 55 R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463  
 R-HEMBA1001866//HS\_2258\_B2\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence.//2.8e-39:397:75//AQ221138

R-nnnnnnnnnnnn//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence./.5.9e-56:303:94//  
AC005065  
R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-  
plete sequence./.1.7e-43:281:88//AC006210  
5 R-HEMBA1001896  
R-HEMBA1001910  
R-HEMBA1001912//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence./.0.10:307:  
61//AC004775  
R-HEMBA1001913  
10 R-HEMBA1001915//HS\_2037\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2037 Col=23 Row=I, genomic survey sequence./.0.071:206:64//AQ233106  
R-HEMBA1001918//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence./.0.97:449:  
59//AC004775  
R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds./.2.0e-105:  
15 534:96//AF000145  
R-HEMBA1001939//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING  
DRAFT SEQUENCE./.4.6e-13:120:82//AL021707  
R-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces./.2.2e-  
36:301:81//AC005629  
20 R-HEMBA1001942//Human PAC clone DJ0205E24 from Xq23, complete sequence./.1.9e-10:208:68//AC003013  
R-HEMBA1001945//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence./.1.2e-06:  
393:60//AE001433  
R-HEMBA1001950//R.prowazekii genomic DNA fragment (clone A437R).//.0.33:122:66//Z82646  
R-HEMBA1001960//Borrelia afzelii VS461 outer surface protein D (ospD) gene, complete cds./.0.0086:427:59//  
25 U05329  
R-HEMBA1001962//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence./.4.5e-07:176:  
70//AC004069  
R-HEMBA1001964//HS\_2215\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2215 Col=1 Row=P, genomic survey sequence./.7.3e-25:215:74//AQ151931  
30 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/  
Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains  
a putative CpG island, ESTs and GSSs, complete sequence./.1.7e-51:209:95//AL031178  
R-HEMBA1001979//CIT-HSP-2387112.TF.1 CIT-HSP Homo sapiens genomic clone 2387112, genomic survey se-  
quence./.4.9e-06:153:71//AQ240461  
35 R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an  
STS and GSSs, complete sequence./.3.1e-46:437:77//AL033521  
R-HEMBA1001991//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like  
gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat./.1.1e-48:446:78//AL020997  
R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta).//.5.1e-90:448:97//AJ005801  
40 R-HEMBA1002008//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs  
and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence./.3.2e-42:317:84//Z97181  
R-HEMBA1002018//HS\_3006\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3006 Col=19 Row=H, genomic survey sequence./.1.0:63:74//AQ089717  
R-HEMBA1002022//Homo sapiens chromosome 18, clone hRPK.453\_M\_1, complete sequence./.0.93:339:59//  
45 AC006203  
R-HEMBA1002035//Mus musculus chromosome 19, clone CIT282B21, complete sequence./.1.4e-11:285:67//  
AC003694  
R-HEMBA1002039  
R-HEMBA1002049//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING  
50 DRAFT SEQUENCE./.5.3e-52:266:84//AL022315  
R-HEMBA1002084//CIT-HSP-2357L11.TR CIT-HSP Homo sapiens genomic clone 2357L11, genomic survey se-  
quence./.0.0013:185:66//AQ063078  
R-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds./.2.7e-70:  
479:86//U92703  
55 R-HEMBA1002100//Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds./.8.5e-32:206:91//  
L40357  
R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence./.4.3e-42:  
302:85//AC005800

R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence./.1.6e-64:550:80//U47924  
R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence./.1.2e-92:435:92//AC000378  
R-HEMBA1002125  
R-HEMBA1002139//Human nebulin mRNA, partial cds./.0.056:68:88//U35637  
5 R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 containing tryptophan hydroxylase gene, complete sequence./.2.0e-26:323:70//AC005728  
R-HEMBA1002150//Human DNA sequence from clone 742C19 on chromosome 22q12.3-13.1. Contains a pseudogene similar to Cytochrome C Oxidase Polypeptide VB and (parts of) up to four novel genes, two with homology to Phorbol genes and one a novel Chromobox protein gene. Contains ESTs, an STS, GSSs and putative CpG islands, complete sequence./.1.0:371:61//AL031846  
10 R-HEMBA1002151  
R-HEMBA1002153//Human BAC 367D17 from chromosome 18, complete sequence./.2.4e-21:322:70//AC003971  
R-HEMBA1002160//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of *S.cerevisiae*, DNA binding protein similar to URE-B1, ESTs and STS./.2.5e-38:216:84//Z97054  
15 R-HEMBA1002161//CIT-HSP-2163F10.TF CIT-HSP Homo sapiens genomic clone 2163F10, genomic survey sequence./.3.1e-58:284:80//B89969  
R-HEMBA1002162//*Caenorhabditis elegans* cosmid F48C11, complete sequence./.0.0079:286:57//Z80789  
R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence./.5.9e-20  
53:326:80//AC002980  
R-HEMBA1002177  
R-HEMBA1002185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745I14, WORKING DRAFT SEQUENCE./.9.5e-37:356:76//AL033532  
R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence./.3.4e-43:244:77//AC003684  
25 R-HEMBA1002191//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces./.4.3e-37:323:78//AC005077  
R-HEMBA1002199//Human Cosmid g5129g124 from 7q31.3, complete sequence./.1.4e-89:564:87//AC002498  
R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence./.1.5e-31:313:71//AC000053  
30 R-HEMBA1002212//*K.lactis* mitochondrial COX1 and A8 genes for cytochrome oxidase subunit I and ATPase subunit 8./.0.0023:346:60//X57546  
R-HEMBA1002215//*M.musculus* mRNA for testin./.4.7e-61:414:84//X78989  
R-HEMBA1002226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE./.4.6e-46:375:77//AL033529  
35 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds./.4.6e-46:238:98//AF089814  
R-HEMBA1002237//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence./.4.3e-26:469:67//AC004242  
40 R-HEMBA1002253//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence./.5.1e-23:162:82//AC005016  
R-HEMBA1002257  
R-HEMBA1002267//*Equus caballus* dermatan sulfate proteoglycan II mRNA, complete cds./.4.6e-44:300:88//AF03 8127  
45 R-HEMBA1002270//Human BAC clone RG067M09 from 7q21-7q22, complete sequence./.1.9e-19:176:85//AC000057  
R-HEMBA1002328//HS\_3061\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=11 Row=G, genomic survey sequence./.1.0:151:65//AQ127617  
50 R-HEMBA1002337//*Saccharomyces cerevisiae* RNA polymerase II holoenzyme component (SRB7) gene, complete cds./.3.7e-07:328:63//U23811  
R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds./.2.4e-128:642:96//AB018314  
R-HEMBA1002348//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence./.3.7e-07:587:58//AL031256  
55 R-HEMBA1002349//*Leishmania tarentolae* maxicircle DNA fragment./.0.018:341:58//X02438  
R-nnnnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds./.1.2e-121:661:93//AF092563  
R-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and

non-small cell lung cancer , segment 11/11.//1.1e-70:559:79//AB020868  
 R-HEMBA1002389//HS\_3218\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=J, genomic survey sequence.//0.0011:122:72//AQ213602  
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//4.2e-81:232:97//  
 5 AC005954  
 R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.50:231:64//  
 AC004848  
 R-HEMBA1002430//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0023:604:56//X95276  
 R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-  
 10 23:183:80//AC006026  
 R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimulation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN. pseudogene similar to hnRNP A1 protein and ESTs, complete sequence.//7.7e-32:161:83//Z83819  
 R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//2.6e-100:305:100//AC005378  
 15 R-HEMBA1002462//Sequence 43 from patent US 5708157.//2.0e-10:131:77//I80068  
 R-nnnnnnnnnnnnn  
 R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.//6.6e-33:279:  
 80//AC004841  
 R-HEMBA1002486//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.//2.1e-50:290:92//U14573  
 20 R-HEMBA1002495//CITBI-E1-2515J10.TR CITBI-E1 Homo sapiens genomic clone 2515J10, genomic survey sequence.//1.0:122:68//AQ261762  
 R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//  
 2.8e-22:210:78//AC004963  
 R-HEMBA1002503//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//2.7e-17:435:58//  
 25 AC003043  
 R-HEMBA1002508//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.7e-09:408:61//AC006213  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//7.1e-112:456:92//AJ011972  
 R-HEMBA1002515  
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds.//1.6e-104:564:93//AB007923  
 30 R-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//2.8e-25:186:86//AQ188792  
 R-HEMBA1002547//Mus musculus agrin gene, exon 36.//0.0095:93:75//M92658  
 R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-49:308:90//AC005378  
 R-HEMBA1002555//Homo sapiens full-length insert cDNA clone YR87G10.//8.3e-65:318:99//AF085957  
 35 R-HEMBA1002558//, complete sequence.//2.3e-38:264:89//AC005409  
 R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.1e-44:192:80//AL008634  
 R-nnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//4.5e-119:587:97//AF075587  
 R-HEMBA1002583  
 40 R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-42:248:88//Z95152  
 R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//2.6e-56:302:84//  
 45 AC004510  
 R-HEMBA1002621  
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//6.7e-76:380:97//AB018351  
 R-HEMBA1002628//P.falciparum complete gene map of plastid-like DNA (IR-A).//8.8e-05:327:60//X95275  
 50 R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence.//4.3e-06:205:66//AF046247  
 R-HEMBA1002645//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.1e-39:281:84//U14567  
 R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//1.1e-104:500:95//  
 AC004839  
 R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.2e-61:280:92//AL022323  
 55 R-HEMBA1002661//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 225E12, WORKING DRAFT SEQUENCE.//3.2e-41:325:81//AL031772  
 R-HEMBA1002666//Homo sapiens full-length insert cDNA clone YY74A07.//0.00037:79:84//AF088008  
 R-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORK-

ING DRAFT SEQUENCE.//2.3e-107:561:94//AL034421  
R-nnnnnnnnnnnn//CIT-HSP-2287E8.TF CIT-HSP Homo sapiens genomic clone 2287E8, genomic survey sequence.//5.4e-17:137:88//B99281  
R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 1354A7 (LBNL H47), complete sequence.//0.033:  
5 146:70//AC004503  
R-HEMBA1002696  
R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//6.2e-44:302:87//AC003982  
R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds.//1.1e-31:332:76//AB004873  
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds.//1.2e-35:287:81//AB014521  
10 R-HEMBA1002730//D.discoideum actin M6 gene, 5' flank.//0.018:233:66//M29109  
R-HEMBA1002742//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING  
DRAFT SEQUENCE.//2.6e-13:419:62//AL033525  
R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//0.019:202:65//  
AC003694  
15 R-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING  
DRAFT SEQUENCE.//0.046:263:60//AL023883  
R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X contains sodium-and chloride-  
dependent glycine transporter 1 (GLYT-1) like, ESTs.//0.052:421:58//Z96810  
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//1.2e-104:545:95//AB011126  
20 R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//3.0e-07:523:59//AC005140  
R-HEMBA1002777  
R-HEMBA1002779//Human HepG2 3' region Mbol cDNA, clone hmd1e03m3.//9.4e-25:158:93//D17139  
R-HEMBA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORK-  
25 ING DRAFT SEQUENCE.//1.6e-42:463:75//AL022344  
R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence.//2.2e-05:417:59//AL034560  
R-HEMBA1002801//Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes,  
ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS.//0.00055:444:59//L76261  
R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//4.4e-115:559:97//AF071185  
30 R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
4.3e-88:329:94//AC005043  
R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SE-  
QUENCE.//1.9e-22:262:67//AP000041  
R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.3e-79:396:  
35 97//AC004707  
R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING  
DRAFT SEQUENCE, 7 unordered pieces.//0.013.393:61//AC005506  
R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//4.1e-73:489:  
85//AC005562  
40 R-HEMBA1002876//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORK-  
ING DRAFT SEQUENCE.//0.21:549:55//AL034557  
R-HEMBA1002886//CIT-HSP-2013C4.TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey se-  
quence.//0.30:431:56//B53836  
R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds.//3.9e-106:541:95//  
45 AF037261  
R-HEMBA1002921  
R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10.//  
4.6e-19:139:78//AB020875  
R-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING  
50 DRAFT SEQUENCE.//7.5e-45:282:89//AL031681  
R-HEMBA1002935//CIT-HSP-2282P14.TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey  
sequence.//1.5e-102:514:97//AQ008584  
R-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745114, WORKING  
DRAFT SEQUENCE.//3.3e-87:444:97//AL033532  
55 R-HEMBA1002939  
R-HEMBA1002944//HS\_3107\_A1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3107 Col=9 Row=E, genomic survey sequence.//6.3e-21:250:73//AQ103952  
R-HEMBA1002951//Xerolycosa miniata mitochondrial 12S rRNA gene.//0.013:228:63//AJ008020

R-HEMBA1002954//HS\_3246\_A2\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-42:258:91//AQ218005  
R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//4.2e-38:300:83//AC005553  
5 R-HEMBA1002970//Slime mold (*D.discoideum*) prestalk D11 gene, complete cds.//5.0e-05:541:57//M11012  
R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:99//AB014579  
R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//9.1e-36:520:69//AC006128  
10 R-nnnnnnnnnnnn//Homo Sapiens Chromosome X clone bWXD691, complete sequence.//0.00040:504:59//AC004386  
R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.7e-66:556:79//U19614  
R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406  
15 R-HEMBA1003033//Homo sapiens full-length insert cDNA clone ZC34B10.//4.6e-78:414:94//AF086194  
R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026  
R-HEMBA1003035//HS\_2008\_A2\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839  
20 20 R-HEMBA1003037//347G15.TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694  
R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983  
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182  
25 R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962  
R-HEMBA1003067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302  
30 R-HEMBA1003071//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ110136  
R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.9e-69:494:84//U42975  
R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of *S.cerevisiae*, DNA binding protein similar to URE-B1, ESTs and STS.//1.1e-11:331:64//Z97054  
35 R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673  
R-HEMBA1003083//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12; 40 HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798  
R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3-unordered pieces.//1.2e-43:281:88//AC006039  
R-HEMBA1003096//Human DNA sequence from clone J506G21, WORKING DRAFT SEQUENCE.//0.00037:421:59//Z82213  
45 R-HEMBA1003098//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.4e-30:303:78//AC005598  
R-HEMBA1003117  
R-HEMBA1003129//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329  
50 R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.9e-99:484:98//AC004472  
R-HEMBA1003136//CIT-HSP-2281L22.TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence.//2.0e-10:93:92//B99861  
55 R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPCI1-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.8e-40:270:87//AC004024  
R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-116:586:96//AJ005670  
R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//6.4e-35:364:70//Z83822

R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta receptor./1.9e-30:282:77//X60459  
R-HEMBA1003197  
R-HEMBA1003199//HS\_2166\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=23 Row=I, genomic survey sequence./0.00026:271:61//AQ164162  
5 R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces./5.4e-44:291:83//AC005480  
R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-7q22, complete sequence./3.1e-10:293:62//AC000118  
R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces./1.0:  
10 118:69//AC006148  
R-HEMBA1003220//HS\_3092\_B1\_F09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=17 Row=L, genomic survey sequence./0.00014:59:91//AQ128202  
R-HEMBA1003222//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y43F8,  
WORKING DRAFT SEQUENCE./0.84:214:62//Z95393  
15 R-HEMBA1003229//RPCI11-16F15.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16F15, genomic survey sequence./0.42:167:64//B83610  
R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic clone 2320G19, genomic survey sequence./3.6e-36:195:81//AQ037231  
20 R-HEMBA1003250//HS\_2168\_A2\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=18 Row=E, genomic survey sequence./1.4e-22:158:89//AQ125356  
R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds./0.96:268:61//U53709  
R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence./1.0e-32:255:84//AC002549  
25 R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces./0.0044:212:60//AC005308  
R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence./1.1e-34:286:74//AC002395  
R-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces./1.8e-53:428:83//AC005840  
30 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds./3.0e-115:551:99//AB011109  
R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic clone 2196L16, genomic survey sequence./2.9e-20:337:65//AQ003073  
R-HEMBA1003304//Sequence 23 from patent US 5552281./1.8e-31:179:97//I25662  
35 R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence./0.00019:334:60//AB017061  
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds./2.8e-111:545:97//AB001872  
R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence./0.60:274:61//AL022153  
40 R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence./0.00028:172:65//AC005099  
R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces./2.2e-44:268:90//AC005081  
45 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds./2.7e-61:312:97//AF026029  
R-HEMBA1003348///\*\*ALU WARNING: Human Alu-J subfamily consensus sequence./7.2e-38:186:83//U14567  
R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequence./0.00012:465:59//Z79600  
R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, complete sequence./3.2e-42:301:87//  
AC002558  
50 R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence./7.4e-34:375:74//AL022721  
55 R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence./1.6e-46:309:88//AC004651  
R-HEMBA1003380//HS\_3184\_B2\_E06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=12 Row=J, genomic survey sequence./1.0e-35:237:88//AQ189144

R-HEMBA1003384//HS\_2193\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, genomic survey sequence./.0.00029:96:76//AQ032212  
R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 un-ordered pieces./.2.6e-21:139:86//AC002993  
5 R-HEMBA1003402//CIT-HSP-2166E19.TR CIT-HSP Homo sapiens genomic clone 2166E19, genomic survey se-quence./.0.99:144:61//B91549  
R-nnnnnnnnnnnnnn  
R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence./.2.5e-112:547:98//AL031321  
10 R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence./.0.082:352:59// AC004879  
R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NBS1) mRNA, complete cds./.9.9e-114:544: 98//AF058696  
15 R-HEMBA1003461  
R-HEMBA1003463  
R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence./.9.1e-106:533:96//AC005041  
R-HEMBA1003528  
R-HEMBA1003531//Human BAC clone GS552A01 from 7q21-q22, complete sequence./.3.4e-08:333:64// AC002454  
20 R-HEMBA1003538//Human mRNA for complement component C1r./.1.4e-23:333:68//X04701  
R-HEMBA1003545//Zebrafish mRNA for zfisl-2 (insulin gene enhancer binding protein homolog), complete cds./.0.030:144:68//D38453  
R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unsorted pieces./.0.0017:487:57//AC004153  
25 R-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE./.2.8e-99:503:96//AL031718  
R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence./.1.6e-114:574:97//AC005913  
R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096./.0.24:116:67//AF034416  
30 R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unsorted pieces./.3.9e-05:422:63//AC006036  
R-HEMBA1003569//Homo sapiens full-length insert cDNA clone ZD82D06./.8.7e-108:545:95//AF086450  
R-HEMBA1003571//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence./.4.6e-51:570:71// AC004914  
35 R-HEMBA1003579//HS\_3237\_B2\_E05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, genomic survey sequence./.8.5e-97:495:95//AQ209302  
R-HEMBA1003581//Mouse mRNA for talin./.8.3e-12:128:82//X56123  
R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2603 (LANL), complete sequence./.2.9e-87:251: 95//AC005774  
40 R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence./.4.5e-52:384:83//AL008715  
R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence./.4.6e-41:442:74//Z84480  
45 R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence./.1.8e-23:177: 88//AC005153  
R-HEMBA1003615  
R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unsorted pieces./.0.039:494:57//AC005139  
50 R-HEMBA100362111\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052I22; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unsorted pieces./.2.3e-26:309:75//AC004599  
R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence./.7.1e- 56:545:75//AC002980  
55 R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete sequence./.2.8e-32:546:68//AF088219  
R-HEMBA1003637//Human BAC clone GS552A01 from 7q21-q22, complete sequence./.8.0e-25:457:68// AC002454  
R-HEMBA1003640//Homo sapiens chromosome X, PAC 671D9, complete sequence./.2.8e-40:280:86//AF031078

R-HEMBA1003645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE./.1.7e-33:297:82//AL023693  
R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence./.0.44:319:59//AL034559  
R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence./.6.9e-  
5 36:242:80//AC004382  
R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence./.8.6e-117:588:  
96//AC005746  
R-HEMBA1003667//Sequence 8 from patent US 5420245./.1.8e-21:170:88//I12222  
R-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence./.1.6e-22:180:87//  
10 AC005065  
R-HEMBA1003680//C. elegans cosmid ZK353./.1.1e-06:270:61//L15313  
R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (cox1) gene, mitochondrial gene  
encoding mitochondrial protein, partial cds./.0.77:171:66//AF044872  
R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPCI-1057I20 (Roswell Park Cancer Institute Human PAC li-  
15 brary) complete sequence./.1.6e-104:523:97//AC004466  
R-HEMBA1003692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING  
DRAFT SEQUENCE./.1.7e-41:414:77//AL021707  
R-HEMBA1003711//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT  
SEQUENCE, 17 unordered pieces./.1.6e-29:304:77//AC000406  
20 R-HEMBA1003714  
R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-685D8, WORKING DRAFT SE-  
QUENCE, 16 unordered pieces./.1.4e-63:578:77//AC005136  
R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered pieces./.2.4e-36:350:78//  
AC002353  
25 R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence./.6.3e-42:250:75//  
AC004699  
R-HEMBA1003729//RPCI11-22D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22D14, genomic survey  
sequence./.1.0:234:62//B86158  
R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS,  
30 GSS, complete sequence./.7.7e-80:558:83//AL008634  
R-HEMBA1003742//HS\_3080\_B2\_H06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3080 Col=12 Row=P, genomic survey sequence./.3.4e-55:331:91//AQ139179  
R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat,  
STS and CpG istand./.4.5e-59:521:75//Z97876  
35 R-HEMBA1003760  
R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds./.2.6e-  
72:467:86//U17343  
R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds./.1.0e-77:557:  
81//AF084259  
40 R-HEMBA1003784  
R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence./.2.1 e-49:390:  
72//AC004455  
R-HEMBA1003803  
45 R-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence./.9.4e-99:359:99//  
AC004596  
R-HEMBA1003805//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of  
the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding  
proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence./.  
8.0e-113:567:96//AL031781  
50 R-HEMBA1003807//Bovine dinucleotide microsatellite HUJII77./.5.4e-18:194:78//M96348  
R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F2545L and R31076 con-  
taining COX6B and UPKA, genomic sequence, complete sequence./.3.4e-40:256:85//AC002115  
R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey se-  
quence./.9.7e-25:150:96//AQ196624  
55 R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseu-  
dogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism,  
complete sequence./.4.8e-33:486:68//Z93929  
R-HEMBA1003864//, complete sequence./.4.4e-100:531:94//AC005300

R-HEMBA1003866//HS\_3203\_B2\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298  
R-HEMBA1003879//Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207  
5 R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036  
R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576  
R-HEMBA1003893//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 113F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421  
10 R-HEMBA1003902//HS\_3031\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549  
R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795  
R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//3.1e-  
15 58:294:85//AC005368  
R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:93//AF109718  
R-HEMBA1003939  
R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:58//AC004904  
R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial gene encoding mito-  
20 chondrial protein, partial cds.//0.034:258:62//AF069619  
R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:492:57//AL034560  
R-HEMBA1003958//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668  
R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase (ahybadh4) gene, complete  
25 cds.//0.11:428:60//AF000132  
R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete sequence.//1.0:222:62//  
AC004414  
R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//I80060  
R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804  
30 R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924  
R-HEMBA1003989//RPCI11-52K22.TJ RPCI11 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484  
R-HEMBA1004000  
35 R-HEMBA1004011  
R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//4.7e-38:284:85//  
AC005670  
R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.48:460:58//AL023575  
40 R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//  
2.5e-21:159:80//AC005081  
R-HEMBA1004038//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054  
R-HEMBA1004042//Homo sapiens clone DJ0968I16, complete sequence.//0.00071:263:68//AC006016  
45 R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//8.8e-23:196:69//  
AC006143  
R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283  
R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677  
50 R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504  
R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
3.5e-61:551:77//AC005484  
R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
0.98:275:63//AC004952  
55 R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//I76237  
R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//1.8e-11:323:63//AF091234  
R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918

R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211\_P\_7, complete sequence./.6.0e-49:491:76//AC003665  
 R-HEMBA1004133//HS\_3229\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence./.1.1e-72:374:97//AQ192003  
 5 R-HEMBA1004138//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE./.3.1e-09:277:66//AL024498  
 R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence./.0.53:239:61//AL008970  
 R-HEMBA1004146//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces./.3.0e-35:165:88//AC004820  
 10 R-HEMBA1004150//CITBI-E1-2517I2.TR CITBI-E1 Homo sapiens genomic clone 2517I2, genomic survey sequence./.0.56:379:59//AQ277616  
 R-HEMBA1004164//Human BAC clone GS200K05 from 7q21-q22, complete sequence./.4.6e-49:448:77//AC002429  
 15 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds./.2.4e-110:563:96//AF067855  
 R-HEMBA1004199//S.pombe chromosome I cosmid c8A4./.0.73:187:64//Z66569  
 R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence./.6.3e-30:293:77//AC004552  
 R-HEMBA1004202//rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].//.3.0e-64:517:80//S72304  
 20 R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces./.1.0e-97:303:98//AC005488  
 R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds./.3.6e-116:573:97//U50748  
 R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12 tRNAs and 7 genes./.5.4e-11:493:60//M37275  
 25 R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds./.6.1e-76:443:86//AF095927  
 R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complete sequence./.1.1e-42:330:83//AC005763  
 R-HEMBA1004241  
 30 R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE./.1.1e-45:288:85//AP000011  
 R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence./.5.2e-09:516:61//AC004903  
 R-HEMBA1004264  
 35 R-HEMBA1004267//HS\_2255\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=O, genomic survey sequence./.8.6e-59:318:95//AQ068854  
 R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCIS-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence./.1.1e-113:576:96//AC005831  
 R-nnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence./.4.4e-110:553:96//AF091081  
 40 R-HEMBA1004276  
 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds./.1.9e-106:538:97//AF022795  
 R-HEMBA1004289//RPCI11-74010.TJ RPCI11 Homo sapiens genomic clone R-74O10, genomic survey sequence./.2.3e-37:248:76//AQ266668  
 45 R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end./.0.0016:273:64//L13174  
 R-HEMBA1004306//HS\_3175\_B2\_F01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, genomic survey sequence./.1.6e-28:190:77//AQ169206  
 R-HEMBA1004312//Human BAC clone RG119P24 from 7q31, complete sequence./.6.3e-36:267:82//AC003088  
 R-HEMBA1004321//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 10155, WORKING DRAFT  
 50 SEQUENCE./.4.1e-111:576:95//AJ009611  
 R-HEMBA1004323//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence./.2.7e-42:136:91//AQ114933  
 R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic clone 2303L24, genomic survey sequence./.1.0:78:67//AQ017600  
 55 R-HEMBA1004330//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUENCE, 5 unordered pieces./.2.3e-119:580:98//AC004987  
 R-HEMBA1004334//Pimpinella brachycarpa Phybl mRNA, complete cds./.3.3e-14:238:69//AF082024  
 R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence./.1.8e-

21:291:71//AC004638  
 R-HEMBA1004341  
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds.//4.1e-74:444:90//D89667  
 R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.//7.0e-38:287:82//AC003002  
 5 R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:92//I58611  
 R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-14:446:63//AC005949  
 R-HEMBA1004372//CIT-HSP-2005C13.TF CIT-HSP Homo sapiens genomic clone 2005C13, genomic survey sequence.//0.010:334:61//B55811  
 10 R-HEMBA1004389//Homo sapiens full-length insert cDNA clone ZE09A11.//1.5e-19:170:83//AF086540  
 R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)23 repeat.//1.0:50:84//X58124  
 R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//8.2e-34:459:  
 69//AC004057  
 R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//2.8e-42:314:84//  
 15 AC005030  
 R-HEMBA1004408  
 R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//1.6e-66:449:82//Z54200  
 R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete  
 20 sequence bases 1..333303.//7.2e-32:460:68//AJ011930  
 R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//  
 3.9e-113:581:96//AC004846  
 R-HEMBA1004461//HS\_3244\_A2\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=3244 Col=24 Row=K, genomic survey sequence.//8.0e-83:397:99//AQ220876  
 R-HEMBA1004479//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-40:485:70//  
 AC006012  
 R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//2.2e-11:  
 513:59//AE001370  
 R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.//2.0e-08:245:  
 66//AC005951  
 30 R-HEMBA1004506//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING  
 DRAFT SEQUENCE.//4.2e-81:582:83//Z84487  
 R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequence.//0.56:235:64//Z70266  
 R-HEMBA1004509  
 R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:83//I76230  
 35 R-HEMBA1004538//HS\_3189\_B2\_C03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3189 Col=6 Row=F, genomic survey sequence.//6.1e-21:140:92//AQ170330  
 R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clone 712K9, genomic survey se-  
 quence.//1.7e-16:116:93//B73329  
 R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-14:213:71//D87457  
 40 R-HEMBA1004573  
 R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome  
 4p16.3 contains protein similar to Mouse SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.0:352:  
 60//Z68279  
 R-HEMBA1004586  
 45 R-nnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.0012:359:60//Z98551  
 R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62//AL022071  
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501./1.4e-50:327:85//  
 AB007970  
 R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library)  
 50 complete sequence.//4.4e-13:527:63//AC004805  
 R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//U31866  
 R-HEMBA1004632  
 R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
 7.7e-117:573:98//AC005534  
 55 R-HEMBA1004638//H.sapiens mRNA for DGCR2.//3.8e-19:118:99//X84076  
 R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence.//  
 0.00013:501:58//AC005171  
 R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel

genes, ESTs, GSSs and CpG islands, complete sequence.//1.5e-120:571:98//AL031432  
 R-HEMBA1004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING DRAFT SEQUENCE.//4.4e-12:110:88//Z93241  
 R-HEMBA1004672//Human DNA sequence from PAC 308I13 on chromosome 1p35-1p36.3.//3.4e-38:324:81//Z99291  
 5 R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//0.86:309:57//AB006702  
 R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T33B22, genomic survey sequence.//0.29:331:61//B97342  
 10 R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//0.051:424:58//AL034559  
 R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.7e-49:497:76//AC004638  
 R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//1.6e-38:362:  
 15 79//AC005562  
 R-HEMBA1004725  
 R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26, complete sequence.//1.1e-58:489:  
 79//AC002085  
 R-HEMBA1004733  
 R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome 6q16.1-16.3. Contains the gene  
 20 for the N-Oct5a (N-Oct3, N-Oct5b) POU domain proteins and an unknown gene. Contains a putative CpG island, ESTs, STS; and GSSs, complete sequence.//0.0030:362:61//AL022395  
 R-HEMBA1004736//Homo sapiens clone DJ0981O07, complete sequence.//1.9e-58:282:87//AC006017  
 R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:  
 25 81//AC004953  
 R-HEMBA1004751//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950  
 R-HEMBA1004752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 495010, WORKING DRAFT SEQUENCE.//3.3e-39:281:85//AL031121  
 30 R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//L06498  
 R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/1,H2B.1A,H4,H2A.1b,H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island.//1.8e-08:516:59//AL021807  
 35 R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:  
 72//AC004057  
 R-HEMBA1004763  
 R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1  
 40 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310  
 R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:  
 45 476:61//AE001371  
 R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human cosmid library) complete sequence.//5.0e-08:113:80//AC003047  
 R-HEMBA1004776  
 R-HEMBA1004778/\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567  
 R-nnnnnnnnnnnn/HS\_3192\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic  
 50 clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855  
 R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:87//AF048728  
 R-HEMBA1004806  
 R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-  
 55 20:333:69//AC005015  
 R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE  
 LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.  
 Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545  
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:85//M74002  
 R-HEMBA1004847//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//7.6e-80:297:85//  
 X53744

R-HEMBA1004850  
R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201  
R-HEMBA1004864  
5 R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPCI11-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297  
R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-49:551:73//AC004826  
10 R-HEMBA1004889//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943  
R-HEMBA1004900//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//6.6e-11:144:7711AC005972  
R-HEMBA1004909//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052  
15 R-HEMBA1004918//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554  
R-HEMBA1004923//Homo sapiens 47kB DNA fragment from Xq28, proximal to MTM1 gene.//2.0e-07:182:69//Y15994  
R-HEMBA1004929  
20 R-HEMBA1004930//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.7e-66:547:79//AC005848  
R-HEMBA1004933//H.sapiens Humig mRNA.//0.13:233:62//X72755  
R-HEMBA1004934//CIT-HSP-2021I16.TF CIT-HSP Homo sapiens genomic-clone 2021I16, genomic survey sequence.//0.66:268:62//B65345  
25 R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sapiens genomic clone 2281L12, genomic survey sequence.//3.8e-20:104:82//B99849  
R-HEMBA1004954//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00082:385:60//AC005341  
R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408  
30 R-HEMBA1004960//Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249  
R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982  
R-HEMBA1004973/\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C124C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.69:179:64//AC003656  
R-HEMBA1004977//Caenorhabditis elegans cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495  
R-HEMBA1004978//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.20:427:60//AL024509  
40 R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP Homo sapiens genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614  
R-HEMBA1004983//Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389  
45 R-HEMBA1004995//Homo sapiens chromosome 16, cosmid clone 306E5 (LANL), complete sequence.//1.6e-90:527:89//AC004224  
R-HEMBA10050087//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83//AL031663  
55 R-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474  
R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//6.3e-104:542:94//AB014548  
R-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c),

H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//3.1e-67:493:83//AL009179  
R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//7.4e-101:537:  
94//AC004596

5 R-HEMBA1005039//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORK-  
ING DRAFT SEQUENCE.//9.5e-30:446:68//AL031650

R-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//1.4e-34:229:88//Z22819

R-HEMBA1005050//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; com-  
plete sequence.//4.0e-43:371:80//AC002404

10 R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//2.3e-15:269:66//  
AC004675

R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//  
4.0e-30:305:74//AC006030

R-HEMBA1005075

15 R-HEMBA1005079//Homo sapiens clone HS 19.11 Alu-Ya5 sequence.//6.5e-48:245:91//AF015156

R-HEMBA1005083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING  
DRAFT SEQUENCE.//1.3e-15:142:83//AL034423

R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//5.3e-110:545:96//  
AF080561

20 R-HEMBA1005113//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53C10,  
WORKING DRAFT SEQUENCE.//0.026:252:64//Z93340

R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains  
one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//  
7.1e-55:306:82//AL022336

25 R-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING  
DRAFT SEQUENCE.//6.4e-45:309:87//AL022345

R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds.//3.2e-31:310:76//  
U81834

R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG  
island.//1.4e-33:361:79//AL021407

30 R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat,  
STS, complete sequence.//2.7e-22:440:66//AL031279

R-HEMBA1005185//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8,  
WORKING DRAFT SEQUENCE.//0.0017:381:58//AL022594

35 R-HEMBA1005201//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.5e-05:457:57//X95276

R-HEMBA1005202//Human 18S ribosomal RNA.//4.7e-38:236:91//X03205

R-HEMBA1005219

R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//  
1.0:209:65//AC004854

40 R-HEMBA1005232//Homo-sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0040:439:58//  
AC004617

R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//4.2e-111:568:96//  
AC005154

R-HEMBA1005244//HS\_3092\_B2\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
45 nomic clone Plate=3092 Col=22 Row=F, genomic survey sequence.//4.9e-12:116:84//AQ127947

R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//3.2e-27:  
210:84//AC004548

R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//4.6e-105:437:  
97//AC005837

50 R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system.//0.011:339:59//  
D86630

R-HEMBA1005275//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//3.4e-17:269:71//  
AC004914

R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region chromosome 13q12-13 con-  
55 tains xs7 mRNA, ESTs.//6.9e-20:193:73//Z75887

R-HEMBA1005296//HS\_3037\_B1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3037 Col=1 Row=H, genomic survey sequence.//0.26:184:64//AQ117120

R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//

1.5e-58:445:78//AC006146  
R-HEMBA1005311//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796E4, WORKING DRAFT SEQUENCE.//9.3e-42:383:78//AL022337  
R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11.//0.80:179:65//AF003389  
5 R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-40:409:71//AC006030  
R-HEMBA1005318//S.pombe chromosome I cosmid c2E11.//0.97:370:61//AL031181  
R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//1.9e-112:577:95//AC005803  
10 R-HEMBA1005353//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 429E7, WORKING DRAFT SEQUENCE.//8.9e-80:406:97//AL031722  
R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-50:320:84//AC005412  
R-HEMBA1005367//RPCI11-85E23.TV RPCI11 Homo sapiens genomic clone R-85E23, genomic survey sequence.//0.39:148:67//AQ281915  
15 R-HEMBA1005372//Homo sapiens full-length insert cDNA YH93B03.//2.6e-108:557:95//AF074997  
R-HEMBA1005374//Homo sapiens full-length insert cDNA clone ZA95D11.//1.9e-110:531:98//AF086142  
R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS (X-linked juvenile retinoschisis precursor protein) gene.  
20 Contains ESTs, STSs and GSSs, complete sequence.//6.0e-41:432:75//Z92542  
R-HEMBA1005394//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE.//4.9e-107:585:93//AL031670  
R-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//5.1e-118:586:97//AL034379  
25 R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds.//1.6e-06:204:68//U95958  
R-HEMBA1005410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//1.2e-23:452:66//AL008722  
30 R-HEMBA1005411//RPCI11-66N19.TK RPCI11 Homo sapiens genomic clone R-66N19, genomic survey sequence.//2.2e-38:222:79//AQ237442  
R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//5.6e-117:453:99//AF041248  
R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//0.86:278:60//Z97196  
35 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment.//5.4e-46:305:87//L40391  
R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//3.3e-79:531:86//AL031054  
R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//4.0e-27:469:  
40 66//AC004894  
R-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//7.2e-40:410:76//AC005212  
R-HEMBA1005472//Human DNA Sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1090E8, WORKING DRAFT SEQUENCE.//3.1e-40:296:85//AL033524  
45 R-HEMBA1005475//HS\_2266\_B2\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence.//0.49:209:61//AQ069377  
R-HEMBA1005497  
R-HEMBA1005500//Homo sapiens PAC clone DJ1093O17 from 7q11.23-q21, complete sequence.//4.5e-116:580:  
50 97//AC004957  
R-HEMBA1005506//Arabidopsis thaliana BAC T26D22.//0.0050:442:59//AF058826  
R-HEMBA1005508//Sigalphus sp. 16S ribosomal RNA gene, partial sequence.//0.020:391:59//AF003509  
R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.44:195:63//Z96811  
55 R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.44:470:57//L14320  
R-HEMBA1005518//M.musculus mRNA for paladin gene.//6.2e-29:183:81//X99384  
R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-40:281:86//AC004913

R-HEMBA1005526//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//3.9e-40:482:73/Z97985  
R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11././/3.8e-84:309:99//AB020860  
5 R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence.//8.1e-25:154:94//U84091  
R-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING DRAFT SEQUENCE.//5.3e-105:534:96//AL034431  
R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//2.8e-69:432:88//  
10 AC004743  
R-HEMBA1005558  
R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//5.9e-33:367:74//AC004087  
R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//2.2e-67:399:91//AL020989  
15 R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence.//1.0:156:631/AC005737  
R-HEMBA1005577  
R-HEMBA1005581//Homo sapiens mRNA for MEGFS, partial cds.//9.7e-27:561:64//AB011538  
20 R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9 -cytochrome oxidase 2 genes.//2.3e-10:404:62//X02171  
R-HEMBA1005583//HS\_3014\_B1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence.//3.0e-81:442:94//AQ154499  
R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-  
25 Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//1.8e-54:490:77//Z98046  
R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//2.2e-28:262:  
79//AC005746  
30 R-HEMBA1005595//HS\_2224\_A2\_G03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence.//3.6e-48:263:95//AQ033446  
R-HEMBA1005606//Human PAC clone DJ0093I03 from Xq23, complete sequence.//2.5e-08:355:63//AC003983  
R-HEMBA1005609//HS\_2182\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence.//2.2e-82:400:99//AQ023130  
35 R-HEMBA1005616//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 124K22, WORKING DRAFT SEQUENCE.//0.80:308:60//AL031176  
R-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//7.4e-76:338:98//AL031731  
R-HEMBA1005627//Homo sapiens full-length insert cDNA clone ZD53D02.//4.5e-72:398:93//AF086321  
40 R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//3.8e-17:548:60//AC004460  
R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.4e-13:172:75//AL022069  
R-HEMBA1005634//RPCI11-13O15.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-13O15, genomic survey sequence.//1.0e-28:153:82//B73293  
45 R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//4.5e-51:343:87//AL021786  
R-HEMBA1005670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//2.5e-33:288:78//AL020995  
R-HEMBA1005679//Human esterase D mRNA, 3'end.//4.2e-49:322:88//M13450  
50 R-HEMBA1005680//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.0e-36:285:83//AC005924  
R-HEMBA1005685//H.sapiens (MAR8) chromosome 19 DNA, 343bp.//0.022:65:86//Z35281  
R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds.//5.4e-46:376:84//U66406  
55 R-HEMBA1005705//RPCI11-13O14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13O14, genomic survey sequence.//0.071:182:59//B76186  
R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATPSG3) like pseudogene, ESTs and STSs.

**EP 1 074 617 A2**

Contains polymorphic CA repeat./.1.0:189:66//Z92545  
R-HEMBA1005732//Human Chromosome 11q12 pac pDJ363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces./.2.1e-47:449:75//AC003023  
R-HEMBA1005737  
5 R-nnnnnnnnnnnn//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//0.11:174:63//X91255  
R-HEMBA1005755//Human DNA-sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence./.0.15:160:65//AL008634  
R-HEMBA1005765//Human Xq28 cosmids U225B5 and U236A12, complete sequence./.5.2e-39:422:74//U71148  
R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15,  
10 WORKING DRAFT SEQUENCE./.0.037:261:61//AP000010  
R-HEMBA1005813//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE./.1.7e-26:242:80//AL023808  
R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds./.0.17:199:62//U52805  
R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence./.0.26:437:56//AL034559  
15 R-HEMBA1005829//Human Cosmid g1572c035, complete sequence./.3.8e-05:366:61//AC000124  
R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence./.8.2e-107:551:96//AL031781  
20 R-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aA4, genomic survey sequence./.2.6e-17:225:72//AL018730  
R-HEMBA1005853//Human Chromosome 15 pac pDJ24m8, complete sequence./.1.1e-27:314:75//AC000379  
R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence./.2.6e-20:328:67//AC006207  
25 R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence./.2.0e-102:  
543:95//AC004945  
R-HEMBA1005894  
R-HEMBA1005909  
R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 2342E5, genomic survey se-  
30 quence./.0.0012:315:60//AQ058081  
R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn, tRNA-Tyr, small subunit rRNA, and ATPase subunit 6./.0.0090:445:58//Z23072  
R-HEMBA1005931//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE./.1.7e-46:351:83//Z98304  
35 R-HEMBA1005934//Homo sapiens chromosome 17, clone hRPK.261\_A\_13, complete sequence./.0.0052:179:  
71//AC005138  
R-HEMBA1005962//Homo sapiens clone RG012D21, complete sequence./.1.1e-11:149:74//AC005045  
R-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3055 Col=15 Row=I, genomic survey sequence./.5.4e-79:403:97//AQ147357  
40 R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds./.6.9e-112:580:95//AF082516  
R-HEMBA1005991//Human DNA sequence from clone 58A9 on chromosome 1q24.1-24.3. Contains STSs, GSSs, genomic marker D1S210 and a ca repeat polymorphism, complete sequence./.2.6e-39:299:82//AL031285  
R-HEMBA1005999//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces./  
45 1.1e-29:260:70//AC004859  
R-HEMBA1006002//Rattus norvegicus s-nexilin mRNA, complete cds./.6.3e-15:174:78//AF056035  
R-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds./.2.6e-112:574:95//AF036405  
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds./.7.6e-27:444:67//AB018268  
R-HEMBA1006035//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING  
50 DRAFT SEQUENCE, 5 unordered pieces./.0.025:373:60//AC005139  
R-HEMBA1006036//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence./.0.0056:  
535:59//AC004125  
R-HEMBA1006042//HS\_2169\_A1\_B11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2169 Col=21 Row=C, genomic survey sequence./.1.7e-73:390:95//AQ132995  
55 R-nnnnnnnnnnnn  
R-HEMBA1006081  
R-HEMBA1006090//HS\_2262\_A2\_A01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2262 Col=2 Row=A, genomic survey sequence./.2.1e-70:360:97//AQ216324

- R-HEMBA1006091  
R-HEMBA1006100//Homo sapiens DNA sequence from PAC 212G6 on chromosome Xp11.3-p11.4. Contains synapsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS, complete sequence.//1.6e-36:354:77//AL009172
- 5 R-HEMBA1006108  
R-HEMBA1006121  
R-HEMBA1006124//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//1.3e-12:327:64//Z95113
- 10 R-HEMBA1006130//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.60:326:62//AC005948  
R-nnnnnnnnnnnn//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//4.3e-52:321:80//AC005777
- 15 R-HEMBA100614211, complete sequence.//1.0e-13:160:78//AC005500  
R-HEMBA1006155//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0013:389:60//AC004688
- 20 R-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.4e-119:574:98//AF048693  
R-HEMBA1006173//Mus musculus protein tyrosine phosphatase STEP61 mRNA, complete cds.//4.1e-43:307:86//U28217
- 25 R-HEMBA1006182//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.7e-30:300:71//AC004491  
R-HEMBA1006198//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.3e-36:284:85//U14567  
R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.1e-110:545:97//AF070557
- 30 R-HEMBA1006248//Homo sapiens mRNA for KIAA0667 protein, partial cds.//0.46:365:58//AB014567  
R-HEMBA1006252//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//2.8e-41:438:71//U91323  
R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds.//1.8e-28:179:91//AF083384  
R-HEMBA1006259//RPCI11-44N14.TJ RPCI11 Homo sapiens genomic clone R-44N14, genomic survey sequence.//1.5e-48:348:85//AQ203161
- 35 R-HEMBA1006268  
R-HEMBA1006272//Human DNA sequence from clone 1198H6 on chromosome 1p36.11-36.31. Contains two Melanoma Preferentially Expressed Antigen PRAME LIKE genes. Contains GSSs and ESTs, complete sequence.//2.8e-73:273:87//AL023753  
R-nnnnnnnnnnnn//H.sapiens PAP mRNA.//1.6e-54:585:71//X76770
- 40 R-HEMBA1006283//Sequence 7 from patent US 5776683.//9.7e-18:113:98//AR016240  
R-HEMBA1006284//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence.//0.97:447:59//AC004585  
R-HEMBA1006291//Homo sapiens full-length insert cDNA clone ZB76B10.//2.9e-94:454:98//AF086161  
R-HEMBA1006293//Sequence 8 from patent US 5721351.//8.1e-10:111:72//I89415
- 45 R-HEMBA1006309//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.6e-37:288:84//AC005412  
R-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.5e-29:132:81//AF076183  
R-HEMBA1006328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 894K16, WORKING DRAFT SEQUENCE.//3.3e-50:340:75//AL034429
- 50 R-HEMBA1006334//Rattus norvegicus nitzin mRNA, partial cds.//8.7e-22:259:72//AF087945  
R-HEMBA1006347//Human prostasin gene, complete cds.//1.8e-78:170:100//U33446  
R-HEMBA1006349//Rat brain calcium channel alpha-1 subunit mRNA, complete cds.//0.00051:120:73//M57682  
R-HEMBA1006359//CITBI-E1-2516C16.TR CITBI-E1 Homo sapiens genomic clone 2516C16, genomic survey sequence.//4.7e-74:576:82//AQ277951
- 55 R-HEMBA1006364//G.gallus gene for transforming growth factor-beta2, exons 5-7.//2.5e-21:118:85//X59080  
R-HEMBA1006377//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//5.7e-68:367:85//AC005239  
R-HEMBA1006380//Human BAC clone RG007J15 from 7q31, complete sequence.//6.1e-47:300:83//AC003989  
R-HEMBA1006381//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//1.5e-47:336:86//AC005914  
R-HEMBA1006398//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.5e-67:501:83//AC005609

R-HEMBA1006416//Homo sapiens chromosome 17, clone 347\_H\_5, complete sequence./.4.4e-37:319:76//AC002119  
 R-HEMBA1006419//Homo sapiens chromosome 17, clone HCIT542B22, complete sequence./.2.9e-50:502:75//AC004253  
 5 R-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes./.4.1e-116:572:97//AF107885  
 R-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence./.9.4e-117:578:97//AL031781  
 10 R-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE./.2.2e-08:353:63//Z93017  
 R-HEMBA1006438//HS\_2008\_A1\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=7 Row=G, genomic survey sequence./.1.2e-29:194:91//AQ245162  
 15 R-HEMBA1006445//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces./.0.011:330:60//AC005075  
 R-HEMBA1006446//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence./.0.032:256:61//AE001398  
 20 R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence./.5.6e-35:229:77//AC002364  
 R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmid clone 34a5, complete sequence./.11.1e-14:354:63//AC002052  
 R-HEMBA1006471  
 25 R-HEMBA1006474//p40, p24 [Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Genomic RNA, 1138 nt, segment 1 of 3].//1.1e-14:442:60//S67502  
 R-HEMBA1006483//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence./.3.7e-37:290:82//U95742  
 R-HEMBA1006485//H.sapiens mRNA for aminopeptidase./.7.6e-91:517:91//Y07701  
 30 R-HEMBA1006486//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces./.1.1e-33:289:81//AC005089  
 R-HEMBA1006489//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence./.6.0e-07:485:60//AL020989  
 R-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence./.4.3e-112:572:95//AC005828  
 35 R-HEMBA1006494//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence./.2.3e-10:186:67//AC002994  
 R-HEMBA1006497//RPCI11-16L10.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16L10, genomic survey sequence./.1.5e-10:75:100//B88015  
 40 R-HEMBA1006502//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence./.3.3e-36:516:70//Z93929  
 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds./.1.2e-115:570:96//AB014566  
 R-HEMBA1006521//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE./.2.2e-20:266:71//Z98304  
 45 R-HEMBA1006530//RPCI11-52M1.TJ RPCI11 Homo sapiens genomic clone R-52M1, genomic survey sequence./.0.00015:227:64//AQ052526  
 R-HEMBA1006535//HS\_2234\_B1\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, genomic survey sequence./.7.5e-33:191:95//AQ129525  
 R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence./.0.026:497:58//AC005007  
 50 R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complete sequence./.5.2e-41:289:86//AC004603  
 R-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds./.3.4e-64:551:78//U06944  
 R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence./.5.7e-09:266:66//AC002554  
 55 R-HEMBA1006566//HS\_2171\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, genomic survey sequence./.0.012:306:61//AQ125421  
 R-HEMBA1006569//Ovis aries beta actin mRNA, complete cds./.3.8e-70:529:82//U39357  
 R-HEMBA1006579//Homo sapiens BAC clone NH0115E20 from Y, complete sequence./.1.0:141:65//AC006032

R-HEMBA1006583//CIT-HSP-2377M16.TR CIT-HSP Homo sapiens genomic clone 2377M16, genomic survey sequence.//1.7e-31:271:76//AQ111875  
R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.093:270:61//AC004709  
5 R-HEMBA1006597//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-45:371:80//AC005031  
R-HEMBA1006612  
R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8B22, WORKING DRAFT SEQUENCE.//2.1e-20:229:77//AL031737  
10 R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//4.8e-40:321:83//AL023284  
R-HEMBA1006631//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2020O8, WORKING DRAFT SEQUENCE.//1.5e-45:477:77//AL031848  
15 R-HEMBA1006635//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//8.0e-40:245:91//U14572  
R-HEMBA1006639  
R-HEMBA1006643  
R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.//2.5e-106:567:94//U40282  
20 R-HEMBA1006652//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//8.7e-54:334:76//AC002089  
R-HEMBA1006653//Homo sapiens 7q telomere, complete sequence.//5.0e-36:207:89//AF027390  
R-HEMBA1006665//HS\_3213\_B2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, genomic survey sequence.//1.2e-21:235:67//AQ175625  
25 R-HEMBA1006674//H.sapiens telomeric DNA sequence, clone 9QTEL023, read 9QTELOO023.seq.//2.6e-32:212:83//Z96776  
R-HEMBA1006676//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-10:436:60//Z98551  
R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//6.1e-06:477:59//L40608-  
30 R-HEMBA1006695//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.8e-30:266:80//AC005096  
R-HEMBA1006696  
R-HEMBA1006708  
R-HEMBA1006709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 715N11, WORKING DRAFT SEQUENCE.//6.8e-14:139:82//AL031674  
35 R-HEMBA1006717  
R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//9.9e-18:365:66//AC005828  
R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.3e-37:380:  
40 75//AC003108  
R-HEMBA1006754//Homo sapiens chromosome 5, P1 clone 962c5 (LBNL H87), complete sequence.//2.1e-75:338:85//AC003951  
R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//1.2e-112:579:95//AC005752  
45 R-HEMBA1006767//Plasmodium falciparum MAL3P6, complete sequence.//0.00022:528:58//Z98551  
R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.3e-46:305:  
87//AC005701  
R-HEMBA10067801//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//7.2e-39:305:82//AL022323  
50 R-HEMBA1006789//Streptomyces coelicolor cosmid 6G4.//0.0085:449:61//AL031317  
R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//4.1e-43:355:  
801//AC006120  
R-HEMBA1006796//HS\_3038\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=22 Row=P, genomic survey sequence.//0.99:158:63//AQ102483  
55 R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//8.4e-47:481:75//AC004854  
R-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_O\_9, complete sequence.//3.0e-08:84:90//AC004797

R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54:496:76//Z93023  
R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence.//0.70:206:65//AC005668  
5 R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-46:281:91//AC004217  
R-HEMBA1006865//Mus musculus clone 101 B1 repeat region sequence.//0.61:115:70//AF056074  
R-nnnnnnnnnnnn//Mus musculus mRNA for oxysterol-binding protein, complete cds.//3.3e-102:618:87//AB017026  
10 R-HEMBA1006885 4.2e-14:379:63//AG006839  
R-HEMBA1006900//CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic clone 2006M20, genomic survey sequence.//2.6e-07:230:66//B56395  
R-HEMBA1006921//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//2.1e-68:267:86//AC005154  
15 R-HEMBA1006926  
R-HEMBA1006929//HS\_3244\_A2\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=2 Row=E, genomic survey sequence.//6.9e-21:191:83//AQ207500  
R-HEMBA1006936  
R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853  
20 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//2.0e-75:371:98//AJ010841  
R-HEMBA1006949//Homo sapiens PAC clone DJ0777G09 from 7q34-q36, complete sequence.//0.47:240:63//AC005518  
R-HEMBA1006973//HS\_2009\_A2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, genomic survey sequence.//9.6e-05:407:60//AQ232302  
25 R-HEMBA1006976//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701  
R-HEMBA1006993//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.9e-47:394:79//U18271  
30 R-HEMBA1006996//CIT-HSP-2172D17.TF CIT-HSP Homo sapiens genomic clone 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406  
R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558  
R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//5.6e-41:437:71//AC005277  
35 R-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//8.2e-73:556:80//X79088  
R-HEMBA1007045  
R-HEMBA1007051//Human DNA sequence from cosmid N69F4 on chromosome 22q11.2-qter contains EST.//9.9e-27:342:71//Z72006  
R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//5.4e-85:558:87//U85056  
40 R-HEMBA1007062  
R-HEMBA1007066  
R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complete sequence.//2.0e-66:476:85//AC006141  
R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60\_A\_24, complete sequence.//1.0e-38:179:82//AC005325  
45 R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.2e-49:551:73//AC006015  
R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequence.//1.0:261:61//AC000385  
50 R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//0.043:295:62//AC004803  
R-HEMBA1007113//Homo sapiens (subclone 6\_a8.from P1 H16) DNA sequence.//1.4e-52:307:87//L43392  
R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547  
55 R-HEMBA1007147//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65f1, reverse read cpg65f1.rt1a.//0.16:187:64//Z62246  
R-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//7.6e-108:543:96//AC005239  
R-HEMBA1007151//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.14:323:58//

AC004875  
R-nnnnnnnnnnnn/Homo sapiens epsin 2a mRNA, complete cds./.5.1e-103:529:94//AF062085  
R-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORKING DRAFT SEQUENCE,  
129 ordered pieces./.5.4e-106:537:96//AC005911

5 R-HEMBA1007194//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human  
PAC Library) complete sequence./.4.1e-39:262:80//AC003035  
R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds./.5.3e-61:332:95//D86987  
R-HEMBA1007206//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains  
ESTs STS and CpG island./.1.9e-50:436:81//Z93023

10 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds./.2.3e-96:471:97//AB018340  
R-HEMBA1007251//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence./.0.011:  
349:62//AC004777  
R-HEMBA1007256//Homo sapiens PAC clone DJ0676L20 from 7q35-q36, complete sequence./.2.8e-10:224:70//  
AC004856

15 R-HEMBA1007267//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library)  
complete sequence./.3.4e-53:362:86//AC005924  
R-HEMBA1007273  
R-HEMBA1007279//Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4./.0.042:454:57//  
AJ235273

20 R-HEMBA1007281//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4./.0.99:288:60//  
AJ235272  
R-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS,  
CpG island, complete sequence./.7.4e-107:554:95//AL031003

25 R-HEMBA1007300//Caenorhabditis elegans cosmid C48C5./.0.22:474:59//U39994  
R-HEMBA1007301  
R-HEMBA1007319//Campylobacter jejuni repetitive DNA, clone pINT./.4.9e-08:524:58//Y14425  
R-HEMBA1007320//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SE-  
QUENCE./.3.4e-16:244:71//AP000043

30 R-HEMBA1007322//Homo sapiens BAC clone RG324D18 from 7p15-p21, complete sequence./.3.9e-83:383:85//  
AC005251  
R-HEMBA1007327//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 7706, WORKING  
DRAFT SEQUENCE./.1.6e-38:533:71//Z96804  
R-HEMBA1007341//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268D13, WORKING  
DRAFT SEQUENCE./.3.6e-21:394:66//AL023513

35 R-HEMBA1007342//Human BAC clone GS368F15 from 7q31, complete sequence./.1.7e-15:190:73//AC003080  
R-HEMBA1007347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone N38G6, WORKING  
DRAFT SEQUENCE./.2.2e-47:455:77//Z96802  
R-HEMBB1000005//Homo sapiens 3p21.1-9 PAC RPCI4-793P23 (Roswell Park Cancer Institute Human PAC Li-  
brary) complete sequence./.1.1e-62:539:79//AC006208

40 R-HEMBB1000008//Homo sapiens chromosome 17, clone hCIT.211\_P\_7, complete sequence./.1.2e-36:285:83//  
AC003665  
R-HEMBB1000018//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces./.1.2e-  
51:416:79//AC004820  
R-HEMBB1000024//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs  
45 and polymorphic CA repeat./.3.9e-18:211:79//Z95113  
R-HEMBB1000025//HS\_3064\_B2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3064 Col=14 Row=D, genomic survey sequence./.5.9e-40:254:90//AQ132765  
R-HEMBB1000030//Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein  
family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS, complete  
50 sequence./.1.5e-32:452:70//Z85986  
R-HEMBB1000036//CIT-HSP-2024L15.TF CIT-HSP Homo sapiens genomic clone 2024L15, genomic survey se-  
quence./.9.3e-63:541:77//B66264  
R-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds./.7.6e-91:467:97//  
AF084928

55 R-HEMBB1000039//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence./.2.4e-44:456:  
68//AC005291  
R-HEMBB1000044//Human BAC clone RG016J04 from 7q21, complete sequence./.1.4e-54:307:80//AC002064  
R-HEMBB1000048//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence./.3.8e-

09:330:63//AC002300  
R-HEMBB1000050//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//6.7e-12:225:65//Z94056

5 R-HEMBB1000054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//8.9e-76:557:82//AL033521

R-HEMBB1000055//Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds.//1.6e-88:350:86//M81806

10 R-HEMBB1000059//Homo sapiens clone DJ0850I01, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.9e-12:356:65//AC006009

R-HEMBB1000083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.7e-41:311:82//AC004840

R-HEMBB1000089//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-34:314:78//AC005520

15 R-HEMBB1000099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//8.8e-32:434:71//AL008715

R-HEMBB1000103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs.//2.5e-16:207:74//Z95115

20 R-HEMBB1000113//HS\_3013\_A1\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3013 Col=15 Row=C, genomic survey sequence.//0.94:211:63//AQ118730

R-HEMBB1000119//Homo sapiens ASMTL gene.//1.9e-106:531:96//Y15521

R-HEMBB1000136//Human Chromosome X, complete sequence.//0.00073:359:59//AC002407

R-HEMBB1000141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//6.8e-41:280:74//AF043945

25 R-HEMBB1000144//Homo sapiens chromosome 17, clone hCIT.507\_E\_2, complete sequence.//0.00083:206:66//AC004134

R-HEMBB1000173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//2.5e-82:401:90//AC004085

30 R-HEMBB1000175  
R-HEMBB1000198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.91:428:56//AL021368

35 R-HEMBB1000215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence.//4.4e-54:298:91//AL021397

40 R-HEMBB1000217  
R-HEMBB1000218//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.8e-32:517:70//AC004216

R-HEMBB1000226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island.//2.5e-77:450:92//Z69706

45 R-HEMBB1000240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//4.1e-05:310:62//AF029308

R-HEMBB1000244//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//1.3e-43:278:85//AL034420

50 R-HEMBB1000250//Human DNA sequence from clone 34B20 on chromosome 6p21.31-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein S10 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-16:484:64//AL031777 R-HEMBB1000258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//4.3e-11:286:67//U91328

55 R-HEMBB1000264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//1.2e-42:406:79//AF079765

R-HEMBB1000266//RPCI11-76C20.TV RPCI11 Homo sapiens genomic clone R-76C20, genomic survey sequence.//1.0:232:59//AQ265533

R-HEMBB1000272//HS\_3032\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence./.0.0082:209:62//AQ096702  
R-HEMBB1000274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence./1.6e-45:277:72//AC000053

5 R-HEMBB1000284//Homo sapiens full-length insert cDNA clone YY88A05./.6.9e-112:572:96//AF088018  
R-HEMBB1000307//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence./.5.7e-96:523:93//AC005244  
R-HEMBB1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE./.7.5e-21:218:67//AL023693

10 R-HEMBB1000317//Toxoplasma gondii chloroplast, complete genome./.0.062:354:58//U87145  
R-HEMBB1000318//Human DNA sequence from PAC 292H14 on chromosome Xp21. Contains STS and CA repeat polymorphism./4.5e-52:302:81//AL008710  
R-HEMBB1000335//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence./1.9e-16:139:84//AC005179

15 R-HEMBB1000336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease./.0.0062:231:64//AJ003147  
R-HEMBB1000337//CIT-HSP-2329010.TF CIT-HSP Homo sapiens genomic clone 2329O10, genomic survey sequence./1.2e-31:192:92//AQ035976  
R-HEMBB1000338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence./1.9e-39:477:71//AC004605

20 R-HEMBB1000339//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE./4.1e-54:357:76//AL031681  
R-HEMBB1000341//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence./1.8e-19:501:63//AC002350

25 R-HEMBB1000343//Homo sapiens chromosome 16, cosmid clone 367E12 (LANL), complete sequence./.3.6e-41:457:72//AC004644  
R-HEMBB1000354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS./.7.2e-36:325:74//Z98751  
R-HEMBB1000369//Homo sapiens chromosome 4 clone B366O24 map 4q25, complete sequence./.9.0e-25:179:79//AC004067

30 R-HEMBB10003741//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING DRAFT SEQUENCE./.8.4e-58:332:79//Z97199  
R-HEMBB1000376//Homo sapiens DNA for amyloid precursor protein, complete cds./.2.1e-47:309:88//D87675  
R-HEMBB1000391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces./.5.7e-46:302:85//AC005080

35 R-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds./.1.0e-107:531:97//AF076838  
R-HEMBB1000402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence./.1.1e-25:441:67//Z98052  
R-HEMBB1000404//HS\_2246\_A2\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence./.0.0025:196:63//AQ084251

40 R-HEMBB1000420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence./1.2e-29:358:72//AC000053  
R-HEMBB1000434//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence./.2.8e-51:299:89//AC004069  
R-HEMBB1000438//HS\_2239\_B2\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence./.1.3e-10:76:100//AQ067700  
R-HEMBB1000441//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE./.4.4e-60:281:90//Z82207

45 R-HEMBB1000449//Homo sapiens clone DJ0898O18, WORKING DRAFT SEQUENCE, 8 unordered pieces./.4.8e-11:228:68//AC004920  
R-HEMBB1000455//Homo sapiens clone GS051M12, complete sequence./.3.1e-14:388:65//AC005007  
R-HEMBB1000472//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence./.4.9e-34:320:79//AC003104

50 R-HEMBB1000480//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence./.3.4e-36:285:82//Z83849  
R-HEMBB1000487

R-HEMBB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE./.1.5e-34:281:81//AL034423

R-HEMBB1000491//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island./.8.5e-37:483:72//Z93023

5 R-HEMBB1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence./.7.6e-14:217:71//AL022721

10 R-HEMBB1000510//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE./.7.1e-44:221:80//AL033397

R-HEMBB1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence./.3.5e-51:280:90//AC002477

15 R-HEMBB1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence./.1.7e-53:304:82//AC004079

R-HEMBB1000530//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence./.4.2e-74:428:92//AC006236

R-HEMBB1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence./.5.6e-13:112:80//U91321

20 R-HEMBB1000554//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE./.5.1e-14:239:63//Z83824

R-HEMBB1000556//Homo sapiens enveloplakin (EVPL) mRNA, complete cds./.0.031:275:60//U53786

R-HEMBB1000564//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence./.3.1e-17:227:76//AC005914

25 R-HEMBB1000573//Borrelia afzelii (strain NT28) DNA, internal transcribed spacer./.0.078:161:63//D84405

R-HEMBB1000575//Homo sapiens chromosome 17, clone hRPC.859\_O\_20, complete sequence./.7.2e-52:260:80//AC003695

R-HEMBB1000586//Human DNA sequence from cosmid V210E9, between markers DDX366 and DDX87 on chromosome X./.2.0e-33:305:79//Z70280

30 R-HEMBB1000589//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence./.1.3e-14:409:65//AC005208

R-HEMBB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence./.6.2e-39:493:71//AC005184

35 R-HEMBB1000592//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence./.1.6e-08:254:64//AC005831

R-HEMBB1000598//Homo sapiens chromosome 11 pac pDJ159ol, complete sequence./.3.3e-38:407:76//AC000381

R-HEMBB1000623//CIT-HSP-2374P17.TR CIT-HSP Homo sapiens genomic clone 2374P17, genomic survey sequence./.1.3e-41:212:100//AQ109717

40 R-HEMBB1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence./.5.2e-31:319:78//AL022724

R-HEMBB1000631//Sequence 28 from patent US 5708157./.6.8e-20:208:80//I80058

R-HEMBB1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces./.7.4e-47:457:75//AC004176

45 R-HEMBB1000637//Human BAC clone RG094H21 from 7q21-q22, complete sequence./.2.9e-45:263:87//AC003085

R-HEMBB1000638//Genomic sequence from Human 6, complete sequence./.9.1e-34:375:73//AC002112

50 R-HEMBB1000643//HS\_2242\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=14 Row=C, genomic survey sequence./.0.010:239:60//AQ065993

R-HEMBB1000649//Homo sapiens RBP56/hTAFII68 gene, exon 7./.8.3e-63:306:100//AB010061

R-HEMBB1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMPR (GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with a polymorphic CA repeat./.3.3e-14:450:64//AL009031

55 R-HEMBB1000665//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence./.0.98:251:63//AB005247

R-HEMBB1000671//Human DNA sequence from PAC 106C24, between markers DDX294 and DDX730 on chro-

mosome X.//6.8e-58:296:85//Z83313  
R-HEMBB1000673//CITBI-E1-2506F20.TR CITBI-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence.//0.98:71:76//AQ264731  
R-HEMBB1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//2.6e-11:153:77//AL031584  
5 R-nnnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds.//2.0e-50:287:93//AF040723  
R-HEMBB1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943  
R-HEMBB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462C17, WORKING  
10 DRAFT SEQUENCE.//4.7e-10:358:64//AL033380  
R-HEMBB1000709//RPCI11-79A8.TV RPCI11 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374  
R-HEMBB1000725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence.//0.00018:386:60//AB017066  
15 R-HEMBB1000726//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//1.5e-48:316:  
88//AC004990  
R-HEMBB1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//  
AC004875  
R-HEMBB1000749//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-  
20 51:438:80//AC005069  
R-HEMBB1000763//Plasmid Col Ib-P9 (from E.coli K12) colicin Ib promoter region and 5' coding region.//1.0:115:  
63//K02071  
R-HEMBB1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:  
86//U83205  
25 R-HEMBB1000781//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//0.00054:  
154:67//AC003046  
R-HEMBB1000789//RPCI11-2I14.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2I14, genomic survey se-  
quence.//3.0e-09:299:64//B63628  
R-HEMBB1000790//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//4.5e-46:185:  
30 85//U95740  
R-HEMBB1000794//HS\_3253\_A1\_G06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291  
R-HEMBB1000807  
R-HEMBB1000810//Human BAC clone RG114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542  
35 R-HEMBB1000821  
R-HEMBB1000822//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey se-  
quence.//4.5e-08:278:64//AQ279944  
R-HEMBB1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SE-  
QUENCE.//1.2e-44:521:72//AP000043  
40 R-HEMBB1000827//Homo sapiens clone DJ0981O07, complete sequence.//6.8e-43:319:84//AC006017  
R-HEMBB1000831//HS\_3247\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850  
R-HEMBB1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Mus-  
45 cular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane  
protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five pre-  
dicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete se-  
quence.//4.2e-17:167:80//AL021368  
R-HEMBB1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
7.9e-26:220:73//AC005283  
50 R-HEMBB1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//  
AC004086  
R-HEMBB1000852//HS\_3075\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816  
R-HEMBB1000870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 72E17, WORKING  
55 DRAFT SEQUENCE.//1.8e-44:454:75//AL033523  
R-HEMBB1000876//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin  
Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//0.0016:227:65//AL024474  
R-HEMBB1000883//Homo sapiens chromosome 19, cosmid F19678, complete sequence.//0.62:238:62//

AC005621  
R-HEMBB1000887//Synthetic human/adenovirus type 5 recombination junction.//9.9e-24:275:76//M34061  
R-HEMBB1000888//CIT-HSP-2282A13.TR CIT-HSP Homo sapiens genomic clone 2282A13, genomic survey sequence.//2.4e-05:310:60//AQ000826

5 R-HEMBB1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//  
6.5e-44:305:84//AC005995  
R-HEMBB1000893//Homo sapiens BAC clone RG363E19 from 7q31.1, complete sequence.//3.7e-30:265:80//  
AC004492

10 R-HEMBB1000908//RPCI11-13P12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13P12, genomic survey sequence.//0.98:183:61//B76199  
R-HEMBB1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//1.7e-28:302:76//AC000024  
R-HEMBB1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//4.1e-34:314:76//AC003037

15 R-HEMBB1000915//Human chromosome 16p11.2-p12 BAC clone CIT987SK-224D6 complete sequence.//6.3e-  
09:536:59//U95739  
R-HEMBB1000917//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING  
DRAFT SEQUENCE.//1.6e-47:234:86//Z93015  
R-HEMBB1000927

20 R-HEMBB1000947//CIT-HSP-2287M13.TF CIT-HSP Homo sapiens genomic clone 2287M13, genomic survey se-  
quence.//0.090:115:69//B99228  
R-HEMBB1000959//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//5.7e-89:544:90//  
AC003098

25 R-HEMBB1000973//Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence.//  
0.038:377:58//AC005560  
R-HEMBB1000975//Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence.//  
1.0e-05:342:62//AC006234

30 R-HEMBB1000981//CIT-HSP-2386J13.TF.1 CIT-HSP Homo sapiens genomic clone 2386J13, genomic survey  
sequence.//1.1e-18:231:74//AQ239443  
R-HEMBB1000985//HS\_3184\_A1\_D12\_T7 CIT Approved Human Genomic Sperm Library D. Homo sapiens ge-  
nomic clone Plate=3184 Col=23 Row=G, genomic survey sequence.//6.3e-52:286:95//AQ150008  
R-HEMBB1000991

35 R-HEMBB1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3,  
complete sequence.//1.4e-42:343:81//AC002368  
R-HEMBB1001004

R-HEMBB1001008//CITBI-E1-2504L23.TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey se-  
quence.//3.1e-57:317:94//AQ262056

40 R-HEMBB1001011//HS\_3017\_B1\_G03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3017 Col=5 Row=N, genomic survey sequence.//7.3e-34:237:86//AQ101944  
R-HEMBB1001014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING  
DRAFT SEQUENCE.//2.4e-49:417:80//AL031662

R-HEMBB1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete se-  
quence.//7.6e-41:303:76//AC002549

45 R-HEMBB1001024//Homo sapiens (subclone 2\_g5 from P1 H16) DNA sequence.//7.4e-48:341:85//L48475  
R-HEMBB1001037//Homo sapiens 22q11 BAC Clone 489d1 In MDR Region, complete sequence.//2.0e-50:416:  
82//AC005527  
R-HEMBB1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//8.4e-22:288:71//  
AC004699

50 R-HEMBB1001051//H.sapiens mRNA for FAN protein.//7.1e-18:114:98//X96586  
R-HEMBB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
6.1e-94:520:93//AC006014

R-HEMBB1001058//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//1.1e-56:242:82//  
AC004187

55 R-HEMBB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.2e-66:323:81//  
U49973  
R-HEMBB1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING  
DRAFT SEQUENCE.//4.0e-114:556:98//AL034375  
R-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.8e-105:512:97//AF034803

- R-HEMBB1001096//Human DNA sequence from PAC 246O8, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//2.4e-13:225:69//Z76735
- 5 R-HEMBB1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.4e-35:295:80//AL022577
- R-HEMBB1001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE.//7.9e-46:380:80//AL031431
- 10 R-HEMBB1001114//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains gly-pican-3 precursor (intestinal protein OCI-5) (GTR2-2),5'UTR. ESTs, STS.//1.1e-38:306:84//Z99570
- R-HEMBB1001117//RPCI11-35I8.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35I8, genomic survey sequence.//1.5e-08:67:100//AQ047113
- R-HEMBB1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//9.0e-26:481:67//AC003071
- 15 R-HEMBB1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.045:127:69//Z99495
- R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds.//5.0e-23:285:73//M25077
- 20 R-HEMBB1001137//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-09, complete sequence.//2.5e-07:334:62//AL010222
- R-HEMBB1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequence.//2.5e-46:412:79//AC002564
- R-HEMBB1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904
- 25 R-HEMBB1001153//RPCI11-10L7.TP RPCI-11 Homo sapiens genomic clone RPCI-11-10L7, genomic survey sequence.//2.3e-34:213:82//B71766
- R-HEMBB1001169//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//0.040:465:56//AC003070
- R-nnnnnnnnnnnn//Sequence 1 from patent US 5618695.//2.8e-15:176:80//I40055
- R-HEMBB1001177
- 30 R-HEMBB1001182//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//1.9e-05:174:70//AL010226
- R-HEMBB1001199
- R-HEMBB1001208
- 35 R-HEMBB1001209//RPCI11-41E13.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41E13, genomic survey sequence.//1.1e-95:473:97//AQ029098
- R-HEMBB1001210//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//6.2e-08:412:61//AC005199
- R-HEMBB1001218//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//1.0e-46:498:74//B75158
- 40 R-HEMBB1001221//RPCI11-62024.TJ RPCI11 Homo sapiens genomic clone R-62024, genomic survey sequence.//3.2e-09:215:68//AQ200950
- R-HEMBB1001234
- R-HEMBB1001242
- R-HEMBB1001249//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.4e-33:361:72//AC005377
- R-HEMBB1001253//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//3.8e-105:517:98//AF042089
- R-HEMBB1001254//Methanococcus jannaschii section 3 of 150 of the complete genome.//0.96:203:61//U67461
- 50 R-HEMBB1001267//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.8e-39:320:80//Z98046
- R-HEMBB1001271//Homo sapiens chromosome 17, clone hRPK.349\_A\_8, complete sequence.//3.9e-47:494:75//AC005544
- 55 R-HEMBB1001282//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//0.0011:97:79//AL031428
- R-HEMBB1001288
- R-HEMBB1001289//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//2.0e-

31:301:78//AC005601  
R-HEMBB1001294//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence//0.053:283:60//  
AC003083  
R-HEMBB1001302  
5 R-HEMBB1001304//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING  
DRAFT SEQUENCE//6.3e-15:396:64//AL033397  
R-HEMBB1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8SpN6, genomic survey sequence//  
3.4e-42:293:86//AG013777  
R-HEMBB1001315//Human NFE genomic fragment//7.5e-30:243:78//M98511  
10 R-HEMBB1001317//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence//2.3e-39:301:  
82//AC004585  
R-HEMBB1001326//HS\_3054\_A1\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3054 Col=23 Row=K, genomic survey sequence//0.90:117:63//AQ106096  
R-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c//  
15 0.037:103:77//D63850  
R-HEMBB1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete  
sequence//9.1e-19:229:77//AC003037  
R-HEMBB1001337  
R-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region//2.9e-45:551:72//U85056  
20 R-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mi-  
tochondrial protein, complete cds//2.7e-59:292:99//AF097441  
R-HEMBB1001348//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces//  
9.1e-41:326:82//AC004859  
R-HEMBB1001356//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING  
25 DRAFT SEQUENCE//1.8e-11:213:67//Z82207  
R-HEMBB1001364//HS\_3050\_A2\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3050 Col=10 Row=K, genomic survey sequence//1.8e-21:158:91//AQ133940  
R-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete se-  
quence//4.1e-37:419:73//AC005876  
30 R-HEMBB1001367//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence//9.5e-15:201:  
75//U91326  
R-HEMBB1001369//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 477J10, WORKING  
DRAFT SEQUENCE//1.8e-28:224:83//AL021686  
R-HEMBB1001380//HS\_2267\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
35 nomic clone Plate=2267 Col=21 Row=L, genomic survey sequence//4.0e-14:100:95//AQ084896  
R-HEMBB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds//9.6e-55:312:81//  
AF071314  
R-HEMBB1001387//Homo sapiens chromosome 9, P1 clone 8660 (LBNL H105), complete sequence//1.0:166:  
63//AC003953  
40 R-HEMBB1001394//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence//1.4e-55:494:  
76//AC005549  
R-HEMBB1001410//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence//0.011:208:  
63//AC006204  
R-HEMBB1001424//Homo sapiens, WORKING DRAFT SEQUENCE, 76 unordered pieces//1.5e-22:325:69//  
45 AC002370  
R-HEMBB1001426//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library)  
complete sequence//1.3e-46:328:84//AC002350  
R-HEMBB1001429/// SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces//6.6e-105:550:95//AC006160  
50 R-HEMBB1001436  
R-HEMBB1001443//HS\_2228\_A1\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2228 Col=9 Row=C, genomic survey sequence//0.37:173:62//AQ066934  
R-HEMBB1001449//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces//  
2.7e-23:339:69//AC005522  
55 R-HEMBB1001454//Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence//1.1e-39:  
299:84//AC005355  
R-HEMBB1001458//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence//6.0e-05:  
486:59//AE001430

R-HEMBB1001463//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//1.2e-50:317:89//AC005154  
 R-HEMBB1001464//CIT-HSP-2370C10.TF CIT-HSP Homo sapiens genomic clone 2370C10, genomic survey sequence.//0.20:95:71//AQ107941  
 5 R-HEMBB1001482//Mus musculus clone OST20235, genomic survey sequence.//4.3e-09:192:70//AF046762  
 R-HEMBB1001500//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu<sup>++</sup>-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.9e-21:253:70//Z94801  
 R-HEMBB1001521//Mus musculus clone OST1209, genomic survey sequence.//7.5e-30:332:75//AF046642  
 R-HEMBB1001527//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.5e-10:55:483:76//AC005000  
 R-HEMBB1001531//Human BAC clone 7E17 from 12q, complete sequence.//1.3e-08:159:71//AC002070  
 R-HEMBB1001535//Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.//4.0e-30:286:79//Z74581  
 R-HEMBB1001536//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.6e-39:342:80//U73169  
 15 R-HEMBB1001537//Genomic sequence from Human 9q34, complete sequence.//3.7e-41:361:77//AC000394  
 R-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.//0.34:212:61//AC003049  
 R-HEMBB1001562//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//8.0e-20:40:267:88//AC002301  
 R-HEMBB1001564//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.1e-30:286:76//AC005225  
 R-HEMBB1001565//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.5e-15:194:75//AC004840  
 25 R-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//2.6e-33:234:79//AL031677  
 R-HEMBB1001586//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-30:371:74//AC005236  
 R-HEMBB1001588//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//8.0e-32:323:73//AC003106  
 30 R-HEMBB1001603//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-59, complete sequence.//0.034:302:59//AL010235  
 R-HEMBB1001618//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and Opg island.//7.1e-31:503:68//Z93023  
 35 R-HEMBB1001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539:72//AC002368  
 R-HEMBB1001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.3e-27:228:82//Z86062  
 40 R-HEMBB1001635//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//1.5e-23:407:69//AC004075  
 R-HEMBB1001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519:74//AC002368  
 R-HEMBB1001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSs, GSSs and 45 genomic marker D6S410, complete sequence.//1.9e-08:464:60//AL024506  
 R-HEMBB1001653//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318:82//AC002344  
 R-HEMBB1001665//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283:90//U14572  
 R-HEMBB1001668  
 50 R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//1.8e-115:573:97//AB014546  
 R-HEMBB1001684//Sequence 1 from patent US 5700927.//1.9e-40:343:77//I86429  
 R-HEMBB1001685//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete sequence.//2.6e-43:31:83//AC005411  
 R-HEMBB1001695  
 55 R-HEMBB1001704//CIT-HSP-2324C15.TR CIT-HSP Homo sapiens genomic clone 2324C15, genomic survey sequence.//0.0074:259:58//AQ028704  
 R-HEMBB1001706//Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.1e-34:296:80//AC004851

R-HEMBB1001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020  
R-HEMBB1001717//CIT-HSP-2378C19.TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992  
5 R-HEMBB1001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBNL H94), complete sequence.//1.8e-10:80:90//AC005613  
R-HEMBB1001736//CIT-HSP-2369K6.TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ075221  
10 R-HEMBB1001747//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671  
R-HEMBB1001749//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.4e-60:242:92//AC005829  
R-HEMBB1001753//RPCI11-59J22.TK RPCI11 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ200046  
15 R-HEMBB1001756//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//3.1e-18:395:67//AC004130  
R-HEMBB1001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050  
20 R-HEMBB1001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (I $\alpha$ lpha) and major histocompatibility protein class II beta chain (I $\beta$ eta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds; NG12 pseudogene, partial sequence; and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157  
R-HEMBB1001785//Torulopsis glabrata mitochondrial intergenic region ATPase 6 -ATPase 9 genes.//0.00073:  
25 189:65//X02170  
R-HEMBB1001797//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140  
R-HEMBB1001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391  
R-HEMBB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING  
30 DRAFT SEQUENCE.//1.3e-71:368:96//Z98882  
R-HEMBB1001816//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//8.4e-21:164:76//AJ006996  
R-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//1.7e-104:498:98//AF056209  
R-HEMBB1001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.2e-44:388:71//  
35 AC005328  
R-HEMBB1001839  
R-HEMBB1001850//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence.//0.00093:488:60//AB005241  
R-HEMBB1001863//Human poly(ADP-ribose) polymerase gene, 5' end.//1.2e-16:458:65//M60436  
40 R-HEMBB1001867//Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.//5.0e-31:399:74//Z68327  
R-HEMBB1001868//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.26:303:59//AB020754  
R-HEMBB1001869//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//7.0e-37:285:85//  
45 AC002553  
R-HEMBB1001872//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y44F5, WORKING DRAFT SEQUENCE.//0.093:367:58//AL009027  
R-HEMBB1001874  
R-HEMBB1001875//Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence.//0.037:406:60//AE001272  
50 R-HEMBB1001880//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//1.3e-49:461:77//AC005922  
R-HEMBB1001899//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y116A8, WORKING DRAFT SEQUENCE.//0.56:295:60//Z98858  
55 R-HEMBB1001905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//1.9e-28:181:75//AL022345  
R-HEMBB1001906  
R-HEMBB1001908//Genomic sequence from Human 17, complete sequence.//2.9e-36:274:76//AC001231

R-HEMBB1001910//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence./.3.5e-41:408:76//AC003070  
 R-HEMBB1001911//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE./.6.1e-64:310:89//AJ011929  
 5 R-HEMBB1001915//Mouse mRNA for arylhydrocarbon receptor, complete cds./.2.0e-20:220:78//D38417  
 R-HEMBB1001921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1141E15, WORKING DRAFT SEQUENCE./.1.9e-47:410:80//AL034422  
 R-HEMBB1001922//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence./.6.2e-32:378:74//AC004099  
 10 R-HEMBB1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces./.8.2e-41:304:84//AC000406  
 R-HEMBB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11./.8.3e-12:202:69//AB020867  
 15 R-HEMBB1001944//P.falciparum gene for beta subunit RNA polymerase./.0.00090:264:62//X75544  
 R-HEMBB1001945//Swietenia humilis DNA for simple tandem repeat (242bp)./.0.056:224:62//AJ000408  
 R-HEMBB1001947//RPCI11-60L13.TJ RPCI11 Homo sapiens genomic clone R-60L13, genomic survey sequence./.7.4e-23:146:94//AQ202335  
 R-HEMBB1001950//Human DNA sequence from clone 415G2 on chromosome 22 Contains synapsin IIIa exon 1, EST and GSS, complete sequence./.0.57:115:68//Z83846  
 20 R-HEMBB1001952//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces./.5.6e-36:283:84//AC004676  
 R-HEMBB1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces./.8.9e-60:334:82//AC005037  
 R-HEMBB1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces./.1.9e-25:56:18:77//AC005077  
 R-HEMBB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence./.3.2e-19:157:86//AC005736  
 R-HEMBB1001967//Homo sapiens DNA for amyloid precursor protein, complete cds./.5.7e-68:314:89//D87675  
 30 R-HEMBB1001973//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC E7.1 / cosmid 40M1, WORKING DRAFT SEQUENCE./.1.4e-37:484:70//AJ009617  
 R-HEMBB1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE./.2.1e-28:286:75//AL034417  
 R-HEMBB1001988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE./.6.9e-29:203:88//AL034420  
 35 R-HEMBB1001990//Homo sapiens full-length insert cDNA clone ZC33G03./.7.8e-95:456:99//AF086192  
 R-HEMBB1001996  
 R-HEMBB1001997//Homo sapiens clone RG050N15, WORKING DRAFT SEQUENCE, 26 unordered pieces./.6.4e-26:162:83//AC005055  
 R-HEMBB1002002//Human DNA sequence from PAC 2A2 on chromosome X contains ESTs./.8.2e-83:362:93//Z84816  
 40 R-HEMBB1002005//Homo sapiens chromosome 3p clone RPCI5-1034C16, WORKING DRAFT SEQUENCE, 45 unordered pieces./.8.5e-36:291:83//AC005903  
 R-HEMBB1002009//Homo sapiens clone DJ0828F13, complete sequence./.5.6e-08:307:65//AC004904  
 R-HEMBB1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 45 Plate=CT 821 Col=19 Row=E, genomic survey sequence./.1.9e-05:375:62//B36336  
 R-HEMBB1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic clone 2313E13, genomic survey sequence./.0.34:241:62//AQ028389  
 R-HEMBB1002043//Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence./.7.4e-35:297:82//AC005612  
 50 R-HEMBB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence./.5.8e-96:582:90//AC005740  
 R-HEMBB1002045//Homo sapiens chromosome 19, cosmid F22676, complete sequence./.4.7e-63:575:77//AC005778  
 R-HEMBB1002049//Human Chromosome X clone bWXD187, complete sequence./.1.9e-21:384:64//AC004383  
 55 R-HEMBB1002050//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence./.2.5e-37:368:76//AC005553  
 R-HEMBB1002068//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence./.0.30:167:65//AC004782

R-HEMBB1002069//Homo sapiens chromosome 19, cosmid R33516, complete sequence./.2.3e-73:449:84//AC004799  
 R-HEMBB1002092//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence./.3.8e-45:307:  
 87//AC005828  
 5 R-HEMBB1002094//Homo sapiens chromosome 19, cosmid R30538, complete sequence./.3.1e-47:457:76//  
 AC005943  
 R-HEMBB1002115//HS\_2223\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2223 Col=19 Row=N, genomic survey sequence./.3.0e-58:295:98//AQ152279  
 R-HEMBB1002139/\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence./.6.6e-49:283:93//U14573  
 10 R-HEMBB1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces./.  
 1.1e-45:451:76//AC006006  
 R-HEMBB1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16 map 10q25, complete sequence./.  
 1.3e-57:359:81//AC005881  
 R-HEMBB1002189//Human Chromosome 11 pac pDJ392a17, complete sequence./.4.5e-43:420:77//AC000385  
 15 R-HEMBB1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces./.  
 8.2e-33:340:64//AC004913  
 R-HEMBB1002193//Sequence 5 from patent US 5709858./.3.2e-23:154:92//I80846  
 R-HEMBB1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence./.2.6e-52:415:81//AF015148  
 R-HEMBB1002218//, complete sequence./.3.4e-17:178:82//AC005300  
 20 R-HEMBB1002232/\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052I22;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces./.1.6e-55:292:88//AC004599  
 R-HEMBB1002247//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence./.2.9e-13:227:  
 70//AC005829  
 R-HEMBB1002249//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING  
 25 DRAFT SEQUENCE./.1.1e-06:284:64//AL031733  
 R-HEMBB1002254//Human Chromosome X, WORKING DRAFT SEQUENCE, 6 unordered pieces./.6.3e-104:  
 593:91//AC002415  
 R-HEMBB1002255//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING  
 DRAFT SEQUENCE./.2.1e-40:284:85//Z93930  
 30 R-HEMBB1002266//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, com-  
 plete sequence./.1.3e-09:371:63//AL010216  
 R-HEMBB1002280//Homo sapiens PAC clone DJ0545C24 from 7q21-q22, complete sequence./.1.3e-39:247:86//  
 AC004534  
 R-HEMBB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence./.4.1e-84:549:86//U73642  
 35 R-HEMBB1002306//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence./.2.5e-10:164:71//  
 AC004129  
 R-HEMBB1002327//Homo sapiens BAC clone GS539F22 from 7p12-p14, complete sequence./.0.39:365:59//  
 AC005028  
 R-HEMBB1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic  
 40 clone Plate=CT 771 Col=9 Row=H, genomic survey sequence./.0.96:180:58//B39313  
 R-HEMBB1002340//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence./.7.9e-17:258:73//  
 AC004849  
 R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein./.6.9e-96:479:97//AJ010841  
 R-HEMBB1002358//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from  
 45 Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence./.2.3e-53:309:  
 83//AC002366  
 R-HEMBB1002359//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces./.  
 4.9e-27:350:74//AC005038  
 R-HEMBB1002364//Homo sapiens Xp22 PAC RPCI1-108M6 (Roswell Park Cancer Center PAC library) complete  
 50 sequence./.8.6e-53:302:79//AC003036  
 R-HEMBB1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapping to chromosome 11, band p13./.3.2e-  
 38:199:100//X04094  
 R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds./.3.2e-07:120:78//AF072467  
 R-HEMBB1002383//Human DNA sequence from cosmid U19H10 on chromosome X. Contains ESTs and CA re-  
 peat./.0.98:351:58//AL021182  
 55 R-HEMBB1002387//HS-1052-B2-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic  
 clone Plate=CT 774 Col=20 Row=N, genomic survey sequence./.2.0e-07:276:67//B41091  
 R-HEMBB1002415//Homo sapiens chromosome 17, clone hRPK.209\_D\_14, complete sequence./.1.4e-25:202:

79//AC005730  
R-HEMBB1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence./.3.6e-60:401:87//  
AC004799

5 R-HEMBB1002442//Homo sapiens clone UWGC:r9a from 6p21, complete sequence./.3.1e-51:358:81//AC006046  
R-HEMBB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING  
DRAFT SEQUENCE./.1.4e-115:557:98//AL034349

R-HEMBB1002457//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS  
and GSSs, complete sequence./.6.3e-37:338:80//AL031012

10 R-HEMBB1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of  
5) of the Complete Nucleotide Sequence./.9.7e-09:314:64//AE000659

R-HEMBB1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAI project).//0.42:110:  
74//AL021635

R-HEMBB1002489//Salvelinus fontinalis microsatellite sequence SFO-12./.6.6e-06:167:71//U50302

15 R-HEMBB1002492//RPCI11-74F21.TK RPCI11 Homo sapiens genomic clone R-74F21, genomic survey se-  
quence./.3.1e-14:410:63//AQ238960

R-HEMBB1002495//HS\_3220\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3220 Col=14 Row=K, genomic survey sequence./.1.3e-24:137:100//AQ180762

R-HEMBB1002502//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence./.9.6e-81:538:  
86//AC006120

20 R-HEMBB1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Trans-  
lation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete  
sequence./.0.0061:482:57//AL031313

R-HEMBB1002510//HS\_2179\_A1\_F03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2179 Col=5 Row=K, genomic survey sequence./.6.9e-35:423:72//AQ298309

25 R-HEMBB1002520//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING  
DRAFT SEQUENCE./.2.0e-62:201:85//AL033397

R-HEMBB1002522//Homo sapiens chromosome 5, Pac clone 61c2 (LBNL H139), complete sequence./.0.99:323:  
58//AC004225

R-HEMBB1002531

30 R-HEMBB1002534//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15,  
WORKING DRAFT SEQUENCE./.1.0e-61:380:79//AP000009

R-HEMBB1002545//RPCI11-2F3.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2F3, genomic survey se-  
quence./.3.5e-12:414:63//B63283

R-HEMBB1002550

35 R-HEMBB1002556/// SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces./.2.6e-62:299:85//AC006160

R-HEMBB1002579//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1141E15, WORK-  
ING DRAFT SEQUENCE./.1.7e-42:286:88//AL034422

R-HEMBB1002582//Homo sapiens clone DJ119N05, complete sequence./.3.0e-14:426:60//AC004968

40 R-HEMBB1002590//Homo sapiens clone RG132J19, complete sequence./.1.1e-30:392:74//AC005163

R-HEMBB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING  
DRAFT SEQUENCE./.8.5e-44:335:83//AL021707

R-HEMBB1002600//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC  
Library) complete sequence./.2.0e-105:470:96//AC005865

45 R-HEMBB1002601//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence./.1.3e-44:445:77//  
AC004223

R-HEMBB1002603//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence./.7.0e-40:321:82//  
AC006162

50 R-HEMBB1002607//CIT-HSP-2347D7.TF CIT-HSP Homo sapiens genomic clone 2347D7, genomic survey se-  
quence./.1.1e-44:234:98//AQ060197

R-HEMBB1002610//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence./.7.0e-22:455:  
65//U91321

R-HEMBB1002613//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC  
Library) complete sequence./.3.0e-72:302:85//AC005908

55 R-HEMBB1002614//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Li-  
brary) complete sequence./.3.8e-10:512:60//AC004801

R-HEMBB1002617//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces./.6.8e-  
24:486:63//AC005520

R-HEMBB1002623//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence./.2.4e-41:326:  
83//AC004953

R-HEMBB1002635//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SE-  
QUENCE, 39 unordered pieces./.2.6e-42:360:80//AC005910

5 R-HEMBB1002664//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence./.9.1e-51:335:87//  
AF042090

R-HEMBB1002677//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2),  
CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein  
(cg2), and CG7 (cg7) genes, complete cds./.0.0011:399:59//AF030694

10 R-HEMBB1002683//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence./.4.1e-55:515:76//  
AF042090

R-HEMBB1002684//Human BAC clone RG066D11 from 7q22, complete sequence./.1.7e-18:504:62//AC002430

R-HEMBB1002686//Homo sapiens full-length insert cDNA clone ZC65D06./.7.0e-85:413:99//AF086217

15 R-HEMBB1002692//Homo sapiens 12p13.3 BAC RPCI11-319E16 (Roswell Park Cancer Institute Human BAC  
Library) complete sequence./.9.8e-69:505:82//AC006206

R-HEMBB1002697//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
DRAFT SEQUENCE, 8 unordered pieces./.0.26:390:58//AC004153

R-HEMBB1002699//Human NFE genomic fragment./.8.0e-32:226:79//M98511

20 R-HEMBB1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sapiens genomic clone 344K23, genomic survey se-  
quence./.8.6e-43:351:8011859764

R-HEMBB1002705//Plasmodium yoelii rhoptry protein, complete cds./.0.0064:454:59//L27838

R-HEMBB1002712//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat  
and GSSs, complete sequence./.9.6e-09:187:67//Z98052

25 R-MAMMA1000009//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces./.  
4.1e-21:201:80//AC005037

R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence./.4.2e-48:  
306:82//AF015720

R-MAMMA1000020//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl  
pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence./.1.4e-41:306:  
30 86//AL022163

R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmo-  
plakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence./.6.1e-36:281:83//AL031058

R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete se-  
quence./.1.3e-67:321:88//AC000090

35 R-MAMMA1000045//Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence./.6.7e-86:559:  
86//AC004054

R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bcamicrol./.0.79:63:77//AF025889

R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S  
40 Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an  
intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice  
products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a  
protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first  
two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135  
SynGAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence./.1.6e-53:397:83//  
AL021366

R-MAMMA1000069//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces./.  
2.0e-37:295:83//AC005057

R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SE-  
QUENCE, 35 unordered pieces./.7.1e-45:296:88//AC005867

50 R-MAMMA1000085

R-MAMMA1000092//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORK-  
ING DRAFT SEQUENCE./.8.2e-34:539:69//AL034410

R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence./.3.4e-39:297:85//  
AC003976

55 R-MAMMA1000117//Homo sapiens p47-phox (NCF1) pseudogene, clone P38, exon 5./.2.6e-07:162:67//U69641

R-MAMMA1000129//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces./.6.1e-  
13:141:80//AC004882

R-MAMMA1000133

R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete sequence./.9.7e-18:171:80//AC005328

R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces./.1.2e-49:366:75//AC005000

5 R-MAMMA1000143//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC D9.2, WORKING DRAFT SEQUENCE./.3.9e-56:318:89//AJ009615

R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence./.2.1e-68:562:78//AL022476

10 R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces./.5.3e-06:408:58//AC005089

R-MAMMA1000171//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence./.1.5e-42:173:89//AQ037381

15 R-MAMMA1000173

R-MAMMA1000175//H.sapiens CpG island DNA genomic Mse1 fragment, clone 186c5, reverse read cpg186c5.rt1b./.0.072:90:72//Z57594

R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence./.1.5e-44:445:75//AC004552

20 R-MAMMA1000198//Homo sapiens clone c102D0968, complete sequence./.1.9e-23:135:85//AF038667

R-MAMMA1000221//HS\_3242\_B2\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, genomic survey sequence./.0.031:167:67//AQ220385

R-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE./.4.5e-36:487:71//AL031728

25 R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence./.6.2e-07:445:59//AL022401

R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complete sequence./.1.6e-25:390:69//AC005266

30 R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence./.1.1e-37:327:80//AL008715

R-MAMMA1000257//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE./.1.3e-22:281:74//AL034549

35 R-MAMMA1000264//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces./.1.7e-29:337:67//AC003656

R-MAMMA1000266//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE./.7.7e-37:339:80//AL031670

R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence./.1.2e-40:283:86//AF001549

40 R-MAMMA1000277//CIT-HSP-516K6.TP CIT-HSP Homo sapiens genomic clone 516K6, genomic survey sequence./.3.0e-29:265:80//B49900

R-MAMMA1000278//Sequence 25 from patent US 5708157./.2.6e-39:282:82//I80056

R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence./.1.6e-52:295:84//AC004494

45 R-MAMMA1000284//CITBI-E1-2522B20.TF CITBI-E1 Homo sapiens genomic clone 2522B20, genomic survey sequence./.1.8e-11:288:61//AQ280722

R-MAMMA1000287

R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence./.4.1e-16:169:77//AC005553

50 R-MAMMA1000307//RPCI11-89L1.TV RPCI11 Homo sapiens genomic clone R-89L1, genomic survey sequence./.1.3e-86:429:97//AQ284795

R-MAMMA1000309//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds./.0.0020:384:60//AF029779

55 R-MAMMA1000312//Ichneutes sp. 16S ribosomal RNA gene, partial sequence./.0.0026:310:60//AF003518

R-MAMMA1000313//Human cosmid Xq28\_IA649, complete sequence./.1.5e-26:317:67//U82694  
 R-MAMMA1000331//Homo sapiens clone DJ1007F24, WORKING DRAFT SEQUENCE, 5 unordered pieces./.3.1e-39:277:86//AC004947  
 5 R-MAMMA1000339//Homo sapiens clone HS19.1 Alu-Ya5 sequence./.3.2e-44:180:89//AF015147  
 R-MAMMA1000340//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence./.0.97:  
 293:64//AE001388  
 R-MAMMA1000348//Homo sapiens BAC129, complete sequence./.4.4e-27:365:72//U85195  
 R-MAMMA1000356//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence./.0.73:  
 332:61//AC002493  
 10 R-MAMMA1000360//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence./.4.6e-80:279:89//  
 AC005189  
 R-MAMMA1000361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 753D4, WORKING  
 DRAFT SEQUENCE./.7.8e-18:346:63//AL031676  
 15 R-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORK-  
 ING DRAFT SEQUENCE./.5.3e-40:299:83//AL022344  
 R-MAMMA1000385//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310013, WORKING  
 DRAFT SEQUENCE./.1.0e-28:225:84//AL031658  
 R-MAMMA1000388//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey se-  
 quence./.4.7e-60:298:99//AQ038102  
 20 R-MAMMA1000395  
 R-MAMMA1000402//Homo sapiens PAC clone DJ1107K12 from 7p12-p14, complete sequence./.1.4e-84:276:88//  
 AC004692  
 R-MAMMA1000410//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence./.6.7e-35:360:  
 76//AC002394  
 25 R-MAMMA1000413//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence./.3.1e-69:327:  
 79//AC004662  
 R-MAMMA1000414//Homo sapiens DNA sequence from PAC 164L12 on chromosome Xq13.1-Xq21.2. Contains  
 GSS (BAC end sequence),STS./.3.6e-41:180:87//AL009028  
 R-MAMMA1000416//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces./.  
 3.1e-59:478:77//AC005377  
 30 R-MAMMA1000421//Human coxVIb gene, last exon and flanking sequence./.5.3e-53:294:82//X58139  
 R-MAMMA1000422//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8B22, WORKING  
 DRAFT SEQUENCE./.1.0:252:59//AL031737  
 R-MAMMA1000423//Homo sapiens clone DA0065G23, complete sequence./.2.0e-50:491:76//AC004816  
 35 R-MAMMA1000424//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribos-  
 mal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat./.3.5e-40:340:80//Z98950  
 R-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds./.0.0019:87:79//AF062484  
 R-MAMMA1000431//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces./.  
 2.0e-58:564:77//AC004821  
 40 R-MAMMA1000444//Human BAC clone RG126M09 from 7q21-q22, complete sequence./.3.0e-43:328:83//  
 AC002067  
 R-MAMMA1000446//Human chromosome X clone Qc15B1, complete sequence./.0.95:209:65//U82672  
 R-MAMMA1000458//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence./.  
 0.99:182:61//AB019236  
 45 R-MAMMA1000468  
 R-MAMMA1000472//Homo sapiens genomic DNA, 21q region, clone: 655M9N34, genomic survey sequence./.  
 1.0e-38:142:88//AG010148  
 R-MAMMA1000478//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING  
 DRAFT SEQUENCE./.1.3e-37:286:83//Z93015  
 50 R-MAMMA1000483//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey se-  
 quence./.4.3e-34:158:86//B54637  
 R-MAMMA1000490//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence./.4.2e-98:569:90//  
 AC006130  
 R-MAMMA1000500//Human BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds./.1.2e-41:  
 334:79//L78833  
 55 R-MAMMA1000501//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORK-  
 ING DRAFT SEQUENCE./.1.4e-38:250:84//AL031118  
 R-MAMMA1000516//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING

DRAFT SEQUENCE://1.3e-43:318:83//Z82207  
R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237  
gene, EST, STS, GSS, complete sequence://4.4e-13:202:73//AL031289  
R-MAMMA1000559//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING  
5 DRAFT SEQUENCE://2.2e-30:245:83//Z93015  
R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01\_183\_B\_7 map 10q24, WORKING DRAFT  
SEQUENCE, 1 ordered pieces://3.6e-39:281:80//U82205  
R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, complete cds.//9.2e-19:216:76//U18419  
R-MAMMA1000576  
10 R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//5.4e-53:297:  
85//AC005666  
R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUENCE, 4 unordered pieces.//  
1.2e-35:450:71//AC006018  
R-MAMMA1000594//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from cosmid 5L5, WORKING DRAFT  
15 SEQUENCE.//4.3e-26:293:75//AJ009613  
R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clone 2341F4, genomic survey se-  
quence.//0.83:110:70//AQ057131  
R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//  
2.6e-50:290:86//AC004956  
20 R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic clone 2334J18, genomic survey se-  
quence.//0.76:132:65//AQ038364  
R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, partial sequence.//6.8e-06:431:59//  
U06970  
R-MAMMA1000621//Human NBR2 mRNA, complete cds.//5.3e-27:258:80//U88573  
25 R-MAMMA1000623  
R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complete sequence.//3.3e-07:325:63//  
AC005498  
R-MAMMA1000643//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39B17, WORKING  
DRAFT SEQUENCE.//1.4e-06:236:68//AL023656  
30 R-MAMMA1000664//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0326F06;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-40:338:81//AC004555  
R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4  
(syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-  
4) STS, GSS, CpG island, complete sequence.//1.2e-46:327:86//AL021578  
35 R-MAMMA1000670  
R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome 6p24. Contains STSs and GSSs,  
complete sequence.//2.2e-29:328:76//AL031785  
R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds.//0.21:247:63//AF054623  
R-MAMMA1000696//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered piec-  
40 es.//2.7e-46:464:71//AC004387  
R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
3.4e-09:244:66//AC005075  
R-MAMMA1000713//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
3.7e-51:439:74//AC005478  
45 R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, complete sequence.//2.8e-29:288:75//  
AC004694  
R-MAMMA1000718//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from  
Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//3.0e-37:231:  
91//AC002366  
50 R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//1.4e-35:299:81//  
AC005781  
R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl  
pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//3.9e-59:409:  
79//AL022163  
55 R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
9.4e-29:560:66//AC005077  
R-MAMMA1000732//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//  
2.4e-14:309:68//AC004832

R-MAMMA1000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE./.4.1e-29:377:71//AL008722

R-MAMMA1000734//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE./.2.0e-108:420:99//AL024507

5 R-MAMMA1000738//Human V beta T-cell receptor (TCRBV) gene locus./.6.6e-41:347:82//U03115

R-MAMMA1000744//T27O8-T7 TAMU Arabidopsis thaliana genomic clone T27O8, genomic survey sequence./.0.095:367:60//B20150

R-MAMMA1000746//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces./.7.4e-95:569:87//AC004661

10 R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequense./.1.3e-48:295:84//AC003071

R-MAMMA1000760//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence./.5.7e-45:347:82//Z82178

15 R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence./.1.1e-32:292:80//U73169

R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces./.2.5e-50:467:79//AC005412

R-MAMMA1000776//Human BAC clone GS552A01 from 7q21-q22, complete sequence./.1.0e-63:429:79//AC002454

20 R-MAMMA1000778//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3./.3.5e-25:234:81//Z95704

R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence./.0.0021:119:74//AL031120

25 R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3./.6.3e-08:269:64//AJ229042

R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence./.1.1e-36:261:80//AC005339

R-MAMMA1000831//CIT-HSP-2387J3.TF.1 CIT-HSP Homo sapiens genomic clone 2387J3, genomic survey sequence./.0.68:156:65//AQ240807

30 R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.726\_O\_12, WORKING DRAFT SEQUENCE, 6 unordered pieces./.4.6e-50:335:86//AC005517

R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence./.1.3e-40:322:77//U91323

R-MAMMA1000842//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE./.4.1e-44:471:74//Z97985

35 R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces./.0.85:394:60//AC004815

R-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE./.0.54:303:63//AL031744

40 R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete sequence./.1.7e-10:115:83//AF030876

R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete sequence./.5.0e-44:352:83//AC004263

R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complete sequence./.1.8e-10:149:74//AC00461

45 R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #16./.8.1e-05:205:66//AF009075

R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence./.2.9e-49:421:80//AC002364

50 R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence./.9.1e-41:302:83//AC002301

R-MAMMA1000867//Human BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds./.1.9e-17:500:61//L78833

R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LANL), complete sequenced./.1.2e-17:211:74//AC004653

55 R-MAMMA1000876//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence./.4.7e-09:160:65//AC003658

R-MAMMA1000877//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains

ESTs STS and CpG island.//3.2e-34:354:75//Z93023  
R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.4e-41:411:74//AC002425  
R-MAMMA1000883  
5 R-MAMMA1000897  
R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence.//1.3e-73:304:91//AC004506  
R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F14150, genomic sequence, complete sequence.//8.4e-23:194:83//AC003110  
10 R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ416i6, complete sequence.//1.5e-09:170:71//AC003024  
R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//8.3e-13:323:67//AC005247  
15 R-MAMMA1000921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//6.8e-28:333:72//AL034379  
R-MAMMA1000931//HS\_3227\_B1\_B03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=D, genomic survey sequence.//1.4e-55:443:79//AQ191777  
R-MAMMA1000940//Homo sapiens clone RG013F03, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:340:84//AC005046  
20 R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.8e-53:330:84//AC002347  
R-MAMMA1000942//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:391:74//AC004383  
R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.6e-75:566:81//AC002477  
25 R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence.//0.013:285:59//AL034559  
R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.2e-45:288:90//AC005096  
R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-108:561:96//AC006001  
30 R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.9e-41:287:87//AC004263  
R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-65:542:79//Z95152  
35 R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303..//3.2e-34:296:80//AJ011930  
R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequence.//1.7e-40:255:87//AF088219  
R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence.//2.5e-39:315:73//AC005190  
40 R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//2.4e-52:296:84//AC006101  
R-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//7.9e-88:432:98//AJ011929  
45 R-MAMMA1001021//Homo sapiens PAC clone DJ0859M06 from 7q11, complete sequence.//3.8e-39:286:87//AC004910  
R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-31:274:80//AC004913  
R-MAMMA1001030//Homo sapiens full-length insert cDNA clone ZD96C01.//3.2e-99:469:99//AF088074  
50 R-MAMMA1001035//RPCI-1-46G8Sp6 RPCI-1 Homo sapiens genomic clone RPCI-1-46G8Sp6, genomic survey sequence.//3.5e-49:270:90//AQ275285  
R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//1.1e-41:285:87//AF042089  
R-nnnnnnnnnnnnn  
55 R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.//1.3e-55:334:91//D84394  
R-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//1.7e-51:481:77//L25125

R-MAMMA1001067//CIT-HSP-2371K20.TF CIT-HSP Homo sapiens genomic clone 2371K20, genomic survey sequence.//7.2e-65:946:95//AQ111326  
R-MAMMA1001073  
5 R-MAMMA1001074//Homo sapiens BAC clone NH0400O10 from Y, complete sequence.//8.6e-33:457:69//AC006040  
R-MAMMA1001075//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.15:  
325:62//AC004605  
R-MAMMA1001078//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.6e-  
45:344:84//AC005609  
10 R-MAMMA1001082//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains  
EST, CA repeat, STS, GSS, CpG island.//8.5e-15:413:64//Z93403  
R-MAMMA1001091//Sequence 7 from patent US 5468610.//0.0027:159:64//I15499  
R-MAMMA1001092//Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.//2.0e-51:267:  
82//AC005951  
15 R-MAMMA1001105//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains gly-  
pican-3 precursor (intestinal protein OCI-5) (GTR2-2), 5'UTR. ESTs, STS.//6.9e-22:178:85//Z99570  
R-MAMMA1001110//Homo sapiens chromosome 17, clone HRPC1169K15, complete sequence.//3.0e-19:141:  
81//AC003963  
20 R-MAMMA1001126//Human DNA from overlapping chromosome 7 PAC and P1 clones containing the XRCC2  
gene, genomic sequence, complete sequence.//2.2e-46:462:75//AC003109  
R-MAMMA1001133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING  
DRAFT SEQUENCE.//1.8e-68:455:86//AL031847  
R-MAMMA1001139//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING  
DRAFT SEQUENCE.//7.1e-09:100:84//AL022345  
25 R-MAMMA1001143//Papio hamadryas lipoprotein lipase (LPL) gene, intron 7.//1.9e-49:362:85//U73684  
R-MAMMA1001145//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//9.5e-49:512:  
74//AC005922  
R-MAMMA1001154//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-88D1 ~complete genomic se-  
quence, complete sequence.//1.5e-29:305:76//AC002289  
30 R-MAMMA1001161//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island,  
complete sequence.//1.1e-64:339:90//AL031286  
R-MAMMA1001162//Human DNA from cosmid DNA MMDB (f10080) and MMDC (f13544) from chromosome  
19q13.3 (obtained by automated sequence analysis).//3.4e-09:243:64//M89651  
R-MAMMA1001181//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered piec-  
es.//3.7e-29:351:74//AC004387  
35 R-MAMMA1001186//Homo sapiens chromosome 19, cosmid R28778, complete sequence.//2.2e-25:415:68//  
AC006125  
R-MAMMA1001191//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5  
of 5) of the Complete Nucleotide Sequence.//0.99:243:61//AE000662  
40 R-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//8.0e-57:223:86//U29156  
R-MAMMA1001202//Mus musculus clone OST13722, genomic survey sequence.//1.0e-30:220:85//AF046748  
R-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2  
ordered pieces.//8.9e-61:567:78//AC005412  
R-MAMMA1001206//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//4.6e-08:  
442:61//AC004763  
R-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//1.3e-117:564:  
97//AC005393  
R-MAMMA1001220//HS-1023-A1-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic  
clone Plate=CT 802 Col=19 Row=M, genomic survey sequence.//6.0e-16:276:68//B33708  
50 R-MAMMA1001222//F17E12TFB IGF Arabidopsis thaliana genomic clone F17E12, genomic survey sequence.//  
0.041:277:61//B97762  
R-MAMMA1001243  
R-MAMMA1001244//HS-1058-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo-sapiens genomic  
clone Plate=CT 780 Col=2 Row=M, genomic survey sequence.//3.5e-05:104:74//B43862  
55 R-MAMMA1001249//H.sapiens DNA for matrix attachment region.//0.0013:95:75//Z54221  
R-MAMMA1001256//Human BAC clone GS188P18, complete sequence.//3.4e-32:356:74//AC000115  
R-MAMMA1001259  
R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//6.3e-20:226:75//AB014561

R-MAMMA1001268//Human DNA sequence from PAC 225D2 on chromosome Xq21. Contains ESTs, CA repeat.//  
1.1e-47:352:85//Z95124  
R-MAMMA1001271  
R-MAMMA1001274//H.sapiens DNA for trapped exon (ID HMC07C06), genomic survey sequence.//3.1e-40:232:  
5 93//X88457  
R-MAMMA1001280//Homo sapiens full-length insert cDNA clone YW26C09.//1.9e-112:574:95//AF087976  
R-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three  
novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB  
10 gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and  
GSSs, complete sequence.//2.9e-114:582:96//AL022314  
R-MAMMA1001296//Human DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Contains an unknown  
gene coding for three alternative mRNAs. Contains ESTs, STSs, a BAC end-sequence (GSS) and a CA repeat  
polymorphism.//1.9e-64:268:88//AL008730  
R-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.5e-38:306:  
15 83//AC005703  
R-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for  
GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat.//  
1.5e-37:306:82//Z83838  
R-MAMMA1001322//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the  
20 HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE  
pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs,  
complete sequence.//2.4e-15:260:71//AL022398  
R-MAMMA1001324//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//4.0e-06:90:83//  
AC005614  
25 R-MAMMA1001330//Human BAC clone RG066D11 from 7q22, complete sequence.//1.4e-45:439:74//AC002430  
R-MAMMA1001341//Human DNA sequence from PAC 211D12 on chromosome 20q12-13.2. Contains Krs-2, K+  
channel protein, stress responsive.//1.3e-24:137:81//Z93016  
R-MAMMA1001343//Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.//5.4e-51:197:  
89//AC002041  
30 R-MAMMA1001346//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//0.99:  
182:64//AC004685  
R-MAMMA1001383//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-42:  
303:86//AC004815  
R-MAMMA1001388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING  
35 DRAFT SEQUENCE.//1.5e-44:324:83//AL021707  
R-MAMMA1001397//Homo sapiens genomic DNA, chromosome 21q11.1, segment 15/28, WORKING DRAFT SE-  
QUENCE.//2.0e-39:254:89//AP000044  
R-MAMMA1001408//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered piec-  
es.//9.4e-36:251:88//AC005805  
40 R-MAMMA1001411//T15F1-T7.1 TAMU Arabidopsis thaliana genomic clone T15F1, genomic survey sequence.//  
1.0:98:71//AQ248928  
R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds.//4.8e-18:117:96//  
AF038957  
R-MAMMA1001420//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//2.8e-  
45 09:377:63//AC005179  
R-MAMMA1001435//S.pombe chromosome I cosmid c26H5.//1.0:356:59//Z99126  
R-MAMMA1001442//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//3.4e-17:259:  
72//AC004047  
R-MAMMA1001446//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.9e-17:231:71//  
50 AC004491  
R-MAMMA1001452//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping  
protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//6.1e-50:558:73//  
AL024493  
R-MAMMA1001465//cSRL-2F3-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone  
55 cSRL-2F3, genomic survey sequence.//3.0e-23:141:96//B04295  
R-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//3.4e-09:309:64//L31783  
R-MAMMA1001487//Homo sapiens chromosome 17, clone hRPC.1108\_L\_11, complete sequence.//5.1e-30:286:  
79//AC005206

R-MAMMA1001501  
R-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B7, WORKING DRAFT SEQUENCE.//4.3e-19:349:64//AL031714  
R-MAMMA1001510  
5 R-MAMMA1001522//Homo sapiens chromosome 5, BAC clone 24h24 (LBNL H194), complete sequence.//1.5e-09:136:75//AC005352  
R-MAMMA1001547//Human Chromosome X, complete sequence.//3.5e-40:300:84//AC002418  
R-MAMMA1001551//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-57:282:89//AL020997  
10 R-MAMMA1001575  
R-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.6e-60:530:78//M61764  
R-MAMMA1001590//Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds.//1.3e-29:161:86//U78027  
R-MAMMA1001600//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library)  
15 complete sequence.//2.1e-18:390:66//AC004216  
R-MAMMA1001604//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//1.0:227:62//AL022238  
20 R-MAMMA1001606//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.3e-17:219:69//AL031985  
R-MAMMA1001620//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//2.1e-51:298:84//AL031650  
R-MAMMA1001627//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING  
25 DRAFT SEQUENCE.//7.8e-45:328:85//Z86090  
R-MAMMA1001630//, complete sequence.//2.5e-08:170:72//AC005399  
R-MAMMA1001633//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//  
2.2e-21:241:70//AC005386  
R-MAMMA1001635//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS  
30 and GSS, complete sequence.//1.1e-32:346:74//Z84466  
R-MAMMA1001649  
R-MAMMA1001663//Homo sapiens clone 162B15, complete sequence.//9.4e-68:267:89//AC004811  
R-MAMMA1001670//Human DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene,  
ESTs, STSs and CpG islands.//1.7e-49:322:88//Z82216  
35 R-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//2.4e-114:575:96//  
AC005614  
R-MAMMA1001679//CIT-HSP-2335N4.TF CIT-HSP Homo sapiens genomic clone 2335N4, genomic survey se-  
quence.//2.4e-82:400:99//AQ037393  
R-MAMMA1001683//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 un-  
40 ordered pieces.//5.7e-47:533:72//AC004166  
R-MAMMA1001686//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.6e-12:194:72//  
AC005261  
R-MAMMA1001692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING  
DRAFT SEQUENCE.//9.6e-44:414:77//AL022345  
45 R-MAMMA1001711//Homo sapiens clone BAC 9H13 chromosome 8 map 8q21, complete sequence.//3.1e-31:  
436:70//AF110324  
R-MAMMA1001715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 73E16, WORKING  
DRAFT SEQUENCE.//8.8e-76:524:84//Z95330  
R-MAMMA1001730  
50 R-MAMMA1001735//Cricetulus griseus (chinese hamster) mRNA for beta tubulin (clone B9T), partial.//2.7e-13:  
382:63//X60786  
R-MAMMA1001740//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SE-  
QUENCE.//3.9e-47:318:87//AP000050  
R-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence.//4.0e-108:566:95//AC006017  
55 R-MAMMA1001744  
R-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//3.5e-113:564:97//  
AF070718  
R-MAMMA1001751//Homo sapiens chromosome 19, cosmid R27328, complete sequence.//3.6e-30:312:75//

AC005625  
R-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//  
4.7e-34:320:77//AF041338

5 R-MAMMA1001757//Homo sapiens chromosome 17, clone hRPC.4\_G\_17, complete sequence.//4.7e-10:244:67//  
AC003688

R-MAMMA1001760//RPCI11-38L16.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38L16, genomic survey  
sequence.//1.3e-10:236:64//AQ029432

R-MAMMA1001764//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//0.74:361:60//AC005140

10 R-MAMMA1001768//Homo sapiens chromosome 17, clone hRPK.147\_L\_13, complete sequence.//1.6e-42:416:  
76//AC005332

R-MAMMA1001769//Homo sapiens chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//1.4e-13:129:  
83//AC004686

R-MAMMA1001771//M.musculus mRNA for semaphorin B.//1.1e-34:530:69//X85991

15 R-MAMMA1001783//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 un-  
ordered pieces.//1.1e-42:282:85//AC000360

R-MAMMA1001785//Human chromosome 16p13.11 BAC clone CIT987SK-98H8 complete sequence.//3.0e-49:  
282:86//U91319

R-MAMMA1001788  
20 R-MAMMA1001790//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
9.8e-43:530:71//AC004913

R-MAMMA1001806//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.8e-  
43:324:79//AC004020

R-MAMMA1001812//Plasmodium falciparum chromosome 2, section 69 of 73 of the complete sequence.//0.65:  
25 183:63//AE001432

R-MAMMA1001815//Homo sapiens clone GS223D04, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
1.1e-10:417:62//AC005018

R-MAMMA1001817//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) com-  
plete sequence.//2.6e-40:313:84//AC005859

30 R-MAMMA1001818  
R-MAMMA1001820//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.2e-45:340:82//  
AC004086

R-MAMMA1001824//Homo sapiens clone DJ1107K15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//  
1.9e-53:291:85//AC004966

35 R-MAMMA1001836//HS\_3164\_B1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3164 Col=3 Row=B, genomic survey sequence.//6.5e-08:79:89//AQ185484

R-MAMMA1001837//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and  
R32804, complete sequence.//8.4e-55:309:85//AC003682

R-MAMMA1001848//Homo sapiens PAC clone DJ0296G17 from Xq23, complete sequence.//1.6e-16:125:90//  
40 AC006144

R-MAMMA1001851//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered pie-  
ces.//2.4e-50:516:74//AC002099

R-MAMMA1001854//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.7e-  
38:308:82//AC002425

45 R-MAMMA1001858//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, com-  
plete sequence.//6.5e-50:283:86//U80460

R-MAMMA1001864//Human Chromosome 15q26.1 PAC clone pDJ398g19, WORKING DRAFT SEQUENCE, 21  
unordered pieces.//3.4e-36:224:86//AC005143

R-nnnnnnnnnnnnnnnnnnn//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//1.4e-11:  
50 495:63//AE001417

R-MAMMA1001874//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3  
unordered pieces.//3.2e-42:446:76//AC003117

R-MAMMA1001878//Human DNA sequence from PAC 431A14 on chromosome 6p21. Contains CYCLOPHILIN  
(PEPTIDYLPROLYL ISOMERASE) like and CIP1 (WAF1, CDKN1, MDA-6, SDI1, PIC1, CAP20) genes.  
55 Contains probable GTPase and receptor genes and ESTs, STSs and CpG islands.//6.9e-44:391:78//Z85996

R-MAMMA1001880//Human DNA sequence from fosmid F77D12 on chromosome 22q12-qter contains ESTs,  
tRNA.//1.3e-15:181:76//Z82097

R-MAMMA1001890//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-670B5 ~complete genomic se-

quence, complete sequence.//1.7e-43:283:86//AC002303  
R-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING DRAFT SEQUENCE.//1.4e-48:420:79//AL031720  
R-nnnnnnnnnnnn//Saccharomyces cerevisiae chromosome IV cosmid 9481.//2.9e-14:505:60//U28373  
5 R-MAMMA1001931//Homo sapiens NACP/alpha-synuclein gene, allele A0, intron 4, partial sequence.//0.51:162:63//AF041008  
R-MAMMA1001956//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING DRAFT SEQUENCE.//1.4e-51:422:79//AL034380  
R-MAMMA1001963//Homo sapiens clone HS19.3 Alu-Ya5 sequence.//1.9e-31:163:91//AF015149  
10 R-MAMMA1001969//Human DNA from chromosome 19 cosmid F19410, genomic sequence, complete sequence.//8.7e-10:186:76//AC002128  
R-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.0e-62:298:86//AC003071  
R-MAMMA1001992//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3  
15 unorderd pieces.//1.8e-44:525:72//AC004581  
R-MAMMA1002009//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 109G6, WORKING DRAFT SEQUENCE.//1.4e-43:282:79//AL023879  
R-MAMMA1002011  
R-MAMMA1002032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING  
20 DRAFT SEQUENCE.//1.1e-39:310:84//AL031284  
R-MAMMA1002033//Homo sapiens chromosome 5, Pac clone 162o17 (LBNL H147), complete sequence.//2.5e-17:170:81//AC003954  
R-MAMMA1002041//Homo sapiens PAC clone DJ0728D04, complete sequence.//8.7e-79:296:85//AC004865  
R-MAMMA1002042//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//8.8e-46:386:  
25 80//U91318  
R-MAMMA1002047//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//1.9e-32:326:  
75//U91318  
R-MAMMA1002056//Homo sapiens chromosome 17, clone hRPK.506\_H\_21, complete sequence.//6.6e-48:367:  
82//AC005962  
30 R-MAMMA1002058//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unorderd pieces.//  
0.25:139:69//AC005052  
R-MAMMA1002068//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered  
pieces.//2.2e-45:406:78//AC004676  
R-MAMMA1002078//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//2.3e-22:357:  
35 64//AC005291  
R-MAMMA1002082//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//2.5e-38:304:82//  
AC004263  
R-MAMMA1002084//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1174N9, WORKING  
DRAFT SEQUENCE.//8.9e-41:319:83//AL031602  
40 R-MAMMA1002093//CIT-HSP-2060J9.TF CIT-HSP Homo sapiens genomic clone 2060J9, genomic survey se-  
quence.//9.7e-17:129:88//B69983  
R-MAMMA1002108  
R-MAMMA1002118//Human DNA sequence from cosmid E116C6, on chromosome 22 Contains ESTs, complete  
sequence.//0.94:168:64//Z73495  
45 R-MAMMA1002125//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//4.8e-40:313:83//  
AC005670  
R-MAMMA1002132//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.0e-70:461:  
83//AC004953  
R-MAMMA1002140//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease  
50 (ATP7A) putative Cu<sup>++</sup>-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.1e-32:477:73//Z94801  
R-MAMMA1002143//Homo sapiens platelet-activating factor acetylhydrolase gene, promoter region and exon 1.//  
6.6e-06:130:73//AF027357  
R-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING  
DRAFT SEQUENCE.//6.0e-19:242:73//AL031447  
55 R-MAMMA1002153//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0281M17;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 3 unorderd pieces.//2.1e-51:291:75//AC006052  
R-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 608E8, WORKING  
DRAFT SEQUENCE.//1.2e-53:461:79//AL022343

R-MAMMA1002156//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//5.1e-37:305:  
82//AC004997

5 R-MAMMA1002158//Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene sim-  
ilar to GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete se-  
quence.//8.1e-34:296:81//AL034418

10 R-MAMMA1002170//Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.3. Contains the 3'  
part of a gene for the ortholog of mouse transmembrane receptor Celsr1, a novel gene for a protein similar to C.  
elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases, and the 3' part  
of a novel gene for a protein similar to mouse B99. Contains ESTs, GSSs and putative CpG islands, complete  
sequence.//7.9e-39:332:82//AL031588

15 R-MAMMA1002174//Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.//4.4e-12:  
189:72//AC005871

R-MAMMA1002198//Homo sapiens clone DJ0800G07, complete sequence.//1.1e-48:338:81//AC004890

15 R-MAMMA1002209//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//1.2e-23:269:  
74//AC005821

R-MAMMA1002215//Homo sapiens clone GS250N06, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
3.2e-12:243:68//AC005158

20 R-MAMMA1002219//Homo sapiens 12p13.3 RPCI4-773N5 (Roswell Park Cancer Institute Human PAC library)  
complete sequence.//3.3e-45:295:88//AC004802

R-MAMMA1002230//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
DRAFT SEQUENCE.//7.3e-41:385:78//AL034379

R-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete  
cds.//7.3e-45:363:79//U38253

25 R-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//2.8e-119:582:  
98//AC005666

R-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//4.7e-42:319:  
84//AC005600

R-MAMMA1002267//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.5e-33:571:  
67//AC006120

30 R-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//2.3e-35:462:70//  
AF068749

R-MAMMA1002269//345I17.TV CIT978SKA1 Homo sapiens genomic clone A-345I17, genomic survey se-  
quence.//4.7e-05:153:69//B15590

35 R-MAMMA1002282//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 112K5, WORKING  
DRAFT SEQUENCE.//8.5e-37:467:71//Z85987

R-MAMMA1002292//Hordeum vulgare lipoxygenase 2 (LoxC) mRNA, complete cds.//0.074:178:61//L37358

R-MAMMA1002293//Homo sapiens chromosome 16, cosmid clone RT167 (LANL), complete sequence.//5.8e-26:  
355:71//AC005568

40 R-MAMMA1002294//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.2e-35:281:  
82//AC004231

R-MAMMA1002297//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome  
4p16.3.//6.7e-48:381:80//Z69375

R-MAMMA1002298//Homo sapiens BAC clone RG208H19 from 7q11.23, complete sequence.//8e-17:296:70//  
AC005074

45 R-MAMMA1002299//HS\_3116\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3116 Col=14 Row=K, genomic survey sequence.//4.1e-60:354:91//AQ140526

R-MAMMA1002308

R-MAMMA1002310//Human DNA sequence from cosmid B10B1 on chromosome 22 Contains ESTs, CA repeat  
and STS, complete sequence.//9.9e-35:283:83//Z73979

50 R-MAMMA1002311//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-  
plete sequence.//1.3e-86:503:90//AC006210

R-MAMMA1002312//H.sapiens gene encoding La autoantigen.//1.3e-23:382:67//X97869

R-MAMMA1002317//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and  
GSSs, complete sequence.//1.3e-59:323:87//AL031054

55 R-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//  
AC005756

R-MAMMA1002322//Homo sapiens genomic DNA, chromosome 21q11.1, segment 13/28, WORKING DRAFT SE-  
QUENCE.//2.3e-48:452:76//AP000042

R-MAMMA1002329//M.musculus mRNA for semaphorin B./.2.0e-12:210:73//X85991  
R-MAMMA1002332//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence./.3.4e-46:393:71//  
AC004973  
R-MAMMA1002333//HS\_3245\_A1\_B04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
5 nomic clone Plate=3245 Col=7 Row=C, genomic survey sequence./.3.1e-21:146:92//AQ205759  
R-MAMMA1002339//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence./.9.7e-39:310:  
79//AF001549  
R-MAMMA1002347//Homo sapiens 12q24.1 PAC RPCI3-305I20 (Roswell Park Cancer Institute Human PAC Li-  
10 brary) complete sequence./.1.2e-46:443:76//AC006088  
R-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORK-  
ING DRAFT SEQUENCE./.1.1e-90:553:89//AL022100  
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2./.8.8e-81:388:92//Y15228  
R-MAMMA1002353//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC li-  
15 brary) complete sequence./.5.5e-35:302:80//AC002996  
R-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING  
DRAFT SEQUENCE./.5.4e-52:361:76//Z93241  
R-MAMMA1002356//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence./.8.3e-28:187:  
91//AC004662  
R-MAMMA1002359//Human DNA sequence from cosmid L118D5, Huntington's Disease Region, chromosome  
20 4p16.3 contains CpG islands./.6.3e-47:297:85//268869  
R-MAMMA1002360//HS\_2163\_B2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2163 Col=16 Row=F, genomic survey sequence./.1.5e-20:374:66//AQ125213  
R-MAMMA1002361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING  
25 DRAFT SEQUENCE./.2.2e-35:264:85//AL033520  
R-MAMMA1002362//H.sapiens PEX gene./.1.8e-40:243:86//Y10196  
R-MAMMA1002380//RPCI11-73J4.TJ RPCI11 Homo sapiens genomic clone R-73J4, genomic survey sequence./.  
1.7e-38:295:77//AQ268168  
R-MAMMA1002384//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Li-  
30 brary) complete sequence./.2.5e-37:311:81//AC004801  
R-MAMMA1002385  
R-MAMMA1002392//Human BAC clone RG066D11 from 7q22, complete sequence./.2.0e-37:365:77//AC002430  
R-MAMMA1002411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING  
DRAFT SEQUENCE./.9.4e-22:496:65//AL031668  
R-MAMMA1002413//Homo sapient 12q24.2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC li-  
35 brary) complete sequence./.2.3e-15:153:77//AC005146  
R-MAMMA1002417//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like  
gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat./.1.8e-23:508:62//AL020997  
R-MAMMA1002427//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence./.2.5e-37:288:  
84//U91321  
40 R-MAMMA1002428//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING  
DRAFT SEQUENCE./.6.0e-05:130:75//AL034423  
R-MAMMA1002434//Homo sapiens DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. Contains  
HB15 gene, ESTs, CA repeat, STS and GSS./.4.8e-18:205:78//AL022396  
R-MAMMA1002446//CIT-HSP-2021L14.TR CIT-HSP Homo sapiens genomic clone 2021L14, genomic survey se-  
45 quence./.4.6e-41:387:72//B65379  
R-MAMMA1002454//Homo sapiens chromosome 19, cosmid F23259, complete sequence./.1.2e-67:491:82//  
AC005512  
R-MAMMA1002461//Homo sapiens PAC clone 166H1 from 12q, complete sequence./.1.4e-28:188:85//AC003982  
R-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205./.6.3e-09:280:61//U10556  
50 R-MAMMA1002475//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs./.1.5e-25:310:  
74//Z83822  
R-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces./.  
1.2e-98:533:93//AC005077  
R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds./.2.7e-114:560:97//AF055460  
55 R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome  
4p16.3./.2.1e-46:329:84//Z69375  
R-MAMMA1002498//Rat mRNA./.0.0068:223:64//M59859  
R-MAMMA1002524//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING

DRAFT SEQUENCE, 5 unordered pieces.//0.012:460:60//AC005139  
R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//  
1.2e-101:529:95//AF065214

5 R-MAMMA1002545//Homo sapiens ribosomal protein s4 Y isoform gene, complete cds.//6.6e-50:471:77//  
AF041427

R-MAMMA1002554//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//5.7e-38:279:  
84//AC004056

R-MAMMA1002556//Homo sapiens chromosome 10 clone CIT-HSP-1255F20 map 10p11.2-10p12.1, complete  
sequence.//9.6e-13:237:67//AC005878

10 R-MAMMA1002566//CITBI-E1-2509P21.TR CITBI-E1 Homo sapiens genomic clone 2509P21, genomic survey  
sequence.//9.7e-14:216:73//AQ261427

R-MAMMA1002571//CITBI-E1-2516L21.TF CITBI-E1 Homo sapiens genomic clone 2516L21, genomic survey  
sequence.//4.6e-25:142:99//AQ279542

R-MAMMA1002573//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 811H13, WORKING  
15 DRAFT SEQUENCE.//1.1e-30:250:82//AL023805

R-MAMMA1002585//Rabbit angiotensin-converting enzyme (ACE) gene, 5' end.//1.0:196:61//M58580

R-MAMMA1002590//H.sapiens CpG island DNA genomic Mse1 fragment, clone 8d5, forward read cpg8d5.f1g.//  
1.0:114:64//Z63758

R-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING  
20 DRAFT SEQUENCE.//9.0e-96:459:98//AL034548

R-MAMMA1002598//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORK-  
ING DRAFTSEQUENCE.//0.79:362:58//AL031847

R-MAMMA1002603//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//1.3e-46:333:  
80//AC005803

25 R-MAMMA1002612//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 269M15, WORK-  
ING DRAFT SEQUENCE.//7.4e-41:283:86//AL021395

R-MAMMA1002617//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING  
DRAFT SEQUENCE.//1.7e-20:308:71//AL031594

R-MAMMA1002618//Homo sapiens clone RG122E10, complete sequence.//1.2e-31:230:76//AC005067

30 R-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.0e-113:551:98//AJ010598

R-MAMMA1002622//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.8e-43:324:  
83//AC004050

R-MAMMA1002623//Homo sapiens chromosome 17, clone hRPC.1171\_I\_10, complete sequence.//2.7e-80:344:  
84//AC004687

35 R-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING  
DRAFT SEQUENCE.//2.6e-34:391:72//AL031727

R-MAMMA1002629//Human DNA from overlapping chromosome 19-specific cosmids R32543., and F15613 con-  
taining ZNF gene family member, genomic sequence, complete sequence.//5.5e-58:346:81//AC003006

R-MAMMA1002636//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//  
40 1.1e-52:285:92//AC004895

R-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//2.1e-13:359:64//AF055666

R-MAMMA1002646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 394I7, WORKING  
DRAFT SEQUENCE.//2.5e-24:285:68//AL023585

R-MAMMA1002650//Human IGF-II gene exon 2 for insulin-like growth factor II located on chromosome 11.//0.64:  
45 237:61//X03424

R-MAMMA1002655//Homo sapiens mini satellite ceb1 repeat region.//0.18:152:65//AF048727

R-MAMMA1002662//Homo sapiens clone DJ0739M23, complete sequence.//2.5e-46:370:82//AC004870

R-MAMMA1002665//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs././/7.4e-55:298:  
92//Z92844

50 R-MAMMA1002671//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey se-  
quence.//0.99:151:66//AQ194411

R-MAMMA1002673//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the  
OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete  
sequence.//3.1e-38:410:76//AL022162

55 R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.4e-107:544:96//D86987

R-MAMMA1002685//HS\_2052\_A1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2052 Col=3 Row=O, genomic survey sequence.//1.2e-23:255:75//AQ231087

R-MAMMA1002698//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)

complete sequence.//1.1e-38:299:83//AC004673  
R-MAMMA1002699//Mus musculus intersectin-EH binding protein lbp1 mRNA, partial cds.//3.3e-05:61:93//AF057285  
R-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//3.5e-39:317:81//AB011399  
5 R-MAMMA1002708//Homo sapiens 12p13.3 PAC RPCI5-977L1 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.26:365:62//AC005293  
R-MAMMA1002711//Homo sapiens chromosome 21 PAC LLNLP704F18108Q13.//2.5e-31:304:77//AJ006995  
R-MAMMA1002721//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//2.3e-40:279:87//Z83826  
10 R-MAMMA1002727//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.45:183:64//AC004710  
R-MAMMA1002728//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.1e-42:410:74//AC002037  
R-MAMMA1002744//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.6e-19:473:63//U96629  
15 R-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//2.2e-108:544:97//AC005856  
R-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-106:551:95//AC006055  
20 R-MAMMA1002754//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-34:305:79//AC005020  
R-MAMMA1002758//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.00014:130:74//U95626  
R-MAMMA1002764//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//8.7e-10:118:81//25 AC005781  
R-MAMMA1002765//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//1.2e-31:290:78//AC006128  
R-MAMMA1002769//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//0.94:260:62//Z82975  
30 R-MAMMA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//2.6e-21:529:62//AL031667  
R-MAMMA1002782//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//2.8e-30:234:72//AL022320  
R-MAMMA1002796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 237J2, WORKING DRAFT SEQUENCE.//1.0:155:66//AL021394  
35 R-MAMMA1002807//Human DNA sequence from BAC 941F9 on chromosome 22q11.2-qter. Contains ESTs, STSs and 3' part of FIBULIN-1 D PRECURSOR like gene, part of a Brain Protein E46 like gene and a CpG island, complete sequence.//5.0e-42:443:75//Z95331  
R-MAMMA1002820//345M16.TVB CIT978SKA1 Homo sapiens genomic clone A-345M16, genomic survey sequence.//1.3e-14:95:87//B17487  
40 R-MAMMA1002830//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//4.1 e-20:223:74//AC002073  
R-MAMMA1002833//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.8e-37:295:84//AC005295  
45 R-MAMMA1002835  
R-MAMMA1002838//Human gene hY3 encoding a cytoplasmic Ro RNA.//4.4e-14:108:92//V00585  
R-MAMMA1002842//CIT-HSP-2017022.TRB CIT-HSP Homo sapiens genomic clone 2017022, genomic survey sequence.//5.2e-43:168:85//B67141  
R-MAMMA1002843//Homo sapiens clone GS051M12, complete sequence.//8.7e-44:525:71//AC005007  
50 R-MAMMA1002844  
R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end.//2.8e-99:361:91//X79067  
R-MAMMA1002868//Homo sapiens clone DJ0852O24, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.6e-39:288:81//AC004906  
R-MAMMA1002871//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//0.0022:490:  
55 57//AC006044  
R-MAMMA1002880//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//1.3e-09:143:76//AC005296  
R-MAMMA1002881//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial

cds for thymopoietin beta //5.1e-41:264:87//U18271  
 R-MAMMA1002886//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence //4.7e-32:216:90//AL022069  
 R-MAMMA1002887  
 5 R-MAMMA1002890  
 3.4e-49:376:81//AG006257  
 R-MAMMA1002892//Homo sapiens PAC clone DJ0765G07 from 7q11, complete sequence //6.0e-60:344:79//AC004881  
 10 R-MAMMA1002895//RPCI11-90K13.TV RPCI11 Homo sapiens genomic clone R-90K13, genomic survey sequence //2.1e-34:300:77//AQ283502  
 R-MAMMA1002908//Human Chromosome X, complete sequence //4.2e-39:297:85//AC004070  
 R-MAMMA1002909//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces //3.4e-23:344:74//AC005798  
 15 R-MAMMA1002930//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence //5.2e-39:261:88//AC006019  
 R-MAMMA1002938//C.pasteurianum gap gene //1.0:343:59//X72219  
 R-MAMMA1002941//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence //6.3e-88:556:  
 20 87//AC006120  
 R-MAMMA1002947  
 0.48:156:69//AC005469  
 R-MAMMA1002964//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat //1.2e-39:473:73//AL020997  
 R-MAMMA1002970//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence //4.7e-47:  
 25 420:77//AC005200  
 R-MAMMA1002972//alpha 1 syntrophin [human, mRNA Partial, 1771 nt] //0.97:305:62//S81737  
 R-MAMMA1002973//Human DNA sequence from cosmid V210E9, between markers DDX366 and DDX87 on chromosome X //2.6e-35:256:85//Z70280  
 R-MAMMA1002982 1.0e-27:110:85//AG005524  
 30 R-MAMMA1002987//Homo sapiens PAC clone DJ1086D14, complete sequence //1.4e-28:527:66//AC004460  
 R-MAMMA1003003//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces //7.9e-48:418:78//AC006109  
 R-MAMMA1003004//, complete sequence //2.0e-12:442:61//AC005406  
 R-MAMMA1003007//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces //1.7e-48:293:91//AC006109  
 35 R-MAMMA1003011//A-306G8.TP CIT978SK Homo sapiens genomic clone A-306G8, genomic survey sequence //0.45:168:64//B18092  
 R-MAMMA1003015//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence //2.9e-44:399:77//AC005740  
 R-MAMMA1003019//RPCI11-9J9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-9J9, genomic survey sequence //2.7e-14:294:68//B71583  
 40 R-MAMMA1003026//HS\_2166\_B2\_C12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=24 Row=F, genomic survey sequence //0.021:189:64//AQ125639  
 R-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence //1.8e-98:525:95//AC005214  
 45 R-MAMMA1003035//Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries) complete sequence //6.7e-06:297:63//AC004550  
 R-MAMMA1003039//RPCI11-56J17.TJ RPCI11 Homo sapiens genomic clone R-56J17, genomic survey sequence //0.21:375:59//AQ081889  
 R-MAMMA1003040//Human DNA sequence from cosmid L108f12, Huntington's Disease Region, chromosome 50 4p16.3 //2.7e-29:298:67//Z49235  
 R-MAMMA1003044//Homo sapiens chromosome 19, cosmid R30676, complete sequence //2.9e-14:113:91//AC004560  
 R-MAMMA1003047  
 R-MAMMA1003049  
 55 R-MAMMA1003055//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 377F16, WORKING DRAFT SEQUENCE //2.3e-45:317:86//Z93783  
 R-MAMMA1003056//Homo sapiens chromosome 19, cosmid R34275, complete sequence //1.0:229:63//AC005305

R-MAMMA1003057//M.domesticus MD6 mRNA.//6.2e-42:326:82//X54352  
R-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//3.1e-49:299:87//Z83826  
5 R-MAMMA1003089//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//2.7e-30:520:67//AC005084  
R-MAMMA1003099//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey sequence.//4.2e-44:338:82//B71494  
R-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//3.4e-48:423:79//U72634  
10 R-MAMMA1003113//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//4.8e-114:567:97//AC006087  
R-MAMMA1003127//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//1.4e-34:283:83//Z99716  
15 R-MAMMA1003135//P.knowlesi Mbn-cutting sites in lambda KBS50.//0.010:243:62//M38776  
R-MAMMA1003140//Homo sapiens chromosome 17, clone HCIT87G17, complete sequence.//6.7e-34:288:81//AC003663  
R-MAMMA1003146//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//4.8e-08:438:59//M97514  
20 R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING DRAFT SEQUENCE.//1.7e-63:149:94//AL021579  
R-MAMMA1003166//HS\_3128\_A1\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=1 Row=C, genomic survey sequence.//3.0e-17:261:70//AQ140766  
R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence.//2.6e-111:593:94//AF070640  
R-NT2RM4000024  
25 R-NT2RM4000027//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//0.026:476:56//AC004993  
R-NT2RM4000030//Mus musculus sex determining protein (Sry) gene, complete cds.//0.00044:378:59//U70653  
R-NT2RM4000046//M.mulatta MHC DR beta 6 gene encoding major histocompatibility complex.//0.27:130:64//Z26239  
30 R-NT2RM4000061  
R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds.//7.2e-112:550:97//AF070639  
R-NT2RM4000086//RPCI11-6J23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6J23, genomic survey sequence.//7.2e-18:277:71//B49463  
35 R-NT2RM4000104//F.rubripes GSS sequence, clone 063K10aG5, genomic survey sequence.//3.6e-08:287:61//Z88817  
R-NT2RM4000139//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//9.4e-08:336:65//AC005199  
R-NT2RM4000155  
40 R-NT2RM4000156//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//3.4e-23:335:72//AC005856  
R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//1.6e-87:551:87//D12646  
R-NT2RM4000169//Human ribosomal protein L37a mRNA sequence.//5.9e-14:122:88//L22154  
45 R-NT2RM4000191  
R-NT2RM4000197//HS\_3241\_A2\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=10 Row=O, genomic survey sequence.//2.8e-86:430:97//AQ206812  
R-NT2RM4000199//Mus musculus Yp BAC GSMB-368G7 (Genome Systems Mouse BAC Library) complete sequence.//0.0047:193:63//AC006056  
50 R-NT2RM4000200  
R-NT2RM4000202//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//2.1e-40:334:76//AC004035  
R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//5.2e-102:546:94//AB018255  
R-NT2RM4000215  
55 R-nnnnnnnnnnnn//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//2.1e-55:303:86//AC005383  
R-NT2RM4000233//Struthio camelus microsatellite sequence OSM 7.//1.2e-07:198:67//AF003735  
R-NT2RM4000244//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.7e-

49:322:88//AC006116  
R-NT2RM4000251//Homo sapiens Chromosome 22q11.2 BAC Clone 72f8 In DGCR Region, complete sequence.//  
0.97:184:66//AC000085  
5 R-NT2RM4000265//Human PAC clone DJ073F11 from Xq23, complete sequence.//6.2e-66:552:78//AC000055  
R-NT2RM4000290//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39417, WORKING  
DRAFT SEQUENCE.//1.4e-05:229:65//AL023585  
R-NT2RM4000324  
R-NT2RM4000327//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING  
DRAFT SEQUENCE.//3.3e-42:443:75//Z97199  
10 R-NT2RM4000344//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
6.4e-64:433:84//AC004826  
R-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds.//7.7e-11:210:69//D13630  
R-NT2RM4000354//Caenorhabditis elegans cosmid T14A8.//0.084:257:60//U50066  
R-NT2RM4000356  
15 R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//8.7e-112:577:95//AB014542  
R-NT2RM4000368  
1.6e-48:348:85//AG006257  
R-NT2RM4000386//Rat mRNA for growth potentiating factor, complete cds.//4.4e-35:141:87//D42148  
R-NT2RM4000395//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey se-  
20 quence.//1.4e-25:207:75//871494  
R-NT2RM4000414//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING  
DRAFT SEQUENCE.//7.1e-17:492:64//AL031985  
R-NT2RM4000421//RPCI11-66B1.TK RPCI11 Homo sapiens genomic clone R-66B1, genomic survey sequence.//  
1.8e-40:311:82//AQ241167  
25 R-NT2RM4000425//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SE-  
QUENCE, 35 unordered pieces.//2.5e-47:316:87//AC005867  
R-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//1.6e-17:133:  
78//AF062476  
R-NT2RM4000457  
30 R-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//4.6e-113:559:96//AJ010952  
R-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22C.//0.00015:170:67//AB000461  
R-NT2RM4000496  
R-NT2RM4000511//Rat troponin T cardiac isoform gene, complete cds.//0.21:290:58//M80829  
R-NT2RM4000514//CIT-HSP-2169K4.TR CIT-HSP Homo sapiens genomic clone 2169K4, genomic survey se-  
35 quence.//1.5e-20:150:89//B95717  
R-nnnnnnnnnnnn//HS-1024-B2-G01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
Plate=CT 803 Col=2 Row=N, genomic survey sequence.//6.3e-10:74:98//B34556  
R-NT2RM4000520//Caenorhabditis elegans cosmid F36H12.//0.15:406:61//AF078790  
R-NT2RM4000531  
40 R-NT2RM4000532//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//1.0:119:  
66//AE001391  
R-NT2RM4000534//paramecium species 4.51er mt dna dimer: replication init. region, clone 2.//9.8e-05:326:60//  
K00909  
R-NT2RM4000585//HS\_3252\_A2\_G08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
45 nomic clone Plate=3252 Col=16 Row=M, genomic survey sequence.//1.9e-69:376:93//AQ219890  
R-NT2RM4000590//CIT-HSP-539O24.TV CIT-HSP Homo sapiens genomic clone 539O24, genomic survey se-  
quence.//1.7e-38:226:93//B50657  
R-NT2RM4000595//Human Chromosome X clone bWXD342, complete sequence.//1.0:239:61//AC004072  
R-NT2RM4000603//RPCI11-49P13.TK RPCI11 Homo sapiens genomic clone R-49P13, genomic survey se-  
50 quence.//0.77:139:64//AQ051950  
R-nnnnnnnnnnnn  
R-NT2RM4000616//HS\_3107\_A2\_B03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3107 Col=6 Row=C, genomic survey sequence.//1.3e-54:272:99//AQ210034  
R-NT2RM4000674  
55 R-NT2RM4000689//Mus musculus pericentrin mRNA, complete cds.//3.5e-70:551:80//U05823  
R-NT2RM4000698  
R-nnnnnnnnnnnn  
R-NT2RM4000712//Homo sapiens clone NH0512E16, complete sequence.//0.54:294:58//AC005039

R-NT2RM4000717//Plasmodium falciparum MAL3P8, complete sequence./.0.050:387:58//AL034560  
 R-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE./.1.0e-107:566:95//AL034379  
 R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds./.1.1e-103:536:95//AB018303  
 5 R-NT2RM4000741//CIT-HSP-2294N4.TR CIT-HSP Homo sapiens genomic clone 2294N4, genomic survey sequence./.5.2e-41:244:93//AQ006361  
 R-NT2RM4000751//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE./.2.7e-28:416:67//AL034405  
 R-NT2RM4000764//Human HepG2 3' region MboI cDNA, clone hmd3g01m3./.2.1e-33:199:96//D17217  
 10 R-NT2RM4000778//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence./.0.00060:241:62//AC002980  
 R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds./.2.9e-104:546:94//AB007920  
 R-NT2RM4000787//Homo sapiens, clone hRPK.3\_A\_1, complete sequence./.5.3e-32:321:77//AC006198  
 15 R-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence./.1.9e-111:552:97//AC005306  
 R-NT2RM4000795//Homo sapiens Chromosome 17p13 Cosmid Clone cos39, complete sequence./.0.74:364:57//U58675  
 R-NT2RM4000796//Homo sapiens full-length insert cDNA clone ZD62D10./.2.7e-105:510:98//AF086348  
 R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end./.7.7e-27:158:96//M21868  
 20 R-NT2RM4000813  
 R-NT2RM4000820//, complete sequence./.2.0e-104:432:97//AC005406  
 R-NT2RM4000833//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence./.2.0e-07:166:68//AB012248  
 R-NT2RM4000848//Rabies virus matrix (M) protein mRNA, complete cds./.0.073:70:84//M22013  
 25 R-NT2RM4000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces./.1.0:237:62//AC004709  
 R-NT2RM4000855  
 R-nnnnnnnnnnnn//HS\_3189\_B2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=16 Row=D, genomic survey sequence./.2.1e-06:114:73//AQ300597  
 30 R-NT2RM4000895//Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence./.3.8e-46:207:91//AF077058  
 R-NT2RM4000950//Human BAC clone RG341D10 from 7p15-p21, complete sequence./.1.0:336:60//AC002530  
 R-NT2RM4000971//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12,  
 35 U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence./.7.1e-09:259:64//AF011889  
 R-NT2RM4000979  
 R-NT2RM4000996//HS\_3164\_A1\_E02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=I, genomic survey sequence./.2.0e-82:443:94//AQ141622  
 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds./.1.2e-112:545:97//AB018272  
 40 R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds./.7.9e-113:556:97//AB014539  
 R-NT2RM4001032//Homo sapiens Surf-5 and Surf-6 genes./.1.2e-10:120:82//AJ224639  
 R-NT2RM4001047//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 163G9, WORKING DRAFT SEQUENCE./.1.0:158:67//AL008733  
 R-NT2RM4001054//CIT-HSP-2292N8.TR CIT-HSP Homo sapiens genomic clone 2292N8, genomic survey sequence./.5.8e-19:118:97//AQ004096  
 R-nnnnnnnnnnnn//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2./.1.0e-05:271:64//M10296  
 R-NT2RM4001092//CITBI-E1-2524J20.TR CITBI-E1 Homo sapiens genomic clone 2524J20, genomic survey sequence./.1.0:186:63//AQ277294  
 50 R-NT2RM4001116  
 R-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence./.3.6e-79:468:90//AC004593  
 R-NT2RM4001151//HS\_2270\_B1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=9 Row=J, genomic survey sequence./.5.5e-62:312:98//AQ163739  
 55 R-NT2RM4001155//Homo sapiens chromosome 12p13.3 clone RPCI4-816N1, WORKING DRAFT SEQUENCE, 31 unordered pieces./.1.4e-107:536:97//AC005841  
 R-NT2RM4001160//HS\_3015\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=19 Row=P, genomic survey sequence./.7.1e-35:201:95//AQ118712

R-NT2RM4001187//X.laevis xUBFbeta2 mRNA for upstream binding factor 1 //0.019:177:63//X57201  
 R-NT2RM4001191//HS\_3002\_A1\_F05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=9 Row=K, genomic survey sequence //3.9e-33:230:75//AQ088791  
 R-NT2RM4001200//Homo sapiens full-length insert cDNA clone YL35H03 //7.5e-69:335:99//AF085857  
 5 R-NT2RM4001203  
 R-NT2RM4001204  
 R-NT2RM4001217  
 R-NT2RM4001256  
 R-NT2RM4001258  
 10 R-NT2RM4001309  
 R-NT2RM4001313//Homo sapiens 12q24.1 PAC RPCI1-71H24 (Roswell Park Cancer Institute Human PAC library) complete sequence //0.00055:183:63//AC004551  
 R-NT2RM4001316//Homo sapiens chromosome 17, clone hCIT.117\_K\_16, complete sequence //4.5e-21:212:79//AC004757  
 15 R-NT2RM4001320//CIT-HSP-2303E22.TR CIT-HSP Homo sapiens genomic clone 2303E22, genomic survey sequence //3.8e-30:86:89//AQ021084  
 R-NT2RM4001340  
 0.0027:493:60//AC005133  
 R-NT2RM4001344  
 20 R-NT2RM4001347//CITBI-E1-2506I20.TR CITBI-E1 Homo sapiens genomic clone 2506I20, genomic survey sequence //6.5e-16:1.01:99//AQ262797  
 R-NT2RM4001371//CITBI-E1-2503G21.TR CITBI-E1 Homo sapiens genomic clone 2503G21, genomic survey sequence //0.063:140:65//AQ265776  
 25 R-NT2RM4001382//HS\_3044\_A1\_F02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=3 Row=K, genomic survey sequence //0.96:103:66//AQ098668  
 R-NT2RM4001384//R.norvegicus mRNA for dendrin //8.5e-07:120:75//Y09000  
 R-NT2RM4001410//Bovine cytochrome P450-scc mRNA fragment //2.3e-15:199:75//M25920  
 R-NT2RM4001411//Rattus norvegicus FceRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds //1.7e-55:235:83//U57391  
 30 R-NT2RM4001412  
 R-NT2RM4001414//Homo sapiens Xp22 Cosmids U98B4 and U24F2 (Lawrence Livermore human cosmid library) complete sequence //1.7e-80:489:89//U69730  
 R-NT2RM4001437//RPCI11-56D2.TJ RPCI11 Homo sapiens genomic clone R-56D2, genomic survey sequence //3.8e-43:250:93//AQ081969  
 35 R-NT2RM4001444//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence //0.0034:224:63//AC005926  
 R-NT2RM4001454//Homo Sapiens Chromosome X clone bWXD90, complete sequence //2.4e-33:360:68//AC004075  
 R-NT2RM4001455//HS\_3229\_B1\_E04\_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=7 Row=J, genomic survey sequence //1.0:183:61//AQ191289  
 40 R-NT2RM4001483//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces //2.2e-51:451:79//AC005282  
 R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds //2.2e-102:547:93//AB014585  
 R-NT2RM4001519//HS\_2208\_A1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=13 Row=K, genomic survey sequence //0.25:214:63//AQ091836  
 45 R-NT2RM4001522//H.sapiens gene for Cu/Zn-superoxide dismutase //3.6e-13:246:70//Z29336  
 R-NT2RM4001557//Plasmodium falciparum MAL3P4, complete sequence //0.055:320:58//AL008970  
 R-NT2RM4001565//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces //3.9e-26:329:72//AC005910  
 50 R-NT2RM4001566//Human trophinin mRNA, complete cds //6.3e-38:296:86//U04811  
 R-NT2RM4001569//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence //2.0e-35:213:89//AL031663

R-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds./.5.4e-60:558:77//AF071317

R-nnnnnnnnnnnn//M.musculus mRNA of enhancer-trap-locus 1./.4.8e-86:565:85//X69942

R-NT2RM4001594//Human interleukin-13 (IL-13) precursor gene, complete cds./.0.083:283:61//U31120

5 R-NT2RM4001597//HS\_2059\_A1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=21 Row=M, genomic survey sequence./.4.4e-09:105:83//AQ245136

R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds./.6.7e-111:565:95//AB018334

R-NT2RM4001611//Homarus americanus ryanodine receptor (RyR) mRNA, partial cds./.1.0:364:61//AF051936

10 R-NT2RM4001629//RPCI11-54G14.TJ RPCI11 Homo sapiens genomic clone R-54G14, genomic survey sequence./.0.0018:347:61//AQ083173

R-NT2RM4001650

R-NT2RM4001662//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein./.0.75:212:62//AL022575

15 R-NT2RM4001666//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence./.2.6e-26:461:65//AC004685

R-NT2RM4001682//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence./.1.5e-107:544:96//AL031775

20 R-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE./.1.8e-110:580:95//AL031447

R-NT2RM4001714//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./.3.1e-10:543:59//AC004153

R-nnnnnnnnnnnn//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence./.8.7e-111:577:94//AL034430

25 R-NT2RM4001731//Ovis aries dinucleotide repeat polymorphism at MAF92 locus./.0.017:93:73//M80527

R-NT2RM4001741//Mouse mRNA for talin./.2.4e-34:273:83//X56123

R-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING DRAFT SEQUENCE./.1.7e-112:567:96//AL031709

30 R-NT2RM4001754//Homo sapiens PAC clone 248O15 from 13q12-q13, complete sequence./.1.4e-64:475:83//AC002483

R-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1./.1.9e-18:202:78//Z83868

R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds./.2.0e-22:236:80//AB018270

R-NT2RM4001783//Homo sapiens clone DJ0981O07, complete sequence./.4.4e-106:551:95//AC006017

35 R-NT2RM4001810//T28D3TF TAMU Arabidopsis thaliana genomic clone T28D3, genomic survey sequence./.0.76:279:60//B27099

R-NT2RM4001813

R-NT2RM4001823

R-NT2RM4001828//HS\_3073\_A2\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=2 Row=I, genomic survey sequence./.1.6e-46:255:96//AQ121030

40 R-NT2RM4001836//Sus scrofa microsatellite S0398 sequence./.9.4e-06:141:69//U78024

R-NT2RM4001841//Salmo salar microsatellite Ssa65 DNA./.1.5e-06:175:65//AF019184

R-NT2RM4001842//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces./.5.0e-07:332:61//AC005077

45 R-NT2RM4001856//Mus musculus clone OST16642, genomic survey sequence./.4.8e-30:235:85//AF046633

R-nnnnnnnnnnnn//Hs\_3244\_B1\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=19 Row=L, genomic survey sequence./.3.0e-40:263:89//AQ252798

R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC./.5.0e-119:592:97//Y17711

R-NT2RM4001876//Megastigmus wachtli dinucleotide microsatellite, clone

50 MWA47CT./.0.13:134:64//AJ001069

R-NT2RM4001880

R-NT2RM4001905//HS\_2016\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=21 Row=P, genomic survey sequence./.0.0066:264:59//AQ226877

R-NT2RM4001922//HS\_2228\_B2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=14 Row=D, genomic survey sequence./.2.5e-35:205:96//AQ065498

55 R-NT2RM4001930//Homo sapiens chromosome 17, clone hRPC.34\_M\_24, complete sequence./.0.26:325:63//AC004562

R-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence./.2.9e-85:421:

98//AC005207  
R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//6.2e-109:556:95//AF098162  
R-NT2RM4001953//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING  
DRAFT SEQUENCE.//1.3e-08:175:70//Z83826

5 R-NT2RM4001965//CIT-HSP-385N14.TR CIT-HSP Homo sapiens genomic clone 385N14, genomic survey se-  
quence.//5.7e-69:532:81//B55044  
R-nnnnnnnnnnnn//R.norvegicus mRNA for IP63 protein.//1.9e-61:352:83//X99330  
R-NT2RM4001979//Homo sapiens full-length insert cDNA clone ZD29F04.//1.1e-98:465:100//AF086241  
R-NT2RM4001984//Borrelia burgdorferi (section 47 of 70) of the complete genome.//0.14:461:60//AE001161

10 R-NT2RM4001987  
R-NT2RM4002013  
R-NT2RM4002018  
R-NT2RM4002034//Homo sapiens chromosome 5, BAC clone 24p24 (LBNL H195), complete sequence.//3.6e-  
42:277:89//AC005353  
15 R-NT2RM4002044//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.83:476:57//  
AC006204  
R-NT2RM4002054  
R-NT2RM4002062//Human microsomal epoxide hydrolase gene, exons 5 and 6.//0.11:136:67//U06659  
R-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//2.9e-99:503 :96//  
20 U82267  
R-nnnnnnnnnnnn//Homo sapiens CAGH45 mRNA, complete cds.//9.6e-41:554:68//U80742  
R-NT2RM4002067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING  
DRAFT SEQUENCE.//7.7e-64:476:81//Z97832  
R-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//1.1e-33:238:85//AF072758  
25 R-NT2RM4002075//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING  
DRAFT SEQUENCE, 3 unordered pieces.//0.0031:403:57//AC005504  
R-NT2RM4002093//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered  
pieces.//9.4e-07:322:62//AC000383  
R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.6e-44:432:74//  
30 D12646  
R-NT2RM4002128//Human HepG2 partial cDNA, clone hmd2e12m5.//2.0e-26:186:90//D17000  
R-NT2RM4002140  
R-NT2RM4002145//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-15:193:76//AF086247  
R-NT2RM4002146//Human ABL gene, intron 1b, partial sequence.//0.66:170:63//U07562  
35 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds.//4.5e-110:560:96//AF084535  
R-NT2RM4002174//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//8.0e-43:302:85//  
AC005696  
R-NT2RM4002189  
R-NT2RM4002194//Human Cosmid g5129g129 from 7q31.3, complete sequence.//0.29:382:60//AC003960  
40 R-NT2RM4002205//Spiroplasma virus (SpV1-R8A2 B) complete genome.//3.5e-05:432:56//X51344  
R-NT2RM4002213  
R-NT2RM4002226//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.94:198:61//  
AC004448  
R-NT2RM4002251  
45 R-NT2RM4002256//Homo sapiens PAC clone DJ0570D02 from 7p13-p14, complete sequence.//2.3e-58:299:85//  
AC004837  
R-NT2RM4002266//H.sapiens CpG island DNA genomic Mse1 fragment, clone 179f11, forward read  
cpg179f11.ft1a.//0.72:97:69//Z57487  
R-NT2RM4002278//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//7.5e-  
49:405:84//AC005069  
50 R-NT2RM4002281//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING  
DRAFT SEQUENCE.//1.7e-13:168:77//AL033531  
R-NT2RM4002287  
R-NT2RM4002294//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered  
pieces.//0.98:208:65//AC004676  
R-NT2RM4002301//HS\_2028\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2028 Col=19 Row=1, genomic survey sequence.//0.94:321:57//AQ233262  
R-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-

gene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence./.1.9e-35:265:84//AL032822  
 R-nnnnnnnnnnnn//Human mRNA for KIAA0319 gene, complete cds./.2.4e-42:569:68//AB002317  
 R-NT2RM4002344//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 5 DRAFT SEQUENCE, 3 unordered pieces./.0.013:391:59//AC004709  
 R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds./.8.6e-121:593:97//AB014549  
 R-NT2RM4002374//Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chro-  
 mosome X contains XK membrane transport protein, ESTs and STS./.3.8e-44:258:86//Z73417  
 R-NT2RM4002383//Human Chromosome 15q26.1 PAC clone pDJ10K5 containing human DNA polymerase gam-  
 10 ma (polg) gene, complete sequence./.0.00084:345:60//AC005316  
 R-NT2RM4002390  
 R-NT2RM4002409//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey se-  
 quence./.0.99:151:66//AQ194411  
 R-NT2RM4002438  
 15 R-NT2RM4002446//Human DNA sequence from clone 360A4 on chromosome 16. Contains ESTs, complete se-  
 quence./.2.8e-103:533:95//AL031008  
 R-NT2RM4002452  
 R-NT2RM4002457//Homo sapiens chromosome 16, cosmid clone 321D4 (LANL), complete sequence./.0.99:171:  
 64//AC004034  
 20 R-NT2RM4002460//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE  
 LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.  
 Contains polymorphic CA repeat./.0.96:94:71//Z92545  
 R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds./.2.9e-102:508:97//  
 AF083255  
 25 R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds./.7.0e-31:172:98//AB014591  
 R-NT2RM4002493//CIT-HSP-2296C24.TF CIT-HSP Homo sapiens genomic clone 2296C24, genomic survey se-  
 quence./.0.46:182:62//AQ006882  
 R-NT2RM4002499//Human v-fos transformation effector protein (Fte-1), mRNA complete cds./.7.3e-24:134:99//  
 M84711  
 30 R-NT2RM4002504//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 geneexons 1,2, and 3,  
 complete sequence./.3.9e-11:334:63//AC002368  
 R-nnnnnnnnnnnn  
 R-NT2RM4002532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING  
 DRAFT SEQUENCE./.3.4e-17:171:79//Z97985  
 35 R-NT2RM4002534  
 R-NT2RM4002567//Homo sapiens chromosome 7 clone UWGC:g1564a040 from 7p14-15, complete sequence././/  
 2.2e-26:181:76//AC005271  
 R-NT2RM4002571  
 R-NT2RM4002593//CIT-HSP-2303L15.TF CIT-HSP Homo sapiens genomic clone 2303L15, genomic survey se-  
 40 quence./.0.034:73:82//AQ015579  
 R-NT2RM4002623//Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence./.0.0014:670:55//  
 AC005862  
 R-NT2RP2000001//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence./.0.00087:  
 251:59//AE001422  
 45 R-NT2RP2000006//Human DNA sequence from PAC 155D22 on chromosome 6q27. Contains EST, STSs and a  
 GSS./.2.7e-37:259:86//Z97205  
 R-NT2RP2000008//RPCI11-41G16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41G16, genomic survey  
 sequence./.4.1e-25:365:70//AQ029090  
 R-NT2RP2000027//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence./.6.0e-05:307:62//  
 50 AC004098  
 R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds./.8.4e-41:223:96//AB018290  
 R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds././/  
 5.8e-63:325:96//AF061749  
 R-NT2RP2000054//Human tyrosinase gene, 5'-flanking region (containing enhancer element responsible for pig-  
 55 ment cell-specific transcription).//.0.88:210:60//D26163  
 R-NT2RP2000056//Mus musculus epsilon tyrosine phosphatase cytoplasmic isoform (Ptpr) mRNA, complete  
 cds./.4.7e-38:377:78//U36758  
 R-NT2RP2000067//Rat mRNA for growth potentiating factor, complete cds./.6.0e-10:137:79//D42148

R-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence./.3.1e-76:  
381:98//AC005754

R-NT2RP2000076//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence./.2.3e-06:  
380:60//AE001372

5 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds./.3.5e-77:379:  
97+++F050079

R-NT2RP2000079//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING  
DRAFT SEQUENCE./.6.5e-32:314:78//AL034549

10 R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds./.5.6e-74:378:96//AB018338

R-NT2RP2000091//Homo sapiens clone RG015P03, complete sequence./.9.3e-21:226:76//AC005048

R-NT2RP2000097//Human DNA sequence from cosmid U209G1 on chromosome X./.9.2e-40:278:81//Z68873

R-NT2RP2000098//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence./.0.34:132:65//AC004015

R-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence./.3.1e-09:259:67//  
AC003973

15 R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds./.1.8e-74:386:95//AB018356

R-NT2RP2000120//CITBI-E1-2503M8.TR CITBI-E1 Homo sapiens genomic clone 2503M8, genomic survey se-  
quence./.5.1e-05:87:77//AQ263909

R-nnnnnnnnnnnnnn

20 R-nnnnnnnnnnnnnn//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence./.4.9e-11:153:69//  
AC004827

R-NT2RP2000147

R-NT2RP2000153//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and  
lactoferrin (lactoferrin) gene, partial cds, complete sequence./.0.0058:261:57//U95626

25 R-NT2RP2000157//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library)  
complete sequence./.2.5e-119:603:96//AC005924

R-NT2RP2000161//CIT-HSP-2045P7.TR CIT-HSP Homo sapiens genomic clone 2045P7, genomic survey se-  
quence./.0.89:173:63//B79728

R-NT2RP2000175

R-NT2RP2000183

30 R-NT2RP2000195//Homo sapiens chromosome 17, clone hRPK.60\_A\_24, complete sequence./.4.3e-39:306:83//  
AC005325

R-NT2RP2000205//Human DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence./.  
7.5e-05:101:78//AL022155

35 R-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence./.7.3e-  
55:306:94//AC004382

R-NT2RP2000232

R-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds./.7.6e-  
13:144:75//U88401

R-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence./.9.6e-63:410:  
86//AC004066

40 R-NT2RP2000248//Caenorhabditis elegans cosmid T01C8./.1.0:282:58//U58726

R-NT2RP2000257//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence./.2.5e-11:163:  
72//AC004894

R-NT2RP2000258//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence./.  
0.58:442:58//AC004077

45 R-NT2RP2000270//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an  
unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c),  
H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene.  
Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence./.1.1e-39:292:84//AL009179

50 R-NT2RP2000274//CIT-HSP-237901.TR CIT-HSP Homo sapiens genomic clone 237901, genomic survey se-  
quence./.6.9e-10:121:81//AQ109409

R-NT2RP2000288

R-NT2RP2000289

R-NT2RP2000297//Homo sapiens full-length insert cDNA clone ZB81C03./.7.7e-109:519:99//AF086165

55 R-NT2RP2000298

R-NT2RP2000310//Homo sapiens p53 induced protein mRNA, partial cds./.1.5e-38:224:93//AF010310

R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the  
HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE

pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence./I4.3e-113:580:96//AL022398  
R-NT2RP2000329//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces./I7.4e-47:367:77//AC006039

5 R-NT2RP2000337//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits)./I4.9e-08:494:58//L04272

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds./I3.4e-46:262:  
10 94//U83981  
R-NT2RP2000369//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces./I3.0e-07:334:61//AC002993  
R-NT2RP2000414//Mouse DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone BAC394, WORKING DRAFT SEQUENCE./I7.0e-08:98:83//AJ004828

15 R-NT2RP2000420//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence./I0.99:150:62//AC005324  
R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds./I4.6e-19:142:  
90//AF102265  
R-NT2RP2000438//RPCI11-62I13.TK RPCI11 Homo sapiens genomic clone R-62I13, genomic survey sequence./I  
20 3.1e-06:103:79//AQ199572  
R-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence./I2.0e-22:276:73//AC004691  
R-NT2RP2000459//CIT-HSP-2013N9.TR CIT-HSP Homo sapiens genomic clone 2013N9, genomic survey se-  
quence./I5.5e-27:205:87//853940

25 R-NT2RP2000498//Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence./I6.0e-12:119:84//AC001234  
R-NT2RP2000503//Human CYP11B2 gene for steroid 18-hydroxylase (P-450 C18), 5'-flanking region and exon 1./I0.48:201:64//D10170  
R-NT2RP2000510//Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence./I3.6e-07:  
30 472:59//AF033929  
R-nnnnnnnnnnnnn  
R-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE./I2.3e-61:317:97//AL022318  
R-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds./I6.6e-29:167:97//AB005543

35 R-NT2RP2000617  
R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds./I2.5e-64:335:96//AB014514  
R-NT2RP2000644//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat./I1.8e-28:383:70//Z92545

40 R-NT2RP2000656//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence./I0.0093:110:70//AL021997  
R-NT2RP2000658//Bacillus thuringiensis chitinase (chi) gene, complete cds./I0.73:301:60//U89796  
R-NT2RP2000668

45 R-NT2RP2000678//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 8/15, WORKING DRAFT SEQUENCE./I2.8e-11:256:66//AP000015  
R-NT2RP2000710//Genomic sequence from Human 17, WORKING DRAFT SEQUENCE, 9 unordered pieces./I  
0.036:176:69//AC002346  
R-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence./I2.7e-110:555:96//AC004540

50 R-NT2RP2000731//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containg transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence./I2.6e-18:319:68//AL023775  
R-NT2RP2000758//CIT-HSP-507A14.TR CIT-HSP Homo sapiens genomic clone 507A14, genomic survey se-  
quence./I1.0:189:60//B50590  
R-NT2RP2000764  
R-NT2RP2000809//Human BAC clone RG356F09 from 7p21, complete sequence./I1.7e-24:215:81//AC004002  
R-NT2RP2000812//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey se-

quence.//9.5e-32:176:97//B99575  
R-nnnnnnnnnnnn/paramecium species 5,87 mt dna dimer: replication init. region.//0.0077:418:57//K00916  
R-NT2RP2000816//F.rubripes GSS sequence, clone 011H02aA6, genomic survey sequence.//0.61:52:73//  
AL011013

5 R-NT2RP2000819  
R-NT2RP2000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 43408, WORKING  
DRAFT SEQUENCE.//0.00012:181:70//AL033504  
R-NT2RP2000842//Mus musculus (C57BL/10 X C3H)F2 clone 4.9 novel mRNA from reninexpressing kidney tumor  
cell line, partial sequence.//3.7e-27:388:72//U13370

10 R-NT2RP2000845//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//0.0022:200:  
68//AC005703  
R-NT2RP2000863  
R-NT2RP2000880//Homo sapiens mRNA for putative GTP-binding protein, partial.//2.3e-43:279:89//AJ006412  
R-NT2RP2000892//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer , segment 7/10.//  
15 0.0028:221:62//AB020875  
R-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//2.2e-55:290:96//AB018266  
R-NT2RP2000938//Homo sapiens full-length insert cDNA clone ZD55G12.//2.1e-37:215:93//AF086336  
R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//3.0e-96:494:96//AB018298  
R-NT2RP2000965

20 R-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs,  
STSs and GSSs and genomic marker D22S56, complete sequence.//4.5e-87:440:97//AL021393  
R-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//5.4e-93:484:  
95//AC005277

25 R-NT2RP2000987//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.1e-06:  
318:62//AE001372  
R-NT2RP2001036//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING  
DRAFT SEQUENCE.//2.0e-24:273:73//AL031732  
R-NT2RP2001044//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//3.3e-07:365:65//AC005140

30 R-NT2RP2001065//Caenorhabditis elegans cosmid F10G7.//9.2e-06:273:59//U40029  
R-NT2RP2001070//CITBI-E1-2503F4.TF CITBI-E1 Homo sapiens genomic clone 2503F4, genomic survey se-  
quence.//0.13:97:72//AQ265973  
R-NT2RP2001094//Mycoplasma mycoides mycoides SC immunodominant protein P72 (p72) gene, complete cds,  
mannitol-1-phosphate dehydrogenase (mt1D) gene, partial cds and insertion sequence IS1296, complete se-  
35 quence.//0.018:373:57//U61140  
R-NT2RP2001119  
R-NT2RP2001127//Homo sapiens HRIHFB2060 mRNA, partial cds.//4.5e-55:304:94//AB015348  
R-NT2RP2001137//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the  
40 TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase  
Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a  
probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted  
CpG island, ESTs, STSs and GSSs, complete sequence.//0.69:129:65//AL022394  
R-NT2RP2001149//Sequence 5 from Patent US 4798885.//8.5e-28:322:77//I01838  
R-NT2RP2001168

45 R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//4.8e-95:490:96//AB 007949  
R-NT2RP2001174//CIT-HSP-2170B18.TR CIT-HSP Homo sapiens genomic clone 2170B18, genomic survey se-  
quence.//1.3e-33:204:93//B89680  
R-NT2RP2001196//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-65, complete  
sequence.//1.7e-06:413:61//AL010134

50 R-NT2RP2001218//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS,  
GSS, complete sequence.//8.5e-15:278:68//AL022153  
R-NT2RP2001226//Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudog-  
ene similar to U-SNRNP associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete  
sequence.//0.0020:462:57//AL030995

55 R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP Homo sapiens genomic clone 2356P23, genomic survey se-  
quence.//8.0e-108:547:96//AQ081110  
R-NT2RP2001245//Spodoptera frugiperda 16S rRNA gene, Val-tRNA, and Leu-tRNA genes, and ND-1 protein  
gene, 5' end.//0.0052:350:58//M76713

R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds./.4.6e-111:544:97//AB018353  
 R-NT2RP2001277//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y59A8,  
 WORKING DRAFT SEQUENCE./.0.0058:327:59//Z98870  
 5 R-NT2RP2001290//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces./.0.96:187:65//AC004709  
 R-NT2RP2001295//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence./.0.59:218:62//  
 AC006041  
 R-NT2RP2001312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING  
 10 DRAFT SEQUENCE./.0.12:117:64//AL033520  
 R-NT2RP2001327//Caenorhabditis elegans cosmid R04D3, complete sequence./.0.31:119:66//Z70212  
 R-NT2RP2001328//HS\_2213\_A1\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2213 Col=13 Row=G, genomic survey sequence./.1.7e-22:200:83//AQ136874  
 R-NT2RP2001347//Plasmodium falciparum MAL3P8, complete sequence./.0.81:509:56//AL034560  
 R-NT2RP2001378//H.sapiens DNA sequence./.0.94:147:63//Z22404  
 15 R-NT2RP2001381//Homo sapiens cyclin E2 mRNA, complete cds./.3.2e-09:75:97//AF091433  
 R-NT2RP2001392//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds./.0.079:178:62//  
 L19301  
 R-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands  
 20 and polymorphic CA repeat./.3.4e-60:351:90//Z93242  
 R-NT2RP2001397//Hamster mRNA for cyclinB2, complete cds./.5.4e-55:320:83//D17294  
 R-NT2RP2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108D11, WORKING  
 DRAFT SEQUENCE./.1.0e-44:246:85//AL034419  
 25 R-NT2RP2001423//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs  
 and a GSS, complete sequence./.3.7e-05:417:61//AL031273 R-NT2RP2001427//Human Chromosome 11 Cosmid  
 cSRL34e5, complete sequence./.0.94:287:59//U73643  
 R-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence./.5.2e-31:299:77//AF046702  
 R-NT2RP2001440//Rattus norvegicus mRNA for 14-3-3 protein gamma-subtype, complete cds./.7.8e-75:548:83//  
 D17447  
 R-NT2RP2001445//Homo sapiens 12q13.1 PAC RPCI-228P16 (Roswell Park Cancer Institute Human PAC Li-  
 30 brary) complete sequence./.1.0e-06:452:59//AC004801  
 R-NT2RP2001449//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces./.  
 5.1e-08:218:67//AC004846  
 R-NT2RP2001450  
 R-NT2RP2001467//Human BAC clone RG343P13 from 7q31, complete sequence./.3.8e-31:254:83//AC002465  
 35 R-NT2RP2001506//C.barati p-47, nt nh, bonT genes./.1.2e-06:415:60//Y12091  
 R-NT2RP2001511//Plasmodium falciparum MAL3P7, complete sequence./.0.11:155:63//AL034559  
 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1./.2.1e-104:545:95//Y14494  
 R-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence./.7.0e-16:283:68//  
 AC004596  
 40 R-NT2RP2001536//Human DNA from chromosome 14-specific cosmid containing XRCC3 DNA repair gene, ge-  
 nomic sequence, complete sequence./.7.7e-16:108:96//AF037222  
 R-NT2RP2001560//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey se-  
 quence./.0.052:112:66//B73597  
 R-NT2RP2001569//CIT-HSP-2335F8.TP CIT-HSP Homo sapiens genomic clone 2335F8, genomic survey se-  
 quence./.6.0e-78:383:98//AQ042029  
 45 R-NT2RP2001576//Homo sapiens sulfonylurea receptor (SUR2) gene, exon 37./.0.33:135:66//AF061322  
 R-NT2RP2001581//Homo sapiens (clone MFD220) PCR primer./.2.7e-07:240:63//L15407  
 R-NT2RP2001597//HS\_3016\_B2\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3016 Col=12 Row=L, genomic survey sequence./.5.3e-45:310:87//AQ118854  
 50 R-NT2RP2001601//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, complete sequence./.0.015:445:58//  
 AC006079  
 R-NT2RP2001613//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence./.3.5e-16:  
 413:63//AF009326  
 55 R-NT2RP2001628//Phytomonas serpens kinetoplast maxicircle ribosomal protein S12 (G6) edited mRNA, com-  
 plete cds./.0.11:190:63//AF034626  
 R-NT2RP2001663//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence./.3.0e-26:  
 157:81//AC004125  
 R-NT2RP2001677//Homo sapiens chromosome 9, P1 clone 11659, complete sequence./.3.0e-58:305:96//

AC004472  
R-NT2RP2001678//Human BAC clone RG222A16 from 7q31, complete sequence./.0.95:107:66//AC002385  
R-NT2RP2001699//Mus musculus erythroid ankyrin and two alternatively spliced erythroid ankyrins (Ank1) gene, putative exon 41 and partial cds./.8.8e-05:211:63//U76758

5 R-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence./.4.7e-68:352:97//AC004079  
R-NT2RP2001721//HS-1052-B1-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=11 Row=N, genomic survey sequence./.7.7e-05:346:59//B40914  
R-NT2RP2001740//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence./.1.1e-16:162:82//AQ175104  
10 R-NT2RP2001748//Human gene for L-histidine decarboxylase, complete cds./.2.0e-33:312:77//D16583  
R-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence./.2.3e-100:435:97//AC004783  
R-NT2RP2001813//Human leukocyte common antigen T200 (CD45, LCA) gene, exon 9./.0.031:261:60//M23468  
15 R-NT2RP2001861  
R-NT2RP2001869//Sequence 5 from patent US 5595900./.4.2e-21:194:77//I34189  
R-NT2RP2001876  
R-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence./.5.0e-111:485:97//AL031864  
20 R-NT2RP2001900  
R-NT2RP2001907//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds./.5.4e-42:382:77//U07563  
R-NT2RP2001926//HS\_3180\_B2\_F02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=L, genomic survey sequence./.2.8e-25:138:80//AQ185415  
25 R-NT2RP2001936//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces./.1.0:320:60//AC005504  
R-NT2RP2001943//Dictyostelium discoideum PkgA (pkgA) gene, partial cds./.1.4e-08:378:59//AF020280  
R-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence./.3.6e-85:409:100//AC005033  
30 R-NT2RP2001947//Human mRNA for KIAA0390 gene, complete cds./.0.85:140:64//AB002388  
R-NT2RP2001969  
R-NT2RP2001976//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence./.2.0e-60:307:98//B99575  
R-NT2RP2001985//Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAll project).//.0.031:282:61//  
35 AL022140  
R-NT2RP2002025  
R-NT2RP2002032//CITBI-E1-2502C19.TF CITBI-E1 Homo sapiens genomic clone 2502C19, genomic survey sequence./.1.2e-52:285:95//AQ264715  
R-NT2RP2002033//Human (lambda) DNA for immunoglobulin light chain./.1.1e-08:389:61//D88270  
40 R-NT2RP2002041//Homo sapiens 12p13.3 BAC RPCI11-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence./.1.1e-49:264:97//AC006206  
R-NT2RP2002046//Human BAC clone GS119P05 from 7q21, complete sequence./.0.0023:429:61//AC004011  
R-NT2RP2002047//P.falciparum PK1 gene./.0.00015:239:62//X83707  
R-NT2RP2002058//HS\_2183\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=1 Row=M, genomic survey sequence./.1.2e-21:185:84//AQ022560  
45 R-NT2RP2002066//G.gallus microsatellite DNA (LEI0222 (=T15ivD04)).//0.18:102:70//Z83792  
R-NT2RP2002070//P.falciparum major merozoite surface antigen (PMMSA) mRNA, complete cds, isolate FC27./.0.95:192:61//M19143  
R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence./.3.8e-25:182:86//AF052183  
50 R-NT2RP2002079//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence./.1.7e-10:97:90//AL009178  
55 R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein./.4.6e-59:376:89//AJ007509  
R-NT2RP2002105  
R-NT2RP2002124//RPCI11-75J16.TJ RPCI11 Homo sapiens genomic clone R-75J16, genomic survey sequence./.0.58:191:64//AQ266779

R-NT2RP2002137//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence./.0.0065:294:61//AC005913  
R-NT2RP2002154  
5 R-NT2RP2002172//RPCI11-90C20.TJ RPCI11 Homo sapiens genomic clone R-90C20, genomic survey sequence./.0.049:160:65//AQ282591  
R-NT2RP2002185//CIT-HSP-2341I15.TF CIT-HSP Homo sapiens genomic clone 2341I15, genomic survey sequence./.6.0e-36:230:90//AQ053355  
R-NT2RP2002192//HS\_2222\_B1\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=15 Row=L, genomic survey sequence./.1.9e-15:249:71//AQ178491  
10 R-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds./.4.7e-35:438:73//AF032872  
R-NT2RP2002208//Hansenula wingei mitochondrial DNA, complete sequence./.0.00057:468:57//D31785  
R-NT2RP2002219//HS\_2058\_A1\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=E, genomic survey sequence./.3.4e-55:512:77//AQ234380  
15 R-NT2RP2002231//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-31, complete sequence./.1.5e-06:398:61//Z98557  
R-nnnnnnnnnnnnnn//Sequence 11 from patent US 5624818./.3.3e-91:553:87//I41141  
R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds./.3.0e14:132:84//AF005418  
R-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING  
20 DRAFT SEQUENCE./.1.6e-96:548:91//AL033527  
R-NT2RP2002270//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence./.5.1e-06:391:60//AC004605  
R-NT2RP2002292//Genomic sequence from Human 13, complete sequence./.0.91:159:64//AC001226  
R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds./.1.3e-101:527:94//  
25 AF069532  
R-NT2RP2002316//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence./.0.00052:389:59//AE001408  
R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds./.2.3e-112:567:95//AF093668  
30 R-NT2RP2002333//Rat POU domain factor (Brn-5) mRNA./.1.5e-22:323:73//L23204  
R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds./.3.7e-102:600:89//AF038958  
R-NT2RP2002394//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
35 DRAFT SEQUENCE, 5 unordered pieces./.0.039:399:59//AC005308  
R-NT2RP2002408//HS\_2212\_A1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=17 Row=I, genomic survey sequence./.9.6e-35:231:88//AQ184632  
R-NT2RP2002426//Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complete sequence./.2.8e-39:308:82//AL021877  
40 R-NT2RP2002439//Leishmania tarentolae mitochondrial electron transport chain component mRNA./.0.022:102:71//M74225  
R-NT2RP2002457//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence./.0.00099:354:59//Z99289  
45 R-NT2RP2002464//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 6/15, WORKING DRAFT SEQUENCE./.0.0015:219:67//AP000013  
R-NT2RP2002475  
50 R-nnnnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds./.3.1e-113:605:92//AB005289  
R-NT2RP2002498//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence./.0.32:210:64//Z98047  
R-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence./.4.0e-86:429:98//AC006213  
R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds./.2.7e-105:583:91//AB018334  
55 R-NT2RP2002520//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes./.0.14:406:58//AJ223323  
R-NT2RP2002537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE./.2.8e-16:188:78//AL023583

R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA./.4.7e-108:571:93//AF009314  
 R-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence./.1.1e-103:422:95//AC005316  
 R-NT2RP2002591//Human DNA binding protein (HPF2) mRNA, complete cds./.1.8e-36:526:67//M27878  
 5 R-NT2RP2002595  
 R-NT2RP2002606//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE./.7.2e-10:211:71//AL033529  
 R-NT2RP2002609  
 R-NT2RP2002618//Plasmodium falciparum MAL3P6, complete sequence./.2.9e-05:566:60//Z98551  
 10 R-NT2RP2002621//Human DNA sequence from PAC 341I10 on chromosome 6q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo)gene, ESTs and STSs./.1.1e-38:348:78//Z97352  
 R-NT2RP2002643//Homo sapiens chromosome 11 clone pTWB15.28 map 11p15.4-p15.5, genomic survey sequence./.1.2e-35:414:66//AF074030  
 15 R-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence./.1.3e-77:403:95//AC005384  
 R-NT2RP2002701  
 R-NT2RP2002706//Homo sapiens chromosome 19, cosmid F22676, complete sequence./.4.0e-42:147:90//AC005778  
 20 R-NT2RP2002710//P.falciparum serine rich protein (SERP I) gene./.0.84:135:67//J03983  
 R-NT2RP2002727//, complete sequence./.1.0:363:59//AC005815  
 R-NT2RP2002736//Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence./.0.44:267:60//AC004138  
 R-NT2RP2002740//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence./.0.0016:474:60//AC004674  
 25 R-NT2RP2002741//HS\_3051\_B1\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=21 Row=P, genomic survey sequence./.1.1e-38:217:86//AQ106283  
 R-NT2RP2002750//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence./.5.0e-36:430:75//AC002395  
 R-NT2RP2002752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366L4, WORKING 30 DRAFT SEQUENCE./.8.2e-41:437:76//AL023494  
 R-NT2RP2002753//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces./.6.8e-100:496:97//AC004882  
 R-NT2RP2002769//paramecium species 5,311 mt dna dimer: replication init. region./.7.4e-10:404:60//K00917  
 R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence./.1.2e-63:341:94//AF070537  
 35 R-NT2RP2002800//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence./.4.9e-60:321:95//AQ029850  
 R-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces./.2.9e-100:492:98//AC006078  
 R-NT2RP2002857//HS\_3026\_B2\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=14 Row=P, genomic survey sequence./.8.9e-06:242:62//AQ 128697  
 40 R-NT2RP2002862//RPCI11-42I15.TJ RPCI11 Homo sapiens genomic clone R-42I15, genomic survey sequence./.1.5e-44:270:85//AQ052700  
 R-NT2RP2002880//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE./.1.0:295:58//AL022318  
 45 R-NT2RP2002891  
 R-NT2RP2002925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 243L18, WORKING DRAFT SEQUENCE./.2.0e-24:395:67//AL034395  
 R-NT2RP2002928//Plasmodium falciparum MAL3P5, complete sequence./.0.044:461:55//AL034556  
 R-NT2RP2002929//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING 50 DRAFT SEQUENCE, 14 unordered pieces./.0.35:491:56//AC005140  
 R-NT2RP2002954//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence./.1.0:275:61//AC005701  
 R-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds./.2.7e-61:508:79//U62483  
 55 R-NT2RP2002979//RPCI11-20F13.TPK RPCI-11 Homo sapiens genomic clone RPCI-11-20F13, genomic survey sequence./.0.88:110:72//AQ008132  
 R-NT2RP2002980//Homo sapiens PAC clone DJ0841B21 from 7q21.1-q31.1, complete sequence./.1.1e-102:433:95//AC004140

R-NT2RP2002986//Human DNA sequence from clone 1147O16 on chromosome Xp21.1-21.3. Contains 13 exons of the DMD muscular dystrophy gene. Contains an STS and GSSs, complete sequence.//0.31:219:62//AL031542  
 R-NT2RP2002987//Homo sapiens chromosome 18, clone hRPK.24\_A\_23, complete sequence.//1.3e-51:283:88//AC005968  
 5 R-NT2RP2002993//Human DNA sequence from PAC 106B9 on chromosome Xq21://4.3e-11:430:63//AL021307  
 R-NT2RP2003000//Saccharomyces cerevisiae mitochondrial transfer RNA- Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.//0.00088:347:62//L36887  
 R-NT2RP2003034//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 2/10.//3.5e-33:271:82//AB020870  
 10 R-NT2RP2003073  
 R-NT2RP2003099//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//1.5e-45:548:69//AC004914  
 R-NT2RP2003108  
 R-NT2RP2003117//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-51:323:88//AC005378  
 15 R-NT2RP2003121//HS\_2238\_A1\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=I, genomic survey sequence.//0.00055:324:61//AQ293058  
 R-NT2RP2003125  
 R-NT2RP2003129  
 R-NT2RP2003137//Human BAC clone RG084D04 from 7q31, complete sequence.//1.1e-46:521:74//AC003084  
 20 R-NT2RP2003161//Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence.//1.0:368:59//AC005879  
 R-NT2RP2003164//Dictyostelium discoideum actin 4 gene, 3' UTR.//1.0:120:64//M25581  
 R-NT2RP2003165//Homo sapiens chromosome 17, clone hRPK.1018\_N\_14, complete sequence.//2.2e-71:467:86//AC005823  
 25 R-NT2RP2003177  
 R-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.1e-95:585:88//AL031597  
 R-NT2RP2003206//P.falciparum interspersed repeat antigen (FIRA) gene.//0.039:338:60//M17877  
 R-NT2RP2003230//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-11:542:60//Z98551  
 30 R-NT2RP2003237//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence.//1.0:311:60//AB016888  
 R-NT2RP2003243//CIT-HSP-2368D12.TR CIT-HSP Homo sapiens genomic clone 2368D12, genomic survey sequence.//0.39:112:66//AQ077738  
 R-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//1.3e-38:273:83//L38481  
 35 R-NT2RP2003272//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//4.4e-15:181:66//AC004187  
 R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//4.2e-110:565:95//AB014525  
 R-NT2RP2003280//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.2e-12:221:70//AC005831  
 R-NT2RP2003286//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//0.86:379:60//AC005261  
 R-NT2RP2003293//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0e-39:418:74//AC005079  
 45 R-NT2RP2003295//HS\_2053\_B1\_A10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=19 Row=B, genomic survey sequence.//0.0016:346:61//AQ235251  
 R-NT2RP2003297//Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence.//0.74:397:56//AC002332  
 R-NT2RP2003308//Homo sapiens PAC clone DJ1098B01 from 7q11.23-q21, complete sequence.//0.99:447:60//AC004960  
 50 R-NT2RP2003329//C.reinhartii psbB 5' flanking region.//0.79:161:59//X59731  
 R-NT2RP2003339//RPCI11-57H15.TK RPCI11 Homo sapiens genomic clone R-57H15, genomic survey sequence.//0.13:184:64//AQ116039  
 R-NT2RP2003347//RPCI11-15B19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15B19, genomic survey sequence.//6.4e-31:218:89//B76357  
 R-NT2RP2003367//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//9.0e-11:101:84/U91321  
 55 R-NT2RP2003391//HS\_2255\_B2\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=2255 Col=8 Row=D, genomic survey sequence.//1.6e-38:247:90//AQ068937  
 R-NT2RP2003393//RPCI11-44K6.TJ RPCI11 Homo sapiens genomic clone R-44K6, genomic survey sequence.//  
 3.9e-31:290:79//AQ202481  
 R-NT2RP2003394//Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I.//5.1e-14:579:61//  
 5 X14910  
 R-NT2RP2003401//Caprine arthritis-encephalitis virus tat protein (tat) and envelope glycoprotein (env) gene, par-  
 tial cds.//0.32:174:66//U81429  
 R-NT2RP2003433//Ascidian mRNA for HRSec61, complete cds.//1.5e-10:193:69//D25536  
 R-NT2RP2003445//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING  
 10 DRAFT SEQUENCE.//4.4e-99:585:89//AL023808  
 R-NT2RP2003446  
 R-NT2RP2003456//Plasmodium falciparum MAL3P7, complete sequence.//0.98:399:57//AL034559  
 R-NT2RP2003480//Homo sapiens full-length insert cDNA clone ZE09A11.//4.7e-111:540:98//AF086540  
 R-NT2RP2003499  
 15 R-NT2RP2003506  
 R-NT2RP2003511  
 R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//4.1e-107:566:93//D87460  
 R-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//1.5e-60:  
 518:79//M12783  
 20 R-NT2RP2003522//HS\_2182\_A1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2182 Col=9 Row=G, genomic survey sequence.//0.053:251:60//AQ024304  
 R-NT2RP2003533//Homo sapiens chromosome 12p13.3 clone RPCI4-816N1, WORKING DRAFT SEQUENCE,  
 31 unordered pieces.//1.5e-37:328:80//AC005841  
 25 R-NT2RP2003543//HS\_3028\_A2\_C12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3028 Col=24 Row=E, genomic survey sequence.//2.0e-39:203:100//AQ094957  
 R-NT2RP2003559//Homo sapiens full-length insert cDNA clone ZD65E09.//2.3e-59:325:95//AF088055  
 R-NT2RP2003564  
 R-NT2RP2003581  
 30 R-NT2RP2003596//HS\_2163\_B1\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2163 Col=21 Row=H, genomic survey sequence.//0.0011:212:67//AQ125143  
 R-NT2RP2003604//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//5.4e-102:501:97//U97067  
 R-NT2RP2003629//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.0012:363:61//AC005507  
 35 R-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminc acid synthetase.//5.1e-37:561:68//  
 AJ006215  
 R-NT2RP2003668//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chro-  
 mosome X contains ESTs.//0.0053:395:58//Z76735  
 R-NT2RP2003687//Human BAC clone RG222A16 from 7q31, complete sequence.//8.0e-10:205:67//AC002385  
 R-NT2RP2003691//HS\_3252\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=3252 Col=22 Row=A, genomic survey sequence.//5.3e-05:332:60//AQ219783  
 R-NT2RP2003702//CIT-HSP-2333P5.TF CIT-HSP Homo sapiens genomic clone 2333P5, genomic survey se-  
 quence.//3.9e-43:431:75//AQ035000  
 R-NT2RP2003704  
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-45:265:93//AB011097  
 45 R-NT2RP2003713//Human DNA sequence from PAC 411B6 on chromosome X \*.//0.64:169:67//Z84470  
 R-NT2RP2003714//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//  
 4.6e-11:152:73//295704  
 R-nnnnnnnnnnnn//H.sapiens mRNA for PIBF1 protein, complete.//0.94:443:59//Y09631  
 R-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//  
 50 2.2e-109:547:96//AC004951  
 R-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//4.1e-  
 109:545:97//AC004626  
 R-NT2RP2003760//B. taurus mRNA for gamma-COP.//6.3e-28:400:69//X70019  
 R-NT2RP2003764//Mouse preprosomatostatin gene.//0.90:285:62//X51468  
 55 R-NT2RP2003769//Schizosaccharomyces pombe gene for protein involved in sexual development, complete  
 cds.//0.96:446:58//D87956  
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds.//1.8e-104:531:96//AF047437  
 R-NT2RP2003777

R-NT2RP2003781//HS\_3109\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=7 Row=D, genomic survey sequence./.1.3e-60:346:92//AQ186749  
R-NT2RP2003793  
R-NT2RP2003840  
5 R-NT2RP2003857//HS\_2205\_A2\_H12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=24 Row=O, genomic survey sequence./.8.1e-22:127:99//AQ151299  
R-NT2RP2003859//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence./.8.3e-60:320:95//AQ029850  
R-NT2RP2003871//HS\_3210\_A1\_C08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3210 Col=15 Row=E, genomic survey sequence./.8.6e-09:322:61//AQ175028  
10 R-NT2RP2003885//RPCI11-7M10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-7M10, genomic survey sequence./.4.7e-67:380:92//B72214  
R-NT2RP2003912//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE./.1.2e-33:379:75//AL023693  
15 R-NT2RP2003952  
R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds./.2.3e-114:568:97//AB014458  
R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds./.1.1e-107:540:97//AB007916  
20 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds./.7.7e-114:568:96//AB018347  
R-NT2RP2003984  
R-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces./.6.6e-99:551:92//AC0003 82  
R-NT2RP2003988  
R-NT2RP2004014  
25 R-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence./.4.9e-114:568:97//AC004780  
R-NT2RP2004042//nbxb0020F03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020F03r, genomic survey sequence./.0.11:195:64//AQ258389  
R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE./.7.6e-110:564:95//AL034555  
30 R-NT2RP2004081//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces./.0.012:503:57//AC005308  
R-NT2RP2004098//H.sapiens CpG island DNA genomic Mse1 fragment, clone 133h3, reverse read cpg133h3.rt1a./.7.9e-25:140:100//Z64530  
35 R-NT2RP2004124  
R-NT2RP2004142//CIT-HSP-2316F21.TR CIT-HSP Homo sapiens genomic clone 2316F21, genomic survey sequence./.2.8e-83:409:98//AQ034964  
R-NT2RP2004152//HS\_3065\_A2\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence./.2.5e-62:304:100//AQ137776  
40 R-NT2RP2004165//Anthocidaris crassispina mRNA for dynein beta-heavy chain, complete cds./.3.4e-20:343:65//D01021  
R-NT2RP2004170///\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces./.2.5e-89:587:86//AC004064  
45 R-NT2RP2004172//Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 3' end./.0.24:440:60//AF017047  
R-NT2RP2004187//RPCI11-59E12.TK RPCI11 Homo sapiens genomic clone R-59E12, genomic survey sequence./.3.1e-05:175:66//AQ198120  
R-NT2RP2004194  
50 R-NT2RP2004196//Fugu rubripes GSS sequence, clone 076D01bE2, genomic survey sequence./.1.6e-22:178:71//AL026601  
R-NT2RP2004207//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence./.0.19:175:64//AC005023  
R-NT2RP2004226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE./.6.1e-17:445:64//AL023808  
55 R-NT2RP2004232//M.musculus (Balb/c) mRNA for serine/threonine protein kinase./.3.2e-25:326:71//Z34524  
R-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds./.8.7e-108:563:94//AB015718  
R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds./.1.1e-101:530:93//AF039687

- R-NT2RP2004242
- R-NT2RP2004245//Homo sapiens DNA sequence from PAC 455H14 on chromosome Xq21.3-22.3. Contains genomic marker DXS1203 with a CA repeat polymorphism, STSs and GSSs, complete sequence.//5.1e-08:236:65//AL023280
- 5 R-NT2RP2004270//Lycopersicon esculentum *ldh2* gene.//0.98:259:61//Y10603
- R-NT2RP2004300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1068F16, WORKING DRAFT SEQUENCE.//5.0e-14:396:65//AL023913
- R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//1.5e-108:544:96//AF000416
- 10 R-NT2RP2004321//*Caenorhabditis elegans* cosmid F47B8, complete sequence.//0.0078:333:61//Z77662
- R-NT2RP2004339//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.4e-75:306:86//AC005229
- R-NT2RP2004347//RPCI11-90N11.TJ RPCI11 Homo sapiens genomic clone R-90N11, genomic survey sequence.//2.9e-87:494:92//AQ284548
- 15 R-NT2RP2004364//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to *C. elegans* C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//4.2e-10:161:76//AL031010
- R-NT2RP2004365//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//3.6e-08:483:57//AE001433
- 20 R-NT2RP2004366//*F.rubripes* GSS sequence, clone 013B16aF3, genomic survey sequence.//2.1e-05:128:67//AL000528
- R-NT2RP2004373//Homo sapiens 12q24.2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.81:205:62//AC006065
- R-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//3.9e-06:82:84//AQ063969
- 25 R-NT2RP2004392//*Ceratovacuna* sp. mitochondrial cytochrome oxidase I (3' end), cytochrome oxidase II (complete cds) and transfer RNA-Leu gene.//2.7e-06:495:58//L39993
- R-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//6.4e-111:572:96//AC005164
- R-NT2RP2004399//*Arabidopsis thaliana* chromosome I BAC F11M15 genomic sequence, complete sequence.//0.13:253:64//AC006085
- 30 R-NT2RP2004400//HS\_3238\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=22 Row=O, genomic survey sequence.//5.1e-23:162:89//AQ211412
- R-NT2RP2004412//*Saccharomyces douglasii* mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//2.6e-09:458:60//M97514
- 35 R-NT2RP2004425//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//0.99:481:56//AL022718
- R-NT2RP2004476//*Rattus norvegicus* activity and neurotransmitter-induced early gene 6 (ania-6) mRNA, 3'UTR.//5.3e-99:600:90//AF030091
- 40 R-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//3.9e-115:575:97//AC005591
- R-NT2RP2004512//Plasmodium falciparum MAL3P3, complete sequence.//0.00034:517:58//Z98547
- R-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//1.8e-115:571:97//AC004890
- 45 R-NT2RP2004538//Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.//1.7e-47:322:87//AC005091
- R-NT2RP2004551//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//0.035:511:58//AC005184
- 50 R-NT2RP2004568//T7C20-Sp6 *Arabidopsis thaliana* genomic clone T7C20, genomic survey sequence.//0.70:446:54//B08766
- R-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 136B1, WORKING DRAFT SEQUENCE.//2.2e-53:397:74//AL031768
- R-NT2RP2004587//CIT-HSP-2376P22.TF CIT-HSP Homo sapiens genomic clone 2376P22, genomic survey sequence.//0.0079:223:63//AQ108976
- 55 R-NT2RP2004594//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.3e-10:493:62//AC004605
- R-NT2RP2004600//Homo sapiens full-length insert cDNA clone ZE04E06.//2.1e-70:343:99//AF086522
- R-NT2RP2004602//Homo sapiens full-length insert cDNA clone YW26E09.//2.0e-96:528:93//AF086033

	R-NT2RP2004614
	R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein //7.3e-117:587:96//AJ006291
	R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds //1.8e-105:520:96//AB007929
5	R-NT2RP2004675//Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds //3.4e-22:197:79//U63721
	R-NT2RP2004681//Rat notch 2 mRNA //8.0e-30:276:78//M93661
	R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds //1.6e-118:600:96//AB014525
	R-NT2RP2004709//Homo sapiens full-length insert cDNA clone ZD42A08 //3.5e-14:139:86//AF086259
10	R-NT2RP2004710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE //6.9e-117:592:96//AL031447
	R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds //4.2e-117:594:96//AB007947
	R-NT2RP2004743//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces //0.53:403:59//AC005505
15	R-NT2RP2004767//Human DNA sequence from PAC 491M17 on chromosome 1p36.2-1p36.3 //2.0e-81:568:84//Z97988
	R-NT2RP2004775//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits) //4.0e-08:365:62//L04272
20	R-NT2RP2004791//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence //7.8e-111:541:98//AC005216
	R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds //2.5e-114:564:96//AF058953
	R-NT2RP2004802
25	R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds //2.7e-118:584:97//AF054179
	R-NT2RP2004841//Human BAC clone RG308B22 from 7q22-q31, complete sequence //4.0e-46:447:72//AC002089
	R-NT2RP2004861//Plasmodium falciparum MAL3P5, complete sequence //0.19:189:66//AL034556
30	R-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence //1.1e-08:330:61//AC004383
	R-NT2RP2004936//CIT-HSP-2374L4.TF CIT-HSP Homo sapiens genomic clone 2374L4, genomic survey sequence //0.99:129:65//AQ110571
	R-nnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence //0.014:402:61//Z98551
	R-NT2RP2004961//RPCI11-45P2.TK RPCI11 Homo sapiens genomic clone R-45P2, genomic survey sequence //9.3e-90:453:97//AQ202282
35	R-NT2RP2004962//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y40H4, WORKING DRAFT SEQUENCE //0.017:291:61//AL022573
	R-NT2RP2004967//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces //4.6e-52:496:77//AC005077
40	R-NT2RP2004978//Homo sapiens chromosome 19, cosmid F23269, complete sequence //0.088:322:63//AC005614
	R-NT2RP2004982//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence //0.025:339:61//AC003071
	R-NT2RP2004985//T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24, genomic survey sequence //0.40:111:70//B78148
45	R-NT2RP2004999//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces //0.23:157:68//AC005682
	R-NT2RP2005000
	R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds //3.0e-111:577:95//AB014515
50	R-NT2RP2005003//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence //2.4e-21:246:77//AC004673
	R-nnnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds //9.5e-115:568:97//AF100141
	R-NT2RP2005018//HS_3108_B1_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=17 Row=J, genomic survey sequence //1.9e-31:222:89//AQ104050
55	R-NT2RP2005020//Rattus norvegicus cationic amino acid transporter-1 (CAT-1) mRNA, complete cds //6.6e-41:566:73//U70476
	R-NT2RP2005031//CIT-HSP-516A2.TV CIT-HSP Homo sapiens genomic clone 516A2, genomic survey sequence //4.1e-31:357:75//B49897
	R-NT2RP2005037

R-NT2RP2005038//Sequence 5 from patent US 5552281./.2.2e-32:178:98//I25644  
R-NT2RP2005108//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence./.3.7e-23:  
475:67//AF009326  
R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds./.8.4e-104:518:97//AB014564  
5 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//1.4e-67:464:85//  
X98743  
R-NT2RP2005139  
R-NT2RP2005140//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA  
10 sequence./.7.9e-08:460:60//U00101  
R-NT2RP2005144//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORKING DRAFT SEQUENCE,  
129 ordered pieces./.2.5e-103:519:96//AC005911  
R-NT2RP2005147//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces./.  
0.068:100:75//AC004971  
R-NT2RP2005159//CITBI-E1-2506A8.TF CITBI-E1 Homo sapiens genomic clone 2506A8, genomic survey se-  
15 quence./.90:113:71//AQ262104  
R-NT2RP2005162//Homo sapiens chromosome 17, clone HCIT307A16, complete sequence./.5.0e-14:183:75//  
AC003041  
R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein./.7.5e-100:513:95//AJ007509  
R-NT2RP2005204  
20 R-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence./.7.2e-119:583:97//  
AC005189  
R-NT2RP2005239//Homo sapiens mRNA for putative tRNA splicing protein, partial./.8.4e-62:312:98//AJ010952  
R-NT2RP2005254//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a  
25 Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloro-  
plast 30S ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691  
and STSs./.5.7e-09:328:62//Z99297  
R-NT2RP2005270//Plasmodium falciparum MAL3P8, complete sequence./.2.3e-05:355:61//AL034560  
R-NT2RP2005276//Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence./.0.0014:541:  
58//AC000107  
30 R-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds./.4.4e-69:459:86//L26335  
R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds./.7.4e-124:594:98//  
AF060219  
R-NT2RP2005289//Homo sapiens mRNA for XRP2 protein./.1.5e-110:545:96//AJ007590  
R-NT2RP2005293//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA  
35 sequence./.1.1e-12:554:61//U00101  
R-NT2RP2005315//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3  
gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence./.9.5e-15:218:77//AL022069  
R-NT2RP2005325//Rattus norvegicus LIM homeodomain protein (LH-2) mRNA sequence./.2.0e-72:478:88//  
L06804  
40 R-NT2RP2005336//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence./.7.3e-33:139:82//U14567  
R-NT2RP2005344//Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS./.  
0.094:451:60//297629  
R-NT2RP2005354//Homo sapiens mRNA for putative thioredoxin-like protein./.1.3e-11:89:96//AJ010841  
R-NT2RP2005360//Homo sapiens clone RG023I15, WORKING DRAFT SEQUENCE, 1 unordered pieces./.0.046:  
45 266:60//AC005049  
R-NT2RP2005393//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence./.6.0e-41:226:86//  
AC005695  
R-NT2RP2005407  
R-NT2RP2005436//Polistes annularis (clone pan117AAT) tandem repeat region./.0.039:169:63//L10835  
50 R-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey se-  
quence./.3.0e-38:263:88//AQ055548  
R-NT2RP2005453//CIT-HSP-2367N1.TR CIT-HSP Homo sapiens genomic clone 2367N1, genomic survey se-  
quence./.67:409:59//AQ079845  
R-NT2RP2005457//Homo sapiens partial XPGC gene, exon 2./.2.0e-42:315:82//X71342  
55 R-NT2RP2005464//CIT-HSP-2359C16.TF CIT-HSP Homo sapiens genomic clone 2359C16, genomic survey se-  
quence./.1.0:251:60//AQ075816  
R-NT2RP2005465//Drosophila melanogaster, chromosome 2R, region 44D1-44D2, P1 clone DS08616, complete  
sequence./.01251288:62//AC005457

R-NT2RP2005472//Chlorarachnion CCMP621 small subunit ribosomal RNA, 5.8S ribosomal RNA, large subunit  
 5 ribosomal RNA, U6 small nuclear RNA, small subunit ribosomal protein S13 (RPS13), pre-mRNA splicing factor  
 PRP 6 homolog, small subunit ribosomal protein 4 (RPS4), small nucleolar ribonucleoprotein E homolog (snRNPE),  
 ATP-dependent clp protease proteolytic subunit homolog (CLPP), putative RNA polymerase II subunit (RNA  
 POLII), and RNA helicase homolog (RNAHEL) genes, complete cds.//1.0:356:59//U58510  
 R-NT2RP2005476//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING  
 DRAFT SEQUENCE.//0.00092:421:60//AL031746  
 R-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//  
 10 6.2e-71:187:100//AC006030  
 R-NT2RP2005491//paramecium species 5,311 mt dna dimer: replication init. region.//1.6e-10:403:62//K00917  
 R-NT2RP2005495//Homo sapiens clone RG037F03, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
 15 1.3e-25:208:82//AC005051  
 R-NT2RP2005496//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the  
 gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cyto-  
 chrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein  
 L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms,  
 20 complete sequence.//1.5e-22:196:84//AL022722  
 R-NT2RP2005498  
 R-NT2RP2005501//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//.7e-29:252:76//  
 25 AC005828  
 R-NT2RP2005509//CIT-HSP-2060J6.TR CIT-HSP Homo sapiens genomic clone 2060J6, genomic survey se-  
 quence.//3.1e-53:402:84//B69979  
 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//9.9e-109:  
 30 570:94//AF092563  
 R-NT2RP2005525//Human clone JkA2 mRNA induced upon T-cell activation, 3' end.//5.1e-32:175:98//U38432  
 R-NT2RP2005531//Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence.//0.94:288:61//  
 AC004911  
 R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.7e-106:560:94//AJ012449  
 R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.3e-114:583:96//AB007963  
 35 R-NT2RP2005549//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//0.91:  
 287:58//AJ011929  
 R-NT2RP2005555//Homo sapiens 12p13.3 PAC RPCIS-927J10 (Roswell Park Cancer Institute Human PAC li-  
 brary) complete sequence.//3.6e-05:222:66//AC004804  
 R-NT2RP2005557//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//8.2e-22:236:76//  
 40 AC004996  
 R-NT2RP2005581//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//  
 7.2e-45:286:85//AC006146  
 R-NT2RP2005600//Human polymorphic microsatellite DNA.//0.043:304:58//M99148  
 R-NT2RP2005605//Human Cosmid g1572c190, complete sequence.//2.4e-17:163:77//AC000126  
 R-NT2RP2005620  
 R-NT2RP2005622//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7,  
 45 genomic survey sequence.//0.010:308:58//B13538  
 R-NT2RP2005637//Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete sequence.//2.5e-26:322:72//  
 AC005996  
 R-NT2RP2005640//Mus musculus squamous cell carcinoma antigen 2 (Scc2) gene, complete cds.//0.030:370:  
 60//AF063937  
 R-NT2RP2005645//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.2e-08:  
 355:62//AE001398  
 R-NT2RP2005651  
 50 R-NT2RP2005654//Leishmania major Friedlin cosmid L5769, complete sequence.//0.96:216:66//AL031908  
 R-NT2RP2005669//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//  
 6.7e-117:594:95//AF069984  
 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//1.8e-89:434:98//  
 AF089814  
 55 R-NT2RP2005683//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7,  
 genomic survey sequence.//0.037:283:58//B13538  
 R-NT2RP2005690//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-  
 38:295:83//AC005478

R-NT2RP2005694//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-106, complete sequence.//0.0026:414:57//AL010210  
 R-NT2RP2005701  
 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//4.1e-104:503:98//AB018342  
 5 R-NT2RP2005719//Caenorhabditis elegans cosmid LLC1, complete sequence.//0.83:275:61//Z82277  
 R-NT2RP2005722//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.2e-21:199:75//AL031985  
 R-NT2RP2005723  
 R-NT2RP2005726//Homo sapiens clone DJ0609N19, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-10 64:503:82//AC004842  
 R-NT2RP2005741//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.5e-09:261:64//AC000384  
 R-NT2RP2005748//RPCI11-64K11.TK RPCI11 Homo sapiens genomic clone R-64K11, genomic survey sequence.//0.00039:215:66//AQ239313  
 15 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//1.3e-40:223:96//AF068868  
 R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//3.7e-103:494:98//AF082516  
 R-NT2RP2005763//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//9.7e-34:172:20 86//AL022098  
 R-NT2RP2005767//Human clone H3 mRNA.//2.5e-21:179:87//U03672  
 R-NT2RP2005773//HS\_2168\_B1\_G12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=N, genomic survey sequence.//0.99:212:63//AQ086414  
 R-NT2RP2005775//Rabbit mRNA for endopeptidase, complete cds.//4.8e-98:591:88//D13310  
 25 R-NT2RP2005781//Streptomyces sp. genomic DNA for sarcosine oxidase.//0.019:384:59//D10623  
 R-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.8e-102:490:99//AL034423  
 R-NT2RP2005804//Homo sapiens chromosome 17, clone hRPK.147\_L\_13, complete sequence.//6.3e-16:481:63//AC005332  
 30 R-NT2RP2005812//Caenorhabditis elegans cosmid F15810.//0.81:147:63//AF036696  
 R-NT2RP2005815  
 R-NT2RP2005835  
 R-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//1.5e-26:512:64//Z68873  
 35 R-NT2RP2005853//Human DNA sequence from clone 1156N12 on chromosome X. Contains an STS and GSSs, complete sequence.//3.7e-16:340:64//AL009047  
 R-NT2RP2005857//Human DNA sequence from cosmid U246D9 on chromosome X. Contains a histone H2B like pseudogene.//1.3e-09:331:65//AL021308  
 R-NT2RP2005859//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-83, complete sequence.//0.0097:363:59//AL010152  
 40 R-NT2RP2005868//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-18, complete sequence.//1.1e-07:508:60//AL008971  
 R-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-31:500:67//AL11316  
 R-NT2RP2005901//Homo sapiens T-cell receptor alpha delta locus from bases 752679 to 1000555 (section 4 of 5) of the Complete Nucleotide Sequence.//0.89:276:60//AE000661  
 45 R-NT2RP2005908  
 R-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//1.2e-40:285:80//U63840  
 R-NT2RP2005942//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.0011:480:58//Z99289  
 50 R-NT2RP2005980//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//8.9e-21:136:78//AC004616  
 R-NT2RP2006023//HS\_2176\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=19 Row=F, genomic survey sequence.//2.5e-66:369:95//AQ023148  
 55 R-NT2RP2006038//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.00029:408:58//AE001369  
 R-NT2RP2006043//Polistes annularis (clone pan117AAT) tandem repeat region.//0.032:195:62//L10835  
 R-NT2RP2006052//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING

DRAFT SEQUENCE, 14 unordered pieces.//0.11:263:61//AC005140  
R-NT2RP2006069  
R-NT2RP2006071//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
DRAFT SEQUENCE, 3 unordered pieces.//0.00044:333:61//AC004709  
5 R-NT2RP2006098//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-77, complete  
sequence.//4.1e-09:393:62//AL010151  
R-NT2RP2006100//HS\_2020\_A2\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2020 Col=4 Row=O, genomic survey sequence.//8.3e-53:304:92//AQ228761  
R-NT2RP2006103//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//1.5e-16:  
10 199:79//M85300  
R-NT2RP2006141  
R-NT2RP2006166//Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete sequence.//8.2e-48:329:  
76//AC002045  
15 R-NT2RP2006184//RPCI11-6O16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6O16, genomic survey se-  
quence.//0.52:273:61//B49539  
R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//1.9e-108:553:95//AB014554  
R-NT2RP2006196//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-57, complete  
sequence.//4.2e-05:420:59//AL008981  
R-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE,  
20 66 unordered pieces.//2.1e-100:409:96//AC006057  
R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//3.8e-93:532:90//X96484  
R-NT2RP2006237//P.falciparum PK1 gene.//2.9e-08:481:59//X83707  
R-NT2RP2006238//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//3.5e-79:405:  
89//U91318  
25 R-NT2RP2006258//Human PAC clone DJ0899B21 from 7p15-p21, complete sequence.//2.2e-08:283:63//  
AC004008  
R-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.2e-13:234:68//X97630  
R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.0e-108:542:97//AF035262  
R-NT2RP2006320//347J16.TVB CIT978SKA1 Homo sapiens genomic clone A-347J16, genomic survey se-  
30 quence.//1.2e-27:215:65//B17768  
R-NT2RP2006321//Human karyopherin beta 3 mRNA, complete cds.//1.7e-48:298:90//U72761  
R-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING  
DRAFT SEQUENCE.//2.8e-104:524:96//AL033531  
R-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.9e-33:298:  
35 78//AC004893  
R-NT2RP2006334  
R-NT2RP2006365//RPCI11-72I15.TK RPCI11 Homo sapiens genomic clone R-72I15, genomic survey sequence.//  
2.6e-35:217:92//AQ267043  
R-NT2RP2006393//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4;  
40 HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//8.0e-40:317:81//AC004046  
R-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING  
DRAFT SEQUENCE.//3.2e-42:184:86//AL022345  
R-NT2RP2006441//Plasmodium falciparum microsatellite TA80 sequence.//0.00021:188:68//AF010568  
R-NT2RP2006454//Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence.//0.30:265:  
45 60//AE001423  
R-NT2RP2006456//Homo sapiens clone 23566 mRNA sequence.//2.5e-104:532:96//AF052098  
R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//6.6e-108:524:97//AJ006266  
R-NT2RP2006467//Sequence 50 from patent US 5691147.//8.3e-22:235:74//I76222  
R-NT2RP2006472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1172A22, WORKING  
50 DRAFT SEQUENCE.//5.4e-12:407:62//AL034386  
R-NT2RP2006534//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.44:111:65//M25216  
R-NT2RP2006554//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//0.19:392:  
58//AE001370  
R-NT2RP2006565//Sus scrofa SCAMP 1 gene, exon 9.//1.5e-13:292:68//AJ223742  
55 R-NT2RP2006571//Homo sapiens chromosome 19, cosmid F17972, complete sequence.//0.0024:409:58//  
AC004660  
R-nnnnnnnnnnnnn//Human BRCA2 region, mRNA sequence CG005.//3.3e-16:334:64//U50532  
R-NT2RP2006598//Mus musculus retinoid X receptor interacting protein (RIP110) mRNA, partial cds.//1.6e-19:

448:64//U22015  
R-NT2RP3000002//Human DNA sequence from cosmid N104C7 on chromosome 22, complete sequence./.4.4e-  
14:501:63//Z82246

5 R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.9e-115:560:97//  
AJ011972

R-NT2RP3000046//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces./.  
3.9e-57:402:83//AC005995

R-NT2RP3000047//Homo sapiens chromosome 17, clone hRPK.138\_P\_22, complete sequence./.1.0:158:66//  
AC005697

10 R-NT2RP3000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING  
DRAFT SEQUENCE./.2.7e-32:411:69//AL033522

R-NT2RP3000055//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1000N6, WORKING  
DRAFT SEQUENCE./.7.9e-17:309:69//AL034378

R-NT2RP3000072//Brassica rapa DNA for S-locus glycoprotein, complete cds./.2.9e-07:516:60//D88192

15 R-NT2RP3000080//Homo sapiens clone DJ1129D05, complete sequence./.1.7e-27:186:90//AC005630

R-NT2RP3000085//Arabidopsis thaliana acetyl-CoA carboxylase biotin-containing subunit mRNA, nuclear gene  
encoding chloroplast protein, complete cds./.0.0051:289:59//U-23155

R-NT2RP3000109//HS\_3065\_A2\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3065 Col=8 Row=G, genomic survey sequence./.2.5e-62:304:100//AQ137776

20 R-NT2RP3000134//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING  
DRAFT SEQUENCE./.0.027:414:57//AL031746

R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds./.3.8e-115:578:96//AB011164

R-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence./.1.3e-67:354:  
95//AC005746

25 R-NT2RP3000186  
R-NT2RP3000197//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic  
CA repeat\*.//2.5e-31:295:78//Z82899

R-NT2RP3000207//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-954B10, complete sequence./.0.016:  
305:61//AC004514

30 R-NT2RP3000220//RPCI11-63O7.TJ RPCI11 Homo sapiens genomic clone R-63O7, genomic survey sequence./.  
0.25:118:66//AQ201832

R-NT2RP3000233//Plasmodium falciparum mRNA for major merozoite surface antigen gp195./.3.2e-11:440:59//  
X15063

R-NT2RP3000235//Mus musculus chromosome 6 clone TB6 subclone TB6pD1//0.81:114:64//U19530

35 R-NT2RP3000247//Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1 27.3. Contains the  
cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSs  
and a CA repeat polymorphism, complete sequence./.4.8e-73:362:86//AL023279

R-NT2RP3000251//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence./.0.025:131:66//  
AC005726

40 R-NT2RP3000252  
R-NT2RP3000255//HS-1025-B2-F08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
Plate=CT 804 Col=16 Row=L, genomic survey sequence./.0.67:119:66//B34879

R-NT2RP3000267

R-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds./.1.2e-23:424:69//  
D29766

45 R-NT2RP3000312//Plasmodium falciparum MAL3P4, complete sequence./.0.55:414:59//AL008970

R-NT2RP3000320//HS\_3056\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3056 Col=5 Row=E, genomic survey sequence./.4.1e-32:214:89//AQ134064

R-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds./.1.5e-22:265:75//  
50 U78090

R-NT2RP3000333//Plasmodium falciparum MAL3P6, complete sequence./.0.68:460:57//Z98551

R-NT2RP3000341//H.sapiens mRNA for TIM17 preprotein translocase./.1.4e-19:137:90//X97544

R-NT2RP3000348//CITBI-E1-2513C11.TF CITBI-E1 Homo sapiens genomic clone 2513C11, genomic survey se-  
quence./.0.0014:118:72//AQ278177

55 R-NT2RP3000350  
R-NT2RP3000359//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces./.  
2.8e-55:320:75//AC006039

R-NT2RP3000361//Homo sapiens mRNA for KIAA0552 protein, complete cds./.0.18:275:61//AB011124

R-NT2RP3000366//CIT-HSP-2317H13.TF CIT-HSP Homo sapiens genomic clone 2317H13, genomic survey sequence//6.7e-42:214:100//AQ041634

R-NT2RP3000397//HS-1012-B1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 787 Col=1 Row=L, genomic survey sequence//0.015:184:63//B31814

5 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.3e-109:529:98//AF071185

R-NT2RP3000418//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510B21, WORKING DRAFT SEQUENCE//6.2e-15:445:65//AL031885

R-NT2RP3000433

10 R-NT2RP3000439

R-NT2RP3000441

R-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE//1.6e-43:300:76//AL031650 R-NT2RP3000451//3'untranslated region of human mRNA for a K<sup>+</sup> channel protein//0.71:101:66//E13519

15 R-NT2RP3000456//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence//5.2e-16:376:65//AF011889

R-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE//0.61:326:58//AL031847

20 R-NT2RP3000487//Sequence 32 from patent US 5476781//8.6e-08:409:61//I16692

R-NT2RP3000512//RPCI11-60F15.TK RPCI11 Homo sapiens genomic clone R-60F15, genomic survey sequence//2.2e-68:379:93//AQ201516

R-NT2RP3000526//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 377F16, WORKING DRAFT SEQUENCE//4.1e-07:224:65//Z93783

25 R-NT2RP3000527//HS\_3228\_A1\_H07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=13 Row=O, genomic survey sequence//4.5e-30:184:93//AQ209131

R-NT2RP3000531//T6M24-Sp6 TAMU Arabidopsis thaliana genomic clone T6M24, genomic survey sequence//0.67:88:68//AQ248538

R-NT2RP3000542//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126B4, WORKING DRAFT SEQUENCE//2.0e-24:145:82//AL022316

30 R-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence//6.1e-107:548:95//AC006012

R-NT2RP3000562//HS\_2041\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=15 Row=J, genomic survey sequence//9.6e-55:279:98//AQ230207

35 R-NT2RP3000578//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence//0.00060:356:58//AL010212

R-NT2RP3000582//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces//4.2e-29:282:67//AC004666

R-NT2RP3000584//Human PAC clone DJ222H05 from Xq25-q26, complete sequence//7.4e-44:245:78//AC002377

40 R-NT2RP3000590//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence//0.66:341:59//AC004077

R-NT2RP3000592//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces//0.022:491:56//AC005505

45 R-nnnnnnnnnnnn//HS\_3025\_A1\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence//2.6e-21:161:88//AQ101452

R-NT2RP3000599//Plasmodium falciparum MAL3P8, complete sequence//1.3e-09:543:58//AL034560

R-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence//5.6e-115:554:98//AC006128

50 R-NT2RP3000622//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 27 unordered pieces//0.15:233:63//AC005414

R-NT2RP3000624//CIT-HSP-2022D4.TR CIT-HSP Homo sapiens genomic clone 2022D4, genomic survey sequence//1.0:166:66//B64262

R-NT2RP3000628//Human BAC clone GS188P18, complete sequence//5.3e-56:384:83//AC000115

55 R-NT2RP3000632//Human cyclin-selective ubiquitin carrier protein mRNA, complete cds//4.0e-61:438:85//U73379

R-NT2RP3000644//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTIC, and RAD23A genes, genomic sequence//1.0e-43:408:77//AD000092

R-NT2RP3000661//F.rubripes GSS sequence, clone 148D22bB9, genomic survey sequence//2.7e-17:234:69//

AL005927

R-NT2RP3000665//Human chromosome 11 46b2 cosmid, complete sequence.//2.1e-42:526:72//U73645  
 R-NT2RP3000685//HS\_3007\_A2\_F02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=4 Row=K, genomic survey sequence.//1.6e-101:506:97//AQ118425

5 R-NT2RP3000690//Plasmodium falciparum MAL3P6, complete sequence.//1.3e-13:411:61//Z98551

R-NT2RP3000736

R-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//0.0071:231:65//U16655  
 R-NT2RP3000753//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.88:366:56//AL021368

10 R-NT2RP3000759//HS\_2055\_A2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=18 Row=G, genomic survey sequence.//0.45:251:60//AQ234828

15 R-NT2RP3000815//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//2.0e-20:293:72//AC005822

R-NT2RP3000825//Plasmodium falciparum MAL3P6, complete sequence.//0.0044:325:62//Z98551

R-NT2RP3000826//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//5.3e-25:375:72//AL022315

20 R-NT2RP3000836//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//1.3e-19:181:81//AL022344

R-NT2RP3000841//Homo sapiens, clone hRPK.1\_A\_1, complete sequence.//0.20:226:61//AC006196

R-NT2RP3000845//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//6.8e-91:512:92//AC005781

25 R-NT2RP3000847//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//7.9e-38:179:86//U14572  
 R-NT2RP3000850//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//4.4e-48:505:76//AC005014

R-NT2RP3000852//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-82:311:98//AL031297

30 R-NT2RP3000859

R-NT2RP3000865//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//1.2e-15:482:63//AL022153 R-NT2RP3000868//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00045:260:59//AB003097

35 R-NT2RP3000869//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//0.0058:172:64//AL031731

R-NT2RP3000875//H.sapiens /Hepatitis B virus fusion mRNA for mevalonate kinase.//1.4e-99:531:93//X75311

R-NT2RP3000901

R-NT2RP3000904//Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence.//0.32:261:57//AC000348

40 R-NT2RP3000917//Plasmodium falciparum MAL3P7, complete sequence.//0.00092:456:58//AL034559

R-NT2RP3000919

R-NT2RP3000968//H.sapiens mRNA for ribosomal protein S15a.//4.5e-24:375:71//X84407

R-NT2RP3000980//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, complete sequence.//0.36:186:62//AC006079

45 R-NT2RP3000994//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.00052:413:60//AC005140

R-NT2RP3001004//Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence.//1.1e-07:330:64//U32857

50 R-NT2RP3001007//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-82, complete sequence.//0.045:286:61//AL010255

R-NT2RP3001055//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.3e-56:348:91//Z95125

R-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//8.2e-84:531:86//X78927

55 R-NT2RP3001081//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//1.1e-08:537:60//AL031746

R-NT2RP3001084

R-NT2RP3001096

R-NT2RP3001107

R-nnnnnnnnnnnn//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence./.7.4e-62:272:73//AC005316  
R-NT2RP3001111  
R-NT2RP3001113  
5 R-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence./.7.2e-112:550:97//  
AC005189  
R-NT2RP3001116//CIT-HSP-2282K23.TR CIT-HSP Homo sapiens genomic clone 2282K23, genomic survey se-  
quence./.0.000.13.160:69//AQ002011  
R-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
10 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,  
complete sequence./.5.9e-99:497:96//AL031864  
R-NT2RP3001120  
R-NT2RP3001126//Plasmodium falciparum MAL3P7, complete sequence./.0.035:266:56//AL034559  
R-NT2RP3001133  
15 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds./.8.1e-114:549:97//AB018305  
R-NT2RP3001147//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence./.0.69:198:63//  
AC004448  
R-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
DRAFT SEQUENCE./.2.4e-108:542:97//AL034379  
20 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein./.2.9e-116:563:98//AJ006266  
R-NT2RP3001176//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
DRAFT SEQUENCE, 4 unordered pieces./.0.44:227:62//AC004688  
R-NT2RP3001214//Borrelia burgdorferi plasmid lp25, complete plasmid sequence./.0.0023:381:61//AE000785  
R-NT2RP3001216//RPCI11-18C15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-18C15, genomic survey  
25 sequence./.7.0e-29:167:97//B88077  
R-NT2RP3001221//Homo sapiens clone 14503, WORKING DRAFT SEQUENCE, 1 ordered pieces./.0.020:211:  
63//AC005827  
R-NT2RP3001232//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic  
30 marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence./.2.7e-08:390:62//  
AL021326  
R-NT2RP3001236//RPCI11-25C17.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25C17, genomic sur-  
vey sequence./.9.5e-41:217:88//AQ014003  
R-NT2RP3001239//Human microtubule-associated protein 1B (MAP1B) gene, complete cds./.2.9e-21:438:63//  
L06237  
35 R-NT2RP3001245//Homo sapiens DNA sequence from PAC 964D12 on chromosome 1q24-q25. Contains EST,  
GSS./.0.00026:439:59//AL021398  
R-NT2RP3001253//HS\_3002\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3002 Col=24 Row=O, genomic survey sequence./.0.98:190:63//AQ251982  
R-NT2RP3001260  
40 R-NT2RP3001268//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUENCE, 2 unordered pieces./.  
0.012:509:57//AC004936  
R-NT2RP3001272//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence./.2.2e-22:134:87//  
AC005589  
R-NT2RP3001274//Sequence 11 from Patent WO9517522./.0.0058:133:66//A45341  
45 R-NT2RP3001281//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS./.  
4.4e-55:558:76//Z96811  
R-NT2RP3001307//HS\_2058\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2058 Col=11 Row=E, genomic survey sequence./.7.2e-33:260:86//AQ305868  
R-NT2RP3001318//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence./.0.27:210:65//  
50 AC004848  
R-NT2RP3001325  
R-NT2RP3001338//Rat tropoelastin gene, intron 17 (partial)./.1.0:184:64//M86367  
R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds./.1.2e-112:566:96//AB007920  
R-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds./.3.2e-86:450:95//AF083105  
55 R-NT2RP3001355  
R-NT2RP3001374//HS\_2184\_A2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2184 Col=8 Row=M, genomic survey sequence./.3.7e-10:101:84//AQ024647  
R-NT2RP3001383//Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence./.7.4e-07:

279:63//AE001397  
R-NT2RP3001384//Homo sapiens chromosome 19, cosmid R33907, complete sequence.//4.4e-75:382:97//  
AC005785

5 R-NT2RP3001392//HS\_3078\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3078 Col=10 Row=H, genomic survey sequence.//1.0:164:64//AQ140587

R-NT2RP3001396//RPCI11-63N18.TJ RPCI11 Homo sapiens genomic clone R-63N18, genomic survey se-  
quence.//0.14:242:61//AQ238544

R-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.8e-10:193:72//U49046

R-NT2RP3001399

10 R-NT2RP3001407//Caenorhabditis elegans cosmid D1046, complete sequence.//0.0011:392:60//Z68160

R-NT2RP3001420//Human BAC clone GS165I04 from 7q21, complete sequence.//3.7e-29:412:74//AC002379

R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence.//1.1e-104:550:94//AF052158

R-NT2RP3001427//Caenorhabditis elegans cosmid K11D5.//0.39:174:64//U53152

15 R-nnnnnnnnnnnn//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//1.4e-94:533:  
91//U69668

R-NT2RP3001432//Homo sapiens DNA sequence from PAC 164C20 on chromosome 6q16.1-22.1. Contains ESTs  
and GSSs (BAC end sequences), complete sequence.//2.5e-12:415:61//AL009029

R-NT2RP3001447//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.6e-36:358:  
77//AC004903

20 R-NT2RP3001449//Homo sapiens clone 24497 mRNA sequence.//1.5e-100:499:97//AF070630

R-NT2RP3001453//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-  
47:295:86//AC004906

R-NT2RP3001457

R-NT2RP3001459

25 R-NT2RP3001472//Crithidia fasciculata kinetoplast apocytochrome b gRNA-mRNA chimera, clone:24.//0.33:150:  
66//D13030

R-NT2RP3001490//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-103, com-  
plete sequence.//2.3e-08:483:60//AL010208

R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//4.4e-60:338:93//U13395

30 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//  
2.1e-110:549:97//AF064801

R-NT2RP3001527//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING  
DRAFT SEQUENCE.//5.3e-32:310:78//AL034549

R-NT2RP3001529//Human Chromosome X, complete sequence.//5.5e-67:280:93//AC002420

35 R-NT2RP3001538

R-NT2RP3001554//Human microtubule-associated protein Ia (MAP1A) mRNA, complete cds.//7.8e-16:391:62//  
U38292

R-NT2RP3001580//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
DRAFT SEQUENCE, 4 unordered pieces.//0.00026:456:58//AC004688

40 R-NT2RP3001587//Homo sapiens HRIHFB2115 mRNA, partial cds.//5.6e-08:86:88//AB015337

R-NT2RP3001589//Homo sapiens chromosome 17, clone hRPK.1096\_G\_20, complete sequence.//0.066:360:  
60//AC005410

R-NT2RP3001607//CIT-HSP-2010M8.TR CIT-HSP Homo sapiens genomic clone 2010M8, genomic survey se-  
quence.//0.041:194:67//B53490

45 R-NT2RP3001608//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-  
aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/  
fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//0.69:151:64//Z83821

R-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21:31-22.2 Contains zinc finger  
protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST,  
STS, GSS, complete sequence.//1.4e-46:354:83//AL021808

R-NT2RP3001629//H.sapiens simple DNA sequence region clone wg1a10.//0.99:137:63//X76572

R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds.//8.5e-108:541:96//AF099149

R-NT2RP3001642

50 R-NT2RP3001646//HS\_3218\_A2\_A01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3218 Col=2 Row=A, genomic survey sequence.//2.6e-32:215:91//AQ303003

R-NT2RP3001671//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-88, complete  
sequence.//0.018:262:61//AL010157

R-NT2RP3001672

R-NT2RP3001676//Homo sapiens cosmid Q95D4, chromosome 21 5' of IFNAR2.//2.1e-48:413:77//AF039905  
R-NT2RP3001678//RPCI11-50C17.TK RPCI11 Homo sapiens genomic clone R-50C17, genomic survey sequence.//0.15:232:62//AQ116359  
5 R-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//7.8e-104:549:95//AB020860  
R-NT2RP3001688//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//6.6e-41:291:86//AC006019  
R-NT2RP3001690//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//3.1e-07:433:59//AE001415  
10 R-NT2RP3001708//Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence.//6.0e-06:237:64//AF053523  
R-NT2RP3001712//CITBI-E1-2516N9.TF CITBI-E1 Homo sapiens genomic clone 2516N9, genomic survey sequence.//1.5e-95:456:99//AQ279562  
15 R-NT2RP3001716//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0012:346:58//AC004617  
R-NT2RP3001724//Human HepG2 3' region MboI cDNA, clone hmd6a06m3.//1.3e-27:163:95//D17273  
R-NT2RP3001730//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.//7.6e-43:409:76//Z98200  
R-NT2RP3001739  
20 R-NT2RP3001752//Human clone 23774 mRNA sequence.//1.9e-08:104:84//U79279  
R-NT2RP3001753//CIT-HSP-2379P21.TF CIT-HSP Homo sapiens genomic clone 2379P21, genomic survey sequence.//8.8e-06:102:78//AQ113378  
R-NT2RP3001764  
25 R-NT2RP3001777//Human mRNA for heparan sulfate proteoglycan (glycan).//0.99:166:66//X54232  
R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//1.3e-111:549:97//AB007928  
R-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.6e-32:266:83//U13262  
R-NT2RP3001799//H.sapiens mRNA for OX40 homologue.//8.5e-44:374:79//X75962  
R-NT2RP3001819  
30 R-NT2RP3001844//Caenorhabditis elegans cosmid C54G7.//0.0042:231:63//U40410  
R-NT2RP3001854//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//1.0:404:59//AF030694  
R-NT2RP3001855  
35 R-NT2RP3001896//CIT978SK-A-686F10.TV CIT978SK Homo sapiens genomic clone A-636F10, genomic survey sequence.//0.0012:68:82//AQ116409  
R-NT2RP3001898//Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence.//0.37:266:65//AC005950  
R-NT2RP3001915//Human BAC clone RG367O17 from 7p15-p21, complete sequence.//0.018:144:66//AC002486  
40 R-NT2RP3001926//Human polyadenylate binding protein (TIA-1) mRNA, complete cds.//2.4e-10:77:100//M77142  
R-NT2RP3001929  
R-NT2RP3001931//Homo sapiens full-length insert cDNA clone YU73B11.//1.0e-110:562:96//AF087969  
R-NT2RP3001938//Human DNA sequence from PAC 447B16 on chromosome Xq13.1-Xq13.3.//0.38:386:56//Z95328  
45 R-NT2RP3001943//Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.//0.87:298:61//AC004500  
R-NT2RP3001944//Bos taurus clone CSSM056 satellite DNA sequence.//0.0095:76:78//U03836  
R-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unorderded pieces.//7.0e-109:552:96//AC005844  
50 R-NT2RP3001989//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.15:111:68//Z81029  
R-NT2RP3002002//Plasmodium falciparum 14-3-3 protein gene, partial cds.//0.016:286:60//AF065987  
R-NT2RP3002004//H.sapiens mRNA for FAST kinase.//5.1e-41:335:82//X86779  
R-NT2RP3002007  
R-NT2RP3002014//Human DNA sequence from clone 228A9 on chromosome 22q12.3-13.32 Contains 85 KDa CALCIUM-INDEPENDENT PHOSPHOLIPASE A2, EST, GSS, CpG island, complete sequence.//6.6e-41:297:86//AL022322  
55 R-NT2RP3002033  
R-NT2RP3002045//Drosophila melanogaster fat protein (fat) gene, complete cds.//0.77:320:60//M80537

R-NT2RP3002054//Caenorhabditis elegans cosmid Y69H2, complete sequence./.0.82:362:57//Z98877  
R-NT2RP3002056//F.rubripes GSS sequence, clone 020E22bF7, genomic survey sequence./.0.010:185:63//  
Z87006  
R-NT2RP3002057  
5 R-NT2RP3002062//Human BAC clone RG356F09 from 7p21, complete sequence./.1.7e-17:164:81//AC004002  
R-nnnnnnnnnnnn  
R-NT2RP3002081//HS\_3082\_A1\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3082 Col=17 Row=M, genomic survey sequence./.4.2e-25:344:73//AQ122260  
10 R-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-  
plete sequence./.2.6e-23:212:80//AC006210  
R-NT2RP3002102//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence./.0.43:168:64//  
AC004746  
R-NT2RP3002108//CIT-HSP-2346P16.TF CIT-HSP Homo sapiens genomic clone 2346P16, genomic survey se-  
quence./.3.5e-08:110:78//AQ059071  
15 R-NT2RP3002146//Streptococcus gordonii competence factor (comC) and histidine protein kinase (comD) genes,  
complete cds, and response regulator (comE) gene, partial cds./.0.11:534:55//U80077  
R-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING  
DRAFT SEQUENCE./.4.1e-108:551:96//AL031710  
R-NT2RP3002151//Mus musculus mRNA for Guanine Nucleotide Regulatory Protein, complete cds./.6.8e-62:347:  
20 80//AB003503  
R-NT2RP3002163//Anolis pulchellus vitellogenin mRNA, partial cds./.0.77:281:63//U46857  
R-NT2RP3002165  
R-NT2RP3002166//D.sargus satellite DNA (clone PSE3).//.0.81:124:62//Z48711  
R-NT2RP3002173  
25 R-NT2RP3002181//HS-1042-A2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
Plate=CT 824 Col=2 Row=K, genomic survey sequence./.1.3e-35:305:81//B36980  
R-NT2RP3002244//Caenorhabditis elegans cosmid R11E3./.0.0024:393:61//AF100669  
R-NT2RP3002248//Human DNA sequence from PAC 170A21 on chromosome 22q12-qter contains ESTs./.0.30:  
217:63//Z82189  
30 R-NT2RP3002255  
R-NT2RP3002273//Homo sapiens BAC clone 393I22 from 8q21, complete sequence./.0.84:463:57//AF070717  
R-NT2RP3002276//HS\_2260\_A1\_MF\_E07 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2260 Col=13 Row=I, genomic survey sequence./.0.0017:198:63//AQ292491  
35 R-NT2RP3002303//Human HMG-17 gene for non-histone chromosomal protein HMG-17./.7.4e-93:510:93//  
X13546  
R-NT2RP3002304//Human BAC clone GS188P18, complete sequence./.6.3e-09:477:59//AC000115  
R-NT2RP3002330//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
DRAFT SEQUENCE, 4 unordered pieces./.0.087:388:58//AC004688  
R-NT2RP3002343  
40 R-NT2RP3002351//Homo sapiens chromosome Y, clone 264,M,20, complete sequence./.0.20:489:56//AC004617  
R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene./.2.4e-104:516:94//Y15164  
R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds./.4.7e-102:524:95//AB014578  
R-NT2RP3002484  
45 R-NT2RP3002501//Human DNA sequence from PAC 92M18, BRCA2 gene region chromosome 13q12-13 con-  
tains BRCA2 exons 25, 26 and 27 ESTs and STS./.5.2e-17:232:75//Z73359  
R-NT2RP3002512  
R-NT2RP3002529//CIT-HSP-2340H2.TR CIT-HSP Homo sapiens genomic clone 2340H2, genomic survey se-  
quence./.0.81:266:58//AQ057387  
50 R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds./.3.3e-82:438:94//AB018272  
R-NT2RP3002549//Medicago truncatula ENBP1 gene, exons 1 to 12./.0.95:381:56//AJ002479  
R-NT2RP3002566//HS\_2036\_A1\_D08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2036 Col=15 Row=G, genomic survey sequence./.0.18:162:64//AQ230627  
R-NT2RP3002587//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces./.5.1e-  
15:213:73//AC004956  
55 R-NT2RP3002590//Arabidopsis thaliana genomic DNA; chromosome 5, P1 clone: MXK3, complete sequence./.  
0.00010:431:59//AB019236  
R-NT2RP3002602//Mus musculus stannin gene, complete cds./.1.6e-20:339:70//AF030522  
R-NT2RP3002603

R-NT2RP3002631//Homo sapiens chromosome 21 PAC  
 RPCIP704A9190Q2://1.0:241:59//AJ006997  
 R-NT2RP3002659//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds://6.8e-24:  
 331:76//M85300

5 R-NT2RP3002660//H.sapiens partial gene for progesterone receptor and Alu element DNA://9.8e-43:273:82//  
 Z49816  
 R-NT2RP3002663//Lymnaea stagnalis 16S ribosomal RNA gene, mitochondrial gene encoding ribosomal RNA,  
 partial sequence://0.60:300:59//U82072

10 R-NT2RP3002671//S.pombe chromosome III cosmid c553://1.2e-20:399:66//AL023704  
 R-NT2RP3002682//RPCI11-44K6.TJ RPCI11 Homo sapiens genomic clone R-44K6, genomic survey sequence://  
 4.7e-09:122:77//AQ202481

R-NT2RP3002687//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.1e-07:494:59//X95276  
 R-NT2RP3002688//Human 7SL RNA sequence://2.7e-32:290:79//X01037

15 R-NT2RP3002701  
 R-NT2RP3002713//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING  
 DRAFT SEQUENCE://0.95:334:59//AL031427  
 R-NT2RP3002763//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//3.9e-40:288:85//U14567  
 R-NT2RP3002770//R.prowazekii genomic DNA fragment (clone A615F).//0.21:174:63//Z82710  
 R-NT2RP3002785//Homo sapiens PAC clone DJ0170D19 from Xq23, complete sequence://0.78:354:59//  
 20 AC004822  
 R-NT2RP3002799//Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flank-  
 ing repeat regions.//1.1e-20:161:77//AF003528  
 R-NT2RP3002810//Caenorhabditis elegans cosmid F10D2.//0.28:441:56//AF022972  
 R-NT2RP3002818//HS\_3053\_A2\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3053 Col=16 Row=A, genomic survey sequence://0.19:220:60//AQ135025

25 R-NT2RP3002861//P.falciparum complete gene map of plastid-like DNA (IR-B).//9.3e-05:414:60//X95276  
 R-NT2RP3002869//Homo sapiens chromosome 19, cosmid F21967, complete sequence://0.14:165:64//  
 AC005256  
 R-NT2RP3002876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING  
 30 DRAFT SEQUENCE://2.6e-59:311:96//AL034380  
 R-NT2RP3002877//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human  
 PAC Library) complete sequence://4.6e-24:422:63//AC003035  
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds://4.7e-109:570:95//AB018314  
 R-NT2RP3002911//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence://3.1e-16:471:64//  
 35 AC005014  
 R-NT2RP3002948//, complete sequence://4.5e-94:516:93//AC005500  
 R-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence://3.4e-111:  
 566:96//AC005754  
 R-NT2RP3002955//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence://0.19:424:  
 40 58//AE001391  
 R-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds://1.1e-89:562:88//D30666  
 R-NT2RP3002972//Stealth virus 5 clone C1311 T7 genomic sequence://1.0:122:67//AF067482  
 R-NT2RP3002978//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING  
 DRAFT SEQUENCE://4.8e-05:249:63//AL031733

45 R-NT2RP3002988//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATI-  
 DYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//  
 0.0097:246:67//Z97195  
 R-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP,  
 G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.9e-24:  
 50 188:78//AF109905  
 R-NT2RP3003032//Arabidopsis thaliana (clone DW1) DNA retrotransposon Ta11-1 integration site.//5.3e-07:376:  
 63//L47211  
 R-NT2RP3003059//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence//1.4e-13:323:66//  
 AC005669

55 R-NT2RP3003061//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hll-10).//3.8e-42:  
 265:91//Y16708  
 R-NT2RP3003068//HS\_3214\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3214 Col=18 Row=N, genomic survey sequence://0.025:207:64//AQ181894

R-NT2RP3003071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE./.0.00014:329:60//Z98044  
 R-NT2RP3003078//T26A1TF *Arabidopsis thaliana* genomic clone T26A1, genomic survey sequence./.0.95:219:63//B27013  
 5 R-NT2RP3003101//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./1.4e-05:285:62//AC004153  
 R-NT2RP3003121//*Homo sapiens* full-length insert cDNA clone ZD62D10./2.1e-47:242:98//AF086348  
 R-NT2RP3003133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE./1.4e-21:199:75//AL031985  
 10 R-NT2RP3003138//Mouse *kif4* mRNA for microtubule-based motor protein *KIF4*, complete cds./5.1e-14:287:68//D12646  
 R-NT2RP3003139//*Rattus norvegicus* kappa opioid receptor gene, exon 4 and complete cds./1.5e-13:122:80//U17995  
 R-NT2RP3003150  
 15 R-NT2RP3003157//*Homo sapiens* 12q15 BAC GSHB-410F4 (Genome Systems Human Bac Library) complete sequence./5.5e-42:289:74//AC005294  
 R-NT2RP3003185//HS\_2058\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2058 Col=5 Row=O, genomic survey sequence./0.025:52:94//AQ231298  
 R-NT2RP3003193//*Homo sapiens* chromosome 17, clone hRPK.628\_E\_12, complete sequence./4.8e-40:349:  
 20 79//AC005701  
 R-NT2RP3003197//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE./5.2e-10:180:71//AL031319  
 R-NT2RP3003203//*Mus musculus* IFN alpha-treated embryonic fibroblast mRNA./1.8e-11:148:77//U51904  
 R-NT2RP3003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 892F13, WORKING DRAFT SEQUENCE./6.6e-41:282:86//AL009183  
 25 R-NT2RP3003212//*Homo sapiens* full-length insert cDNA clone ZB91B11./1.7e-68:363:95//AF086173  
 R-NT2RP3003230//*Caenorhabditis elegans* cosmid T12B5./.0.0018:279:64//AF100307  
 R-NT2RP3003242//*Homo sapiens* chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence./1.  
 30 0:346:57//AC005272  
 R-NT2RP3003251//*Homo sapiens* BAC clone RG060N22 from 7q21, complete sequence./2.5e-10:436:62//AC003083  
 R-NT2RP3003264//CIT-HSP-2296M7.TR CIT-HSP *Homo sapiens* genomic clone 2296M7, genomic survey se-  
 quence./5.8e-05:308:61//AQ005862  
 R-NT2RP3003278//Human HepG2 partial cDNA, clone hmd3b11m5./9.4e-47:302:89//D17022  
 35 R-NT2RP3003282//*Homo sapiens* dynamin (DNM) mRNA, complete cds./7.4e-101:550:93//L36983  
 R-NT2RP3003290//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE./3.0e-22:228:78//AL031662  
 R-NT2RP3003301  
 R-NT2RP3003302//CIT-HSP-2319H19.TF CIT-HSP *Homo sapiens* genomic clone 2319H19, genomic survey se-  
 40 quence./1.5e-69:367:95//AQ034950  
 R-NT2RP3003311//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./5.1e-08:398:64//AC005505  
 R-NT2RP3003313//*Caenorhabditis elegans* cosmid F39B1, complete sequence./0.00022:436:58//Z69660  
 R-NT2RP3003327//*Homo sapiens* Chromosome 16 BAC clone CIT987-SKA-237H1 ~complete genomic se-  
 45 quence, complete sequence./1.5e-16:334:70//AC002287  
 R-NT2RP3003330//*Homo sapiens* full-length insert cDNA YI24C02./4.4e-96:458:99//AF075015  
 R-NT2RP3003344//HS\_3235\_B2\_H09\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* ge-  
 nomic clone Plate=3235 Col=18 Row=P, genomic survey sequence./4.1e-18:197:80//AQ303203  
 R-NT2RP3003346  
 50 R-NT2RP3003353//CITBI-E1-2523B18.TR CITBI-E1 *Homo sapiens* genomic clone 2523B18, genomic survey se-  
 quence./8.3e-06:130:73//AQ278834  
 R-NT2RP3003377//*Homo sapiens* clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces./  
 1.9e-97:481:94//AC005519  
 R-NT2RP3003384//*Homo sapiens* clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces./2.3e-  
 55 10:226:71//AC004820  
 R-NT2RP3003385  
 R-NT2RP3003403//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin,  
 Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence./2.8e-40:496:

72//AL031585  
R-NT2RP3003409//Rat POU domain factor (Brn-5) mRNA.//1.5e-20:375:68//L23204  
R-NT2RP3003411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 438L4, WORKING  
DRAFT SEQUENCE.//1.0:180:61//Z97635  
5 R-NT2RP3003427//RPCI11-45J23.TJ RPCI11 Homo sapiens genomic clone R-45J23, genomic survey se-  
quence.//0.82:162:69//AQ195566  
R-NT2RP3003433//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//1.1e-10:379:  
61//AC006031  
R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//1.1e-95:479:96//  
10 AF004828  
R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.3e-100:527:93//AB018268  
R-NT2RP3003491//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-08:  
495:59//AE001398  
R-NT2RP3003500//W.suaveolens mitochondrial ATP9 gene.//0.0074:514:59//X77238  
15 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA.//1.3e-31:217:88//  
U00952  
R-NT2RP3003552  
R-NT2RP3003555//Dictyostelium discoideum interaptin (abpD) gene, complete cds.//0.98:321:61//AF057019  
R-NT2RP3003564  
20 R-NT2RP3003572//Human DNA sequence from BAC 992D9 on chromosome 22q12.1 contains STS.//0.0015:507:  
59//AL008638  
R-NT2RP3003576//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//1.2e-39:359:  
79//AC003007  
R-NT2RP3003589//Plasmodium falciparum MAL3P8, complete sequence.//0.014:539:58//AL034560  
25 R-NT2RP3003625//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the AD-  
SL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable  
rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete  
sequence.//1.8e-44:448:77//AL022238  
R-NT2RP3003656//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//0.34:257:62//  
30 AC005291  
R-NT2RP3003659//O.fuscipennis 16S rRNA gene, partial.//0.021:145:65//Z93701  
R-NT2RP3003665//HS\_3078\_B2\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3078 Col=18 Row=F, genomic survey sequence.//1.3e-75:397:95//AQ140580  
R-NT2RP3003672  
35 R-NT2RP3003686  
R-NT2RP3003701//Human BAC clone GS310A05 from 7q21-q22, complete sequence.//6.4e-17:464:62//  
AC002452  
R-NT2RP3003716//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING  
DRAFT SEQUENCE.//0.00072:425:62//AL034410  
40 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//1.7e-101:492:97//AB018300  
R-NT2RP3003746//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//3.7e-  
07:217:66//AC003009  
R-NT2RP3003795//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat  
and GSSs, complete sequence.//8.1e-26:456:68//Z98052  
45 R-NT2RP3003799//cSRL-138g10-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
clone cSRL-138g10, genomic survey sequence.//4.9e-09:117:77//B01736  
R-NT2RP3003800//Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds.//2.8e-106:551:  
95//AF077754  
R-NT2RP3003805  
50 R-NT2RP3003809//Homo sapiens full-length insert cDNA clone YZ95A01.//3.6e-106:533:97//AF086107  
R-NT2RP3003819//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING  
DRAFT SEQUENCE.//6.0e-44:288:81//Z84487  
R-NT2RP3003825//Mus domesticus interleukin 1 receptor antagonist (IL-1RA) mRNA.//0.0014:410:58//M64404  
R-NT2RP3003828  
55 R-NT2RP3003831//\*\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//2.3e-41:289:85//U14567  
R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.6e-108:541:97//AF070611  
R-NT2RP3003842//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//1.5e-  
46:457:74//AC002980

R-NT2RP3003846//Plasmodium falciparum MAL3P3, complete sequence./.3.5e-06:356:62//Z98547  
R-NT2RP3003870//Homo sapiens full-length insert cDNA clone ZD75H11./.8.2e-09:68:98//AF086402  
R-NT2RP3003876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE./.0.0027:180:66//AL031650  
5 R-NT2RP3003914//Dictyostelium discoideum DNA for transposable element Tdd-3 tandem array./.0.029:234:62//X53439  
R-NT2RP3003918  
R-NT2RP3003932//Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds./.0.00087:164:  
67//AF029215  
10 R-NT2RP3003989  
R-NT2RP3003992//Sequence 1 from patent US 5591825./.0.56:235:59//I33465  
R-NT2RP3004013//HS\_3018\_A1\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=17 Row=M, genomic survey sequence./.0.00026:421:60//AQ119904  
15 R-NT2RP3004016//Drosophila melanogaster DNA sequence (P1s DS03465 (D149) and DS08544 (D187)), complete sequence./.4.8e-12:308:62//AC004532  
R-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING DRAFT SEQUENCE./.0.42:190:64//AL021579  
R-NT2RP3004051//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence./.3.6e-21:332:69//  
20 AC006130  
R-NT2RP3004070//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces./.2.0e-05:476:57//AC005308  
R-NT2RP3004078//Homo sapiens chromosome 19, cosmid R30335, complete sequence./.2.0e-86:486:93//  
25 AC005784  
R-NT2RP3004093//Human PAC clone 257C22A from 13q12-q13, complete sequence./.5.3e-11:230:69//  
AC002525  
R-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces./.7.5e-  
93:551:92//AC005038  
R-NT2RP3004110//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence./.1.6e-104:317:100//AC006064  
30 R-NT2RP3004125//Pongo pygmaeus CT microsatellite, clone #3, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus)./.0.73:168:60//U36532  
R-NT2RP3004145//Homo sapiens full-length insert cDNA clone ZE09H03./.2.3e-89:427:99//AF086542  
R-NT2RP3004148//Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence./.  
35 0.013:134:70//U78721  
R-NT2RP3004155//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence./.3.8e-10:101:87//  
AC004081  
R-NT2RP3004206//Homo sapiens clone DJ0794K21, complete sequence./.1.5e-06:442:57//AC005533  
R-NT2RP3004207//Mouse mRNA for seizure-related gene product 6./.1.7e-07:220:69//D29763  
R-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence./.7.3e-89:504:92//D42052  
40 R-NT2RP3004215//Caenorhabditis elegans cosmid F11A6, complete sequence./.0.018:353:59//Z81498  
R-NT2RP3004242//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence./.4.5e-06:  
407:60//AE001415  
R-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence./.  
2.8e-105:534:97//AC005385  
45 R-NT2RP3004253//RPCI11-78J12.TJ RPCI11 Homo sapiens genomic clone R-78J12, genomic survey sequence./.4.0e-64:382:90//AQ281324  
R-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds./.7.0e-60:417:84//AF013967  
R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, complete cds./.2.7e-43:528:73//AF092536  
50 R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence./.1.4e-06:435:  
62//AC004231  
R-NT2RP3004341//CITBI-E1-2503F11.TR CITBI-E1 Homo sapiens genomic clone 2503F11, genomic survey sequence./.0.0018:210:65//AQ263365  
R-NT2RP3004348//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence./.7.1 e-46:340:83//  
AC005695  
55 R-NT2RP3004349//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117O3, WORKING DRAFT SEQUENCE./.9.4e-29:263:79//AL020995  
R-NT2RP3004378//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats./.2.0e-67:422:90//Z95125

R-NT2RP3004399//HS\_3046\_A1\_E02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=3 Row=1, genomic survey sequence.//0.00014:186:67//AQ137619  
 R-NT2RP3004424//RPCI11-59I14.TJ RPCI11 Homo sapiens genomic clone R-59I14, genomic survey sequence.//7.4e-71:370:95//AQ201461  
 5 R-NT2RP3004428//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y66A7, WORKING DRAFT SEQUENCE.//0.096:205:64//AL022282  
 R-NT2RP3004451//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//0.0029:396:60//AC005824  
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//2.9e-106:526:98//AB007917  
 10 R-NT2RP3004466  
 R-NT2RP3004470//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//8.3e-06:229:64//AC005895  
 R-NT2RP3004472//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.87:442:59//AC005504  
 15 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.6e-105:521:97//AB007925  
 R-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//3.9e-38:322:81//U47024  
 R-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//4.2e-96:527:92//AC003982  
 R-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.3e-43:342:82//AC006023  
 20 R-NT2RP3004503//Human cosmid g1572c101, complete sequence.//2.3e-25:392:68//AC000357  
 R-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.8e-28:387:70//Y08260  
 R-NT2RP3004507  
 R-NT2RP3004527//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//0.68:244:62//AC004518  
 25 R-nnnnnnnnnnnn//Mouse oncogene (ect2) mRNA, complete cds.//2.6e-79:525:84//L11316  
 R-NT2RP3004544  
 R-NT2RP3004566  
 R-NT2RP3004569//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:296:58//AC004709  
 30 R-NT2RP3004572//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//8.2e-12:457:63//AC005083  
 R-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//2.4e-97:488:96//AB007946  
 R-NT2RP3004594//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//1.7e-10:368:61//AC005234  
 35 R-NT2RP3004617  
 R-NT2RP3004618//F2H16TF IGF Arabidopsis thaliana genomic clone F2H16, genomic survey sequence.//0.96:212:64//B26414  
 R-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase e (GlcNAc6ST), complete cds.//2.2e-55:291:95//AB014679  
 40 R-NT2RP4000008//H.sapiens polyA site DNA sequence.//2.5e-25:202:85//Z24749  
 R-NT2RP4000023//CIT-HSP-2372A9.TF CIT-HSP Homo sapiens genomic clone 2372A9, genomic survey sequence.//3.6e-51:313:89//AQ112388  
 R-NT2RP4000035//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.3e-69:536:81//AC005015  
 45 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds.//2.1e-58:289:82//AF016266  
 R-NT2RP4000051//Homo sapiens Chromosome 22q11.2 Cosmid Clone 20b In DGCR Region, complete sequence.//0.56:462:58//AC000074  
 R-NT2RP4000078//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00021:460:60//AC005506  
 50 R-NT2RP4000102//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//1.6e-08:518:58//AC004648  
 R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//3.5e-106:536:96//AB011538  
 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//1.1e-110:554:97//AB007952  
 R-NT2RP4000147  
 55 R-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//3.5e-46:395:83//L20681  
 R-NT2RP4000151  
 R-NT2RP4000159//Caenorhabditis elegans cosmid R02F11.//0.00011:261:63//AF016439  
 R-NT2RP4000167//RPCI11-59L8.TK RPCI11 Homo sapiens genomic clone R-59L8, genomic survey sequence.//

6.2e-26:163:93//AQ200049  
 R-NT2RP4000185  
 R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.6e-99:505 :96//AB014600  
 R-NT2RP4000212//, complete sequence.//1.0e-106:538:96//AC005300  
 5 R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.2e-39:272:88//  
 AC005261  
 R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//1.6e-09:457:60//  
 AC004081  
 R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//9.0e-69:354:96//AJ006470  
 10 R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0e-27:344:73//D10727  
 R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//9.7e-78:381:99//AF091092  
 R-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey se-  
 quence.//0.26:124:69//AQ043515  
 15 R-nnnnnnnnnnnn//ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homolog [herpesvirus saimiri HVS, host-  
 squirrel monkey, Genomic, 4 genes, 3720 nt].//0.12:326:61//S76368  
 R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.2-12.3 Contains ESTs STS  
 and GSSs, complete sequence.//2.2e-111:538:98//AL033384  
 R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99//AF070524  
 R-NT2RP4000323//S.cerevisiae telomeric sequence DNA, clone YLP108CA-2-i.//0.048:107:69//M34311  
 20 R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-  
 39:350:79//AC004972  
 R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281  
 R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//  
 8.7e-109:527:98//AF044195  
 25 R-NT2RP4000370//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//9.9e-25 :348:72//  
 AC005154  
 R-NT2RP4000376//Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.//2.2e-  
 69:391:89//U17901  
 R-NT2RP4000381//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//0.066:197:63//  
 30 AC006080  
 R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens genomic clone A-345F19, genomic survey se-  
 quence.//0.10:79:75//B15527  
 R-NT2RP4000417//Homo sapiens full-length insert cDNA clone ZD52B10.//9.6e-96:468:97//AF086313  
 R-NT2RP4000424//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2  
 35 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethyl-  
 aniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for  
 another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete se-  
 quence.//1.8e-08:489:59//AL021026  
 R-NT2RP4000448//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
 40 DRAFT SEQUENCE, 8 unordered pieces.//3.3e-07:510:60//AC005505  
 R-NT2RP4000449//HS\_2037\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2037 Col=18 Row=B, genomic survey sequence.//1.3e-58:375:88//AQ243047  
 R-NT2RP4000455//Phocine herpesvirus type 1 glycoprotein D (gD) gene, partial cds.//0.62:133:63//U92271  
 R-nnnnnnnnnnnn  
 45 R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
 clone CSRL-54b11, genomic survey sequence.//2.1e-19:145:88//B05082  
 R-nnnnnnnnnnnn  
 R-NT2RP4000500  
 R-NT2RP4000515//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 50 DRAFT SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC005140  
 R-NT2RP4000517//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//2.7e-21:230:  
 77//AC003007  
 R-NT2RP4000518//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced  
 Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseu-  
 55 dogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor  
 JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//0.0080:461:59//AL021068  
 R-NT2RP4000519  
 R-NT2RP4000524

R-NT2RP4000528//Homo sapiens chromosome 17, clone hRPK.138\_P\_22, complete sequence./.0.99:158:66//AC005697

R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Cosmid Clone 33e In DGCR Region, complete sequence./1.0:309:59//AC000078

5 R-NT2RP4000556//Rattus norvegicus cell cycle protein p55CDC gene, complete cds./.0.0031:126:72//AF052695

R-NT2RP4000588//Homo sapiens BAC clone RG208K23 from 7q31, complete sequence./1.0:186:64//AC004161

R-NT2RP4000614//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-62, complete sequence./1.4e-06:526:58//AL009013

10 R-NT2RP4000638//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces./6.9e-48:497:75//AC004666

R-NT2RP4000648//CIT-HSP-2300I7.TR CIT-HSP Homo sapiens genomic clone 2300I7, genomic survey sequence./0.22:110:68//AQ012747

R-NT2RP4000657//Lycodichthys dearborni type III antifreeze peptide gene, clone 5'LD-1/NotI-EcoRI subclone SphI-XbaI, partial cds./.0.0065:189:63//U20443

15 R-NT2RP4000704//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE./0.22:334:60//Z83824

R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Cosmid Clone 56c In DGCR Region, complete sequence./2.2e-70:448:88//AC000080

20 R-NT2RP4000728//CIT-HSP-2310K14.TF CIT-HSP Homo sapiens genomic clone 2310K14, genomic survey sequence./0.00013:289:61//AQ019669

R-NT2RP4000739//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces./0.53:254:61//AC004765

R-NT2RP4000781//P.cepacia fusaric acid-resistance genes encoding 5 proteins, complete cds./1.0:392:59//D12503

25 R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence./0.59:378:58//AC003037

R-NT2RP4000833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE./3.4e-53:307:85//AL023808

R-NT2RP4000837//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence./7.0e-50:367:77//AE000660

R-NT2RP4000855

R-NT2RP4000865//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence./1.5e-78:479:88//AC003098

30 R-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein./4.5e-09:186:69//AJ001616

R-NT2RP4000879//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./7.8e-08:364:60//AC004153

R-nnnnnnnnnnnn//Human S-adenosylmethionine decarboxylase (AMD1) gene, exons 5-9./3.5e-90:459:96//M88006

35 R-nnnnnnnnnnnn//H.sapiens ung gene for uracil DNA-glycosylase./7.6e-09:392:61//X89398

R-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds./5.8e-45:264:92//U42975

R-nnnnnnnnnnnn//epstein-barr virus simple repeat array (ir3).//0.00012:367:61//J02079

R-NT2RP4000928//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence./1.0:138:68//AB006698

40 R-NT2RP4000929//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence./0.45:288:62//Z82197

R-NT2RP4000955//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633O19, WORKING DRAFT SEQUENCE./1.1e-09:322:62//AL022302

45 R-NT2RP4000973//Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions./2.3e-06:326:62//AF003528

R-NT2RP4000975

R-NT2RP4000979//HS\_3009\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=15 Row=L, genomic survey sequence./2.3e-14:117:89//AQ090957

50 R-NT2RP4000984//Human immunodeficiency virus type 1 envelope glycoprotein (env) gene, C2-V3 region, isolate HIV194UG011TIN.01\_di1PD, partial cds./0.11:219:62//U44882

R-NT2RP4000989//Sequence 30 from patent US 5552281./3.5e-25:154:97//I25669

R-NT2RP4000996//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2),

CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//3.8e-07:421:59//AF030694  
 R-NT2RP4000997//Homo sapiens chromosome 17, clone 104H12, complete sequence.//4.2e-37:499:72//AC000003

5 R-NT2RP4001004//HS\_3163\_A2\_H02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=4 Row=O, genomic survey sequence.//2.8e-38:241:90//AQ168515  
 R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//7.1e-55:372:73//AC006023  
 R-NT2RP4001010//Homo sapiens full-length insert cDNA clone ZD38E12.//3.3e-09:153:74//AF086247

10 R-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.1e-34:361:78//U20086  
 R-NT2RP4001041//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//9.9e-84:435:96//AC005216  
 R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds.//6.2e-50:282:94//AB007859  
 R-NT2RP4001064//H.sapiens NOS2 gene, exon 15.//0.71:183:61//X85771

15 R-NT2RP4001078//Human D-site binding protein gene, exon 4 and complete cds.//1.9e-114:569:97//U48213  
 R-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase, partial.//2.4e-118:574:98//AJ010953  
 R-NT2RP4001080//Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence.//0.013:430:58//AE001429

20 R-nnnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds.//1.8e-119:548:95//AB011164  
 R-NT2RP4001095//Homo sapiens cosmids IM0525, LC1233, Qc3C1, LB1439, Qc12C11 and 220B3 from Xq28, complete sequence.//2.8e-39:312:81//AF003626  
 R-NT2RP4001100//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//8.7e-41:389:78//Z78021

25 R-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//2.8e-12:292:68//M96629  
 R-NT2RP4001122//Caenorhabditis elegans cosmid F44D12, complete sequence.//0.97:129:66//Z68298  
 R-NT2RP4001126//HS\_3146\_A1\_805\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=9 Row=C, genomic survey sequence.//0.013:268:63//AQ141093  
 R-NT2RP4001138

30 R-NT2RP4001143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//1.8e-31:380:68//AL031668  
 R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-83:325:92//AC005095  
 R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//8.1e-32:553:67//D67067

35 R-NT2RP4001150//AK011 Genomic DNA Hordeum vulgare genomic clone tel44a similar to barley TAS, genomic survey sequence.//0.91:132:63//AQ248412  
 R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence.//4.0e-118:437:97//AB003468  
 R-NT2RP4001174//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//1.7e-33:289:82//AC002996  
 R-nnnnnnnnnnnn//P.falciparum mRNA for AARP2 protein.//0.93:187:64//Y08924

40 R-NT2RP4001207  
 R-NT2RP4001210//CIT-HSP-2042D13.TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence.//3.8e-06:268:63//B74772  
 R-NT2RP4001213//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//4.7e-16:371:66//M99593

45 R-NT2RP4001219//HS\_2190\_A1\_A06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence.//2.4e-06:288:61//AQ216635  
 R-NT2RP4001228//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.024:357:58//AL031745

50 R-NT2RP4001235//HS\_3047\_A1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=L, genomic survey sequence.//0.0033:301:63//AQ126918  
 R-NT2RP4001256//HS\_3007\_A2\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence.//1.5e-11:140:80//AQ118389  
 R-NT2RP4001260//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//0.0013:486:59//AE001426

55 R-NT2RP4001274//RPCI11-24O21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24O21, genomic survey sequence.//3.9e-25:142:99//AQ013887

R-nnnnnnnnnnnn//Homo sapiens full-length insert cDNA clone ZD55D10./.1.2e-10:90:92//AF086334  
 R-NT2RP4001313//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence./.7.7e-23:  
 466:66//AF009326  
 R-NT2RP4001315//CIT-HSP-2312C6.TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey se-  
 quence./.0.98:305:62//AQ018036  
 5 R-NT2RP4001339  
 R-NT2RP4001345  
 R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence./.0.00082:260:59//  
 AB003097  
 10 R-NT2RP4001353//RPCI11-55N17.TJ RPCI11 Homo sapiens genomic clone R-55N17, genomic survey se-  
 quence./.0.74:106:66//AQ081821  
 R-NT2RP4001372  
 R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence./.1.5e-09:473:  
 60//AC006080  
 15 R-NT2RP4001375  
 R-NT2RP4001379//CIT-HSP-2335A10.TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey se-  
 quence./.9.4e-41:441:75//AQ040083  
 R-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence./.2.4e-22:276:73//  
 AC004691  
 20 R-NT2RP4001407//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 DRAFT SEQUENCE, 14 unordered pieces./.0.49:254:61//AC005140  
 R-NT2RP4001414  
 R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7./.6.6e-66:357:90//L14272  
 R-NT2RP4001442//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 25 DRAFT SEQUENCE, 5 unordered pieces./.0.11:307:59//AC005308  
 R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone  
 cSRL-58d2, genomic survey sequence./.0.0039:112:71//B05220  
 R-NT2RP4001474  
 R-NT2RP4001483  
 30 R-NT2RP4001498//Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds./.1.2e-07:339:  
 61//L34027  
 R-NT2RP4001502//HS\_2187\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2187 Col=19 Row=F, genomic survey sequence./.1.3e-20:183:81//AQ214108  
 R-NT2RP4001507//Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE,  
 35 4 unordered pieces./.0.15:333:62//AC005916  
 R-NT2RP4001524//Genomic sequence from Human 13, complete sequence./.0.96:159:65//AC001226  
 R-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds./.9.5e-34:337:80//U20086  
 R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING  
 40 DRAFT SEQUENCE, 2 unordered pieces./.0.00027:336:63//AC004710  
 R-nnnnnnnnnnnn//Arabidopsis thaliana BAC T12H20./.1.5e-11:517:60//AF080119  
 R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs./.0.0069:305:62//  
 Z82212  
 R-NT2RP4001567//RPCI11-61A2.TJ RPCI11 Homo sapiens genomic clone R-61A2, genomic survey sequence./.  
 0.0072:180:60//AQ200771  
 45 R-NT2RP4001568  
 R-NT2RP4001571//Trypanoplasma borrelii kinetoplast ribosomal protein S12 (RPS12), putative cryptogene (GRII),  
 12S ribosomal RNA, and apocytochrome b (CYb) genes, primary transcripts, and cytochrome c oxidase subunit  
 III (COIII) gene, complete cds./.1.6e-09:555:58//U14181  
 R-NT2RP4001574//HS\_2247\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 50 nomic clone Plate=2247 Col=9 Row=D, genomic survey sequence./.1.1e-41:254:90//AQ182345  
 R-NT2RP4001575//Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the  
 BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18  
 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseu-  
 dogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6  
 55 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type  
 XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG  
 islands, ESTs, STSs, and GSSs, complete sequence./.1.1e-118:567:98//AL031228  
 R-NT2RP4001592//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING

DRAFT SEQUENCE.//2.5e-09:370:61//AL031650  
 R-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//0.99:73:75//AC002364  
 R-NT2RP4001614  
 5 R-NT2RP4001634//Homo sapiens full-length insert cDNA clone YU73B11.//5.8e-101:526:94//AF087969  
 R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds.//5.4e-115:559:97//AF007151  
 R-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092  
 R-NT2RP4001656//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.2e-109:515:99//AC000384  
 10 R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.19:504:58//AC000397  
 R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//4.5e-115:583:96//U96629  
 R-NT2RP4001725//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.98:301:60//AC000380  
 15 R-nnnnnnnnnnnn//Caenorhabditis elegans cosmid F48E3.//2.2e-17:328:64//U28735  
 R-NT2RP4001739//RPCI11-74E7.TJ RPCI11 Homo sapiens genomic clone R-74E7, genomic survey sequence.//1.1e-08:141:65//AQ268408  
 R-NT2RP4001753//H.sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:552:96//X78926  
 R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//9.3e-27:358:72//L11316  
 20 R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-99:484:98//AC005020  
 R-NT2RP4001803//HS\_3087\_B2\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3087 Col=10 Row=D, genomic survey sequence.//2.7e-96:471:97//AQ121405  
 R-NT2RP4001822  
 25 R-NT2RP4001823  
 R-NT2RP4001828//Human DNA sequence from PAC 179115, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//4.1e-14:136:83//Z92540  
 R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.5e-06:418:60//AE001372  
 30 R-NT2RP4001849//P.falciparum serine rich protein (SERP I) gene.//0.64:135:67//J03983  
 R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548  
 R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-111:570:96//AC005014  
 35 R-NT2RP4001896  
 R-NT2RP4001901  
 R-NT2RP4001927//Borrelia burgdorferi (section 32 of 70) of the complete genome.//1.0:242:60//AE001146  
 R-NT2RP4001938//Human aminopeptidase N gene, exon 1.//3.3e-42:195:85//M55523  
 R-NT2RP4001946//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
 40 DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//AC004157  
 R-NT2RP4001950//RPCI11-69C18.TJ RPCI11 Homo sapiens genomic clone R-69C18, genomic survey sequence.//4.7e-91:552:89//AQ236641  
 R-NT2RP4001953//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//6.6e-70:325:84//Z93023  
 45 R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//5.5e-37:141:86//D42148  
 R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, partial 3'UTR region.//1.0e-46:242:98//U25276  
 R-NT2RP4002018//RPCI11-76I23.TV RPCI11 Homo sapiens genomic clone R-76I23, genomic survey sequence.//7.9e-89:438:97//AQ268536  
 50 R-NT2RP4002047//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//4.1e-07:325:62//AL031297  
 R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13.1-13.31. Contains GSSs, complete sequence.//0.31:452:57//AL022353  
 R-NT2RP4002058//RPCI11-69O1.TJ RPCI11 Homo sapiens genomic clone R-69O1, genomic survey sequence.//0.23:163:64//AQ268418  
 55 R-NT2RP4002071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1172A22, WORKING DRAFT SEQUENCE.//1.1e-11:407:62//AL034386  
 R-NT2RP4002075//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon

of a putative new gene and STSs and GSSs, complete sequence./.0.085:350:61//AL033375  
R-NT2RP4002078//RPCI11-79I16.TV RPCI11 Homo sapiens genomic clone R-79I16, genomic survey sequence./.3.3e-87:452:95//AQ283131  
R-nnnnnnnnnnnnn  
5 R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5./.0.50:256:61//AF068619  
R-NT2RP4002408//CIT-HSP-2376023.TF CIT-HSP Homo sapiens genomic clone 2376O23, genomic survey se-  
quence./.6.8e-62:320:96//AQ111163  
R-NT2RP4002791//Human PAC clone DJ318C15 from Xq23, complete sequence./.0.022:435:61//AC002476  
10 R-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence./.6.0e-56:660:71//  
AC002383  
R-NT2RP4002905//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete  
sequence./.0.0017:533:57//AL008972  
R-OVARC100001//Homo sapiens mRNA for KIAA0465 protein, partial cds./.8.7e-114:605:94//AB007934  
15 R-OVARC100004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence./.2.1e-43:326:  
74//AC005510  
R-OVARC100006//HS\_2253\_B1\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2253 Col=1 Row=L, genomic survey sequence./.3.7e-35:191:98//AQ069124  
R-OVARC100013//HS\_2212\_A2\_G06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2212 Col=12 Row=M, genomic survey sequence./.0.14:212:63//AQ210584  
20 R-OVARC100014//Human DNA sequence from PAC 463A9, on chromosome Xq25 contains STS./.0.0053:356:  
62//Z80232  
R-OVARC100017  
R-OVARC100035//RPCI11-65E1.TJ RPCI11 Homo sapiens genomic clone R-65E1, genomic survey sequence./.  
3.3e-05:236:63//AQ237194  
25 R-OVARC1000058//Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains  
an Immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSs, GSSs and taga  
and tat repeat polymorphisms, complete sequence./.2.7e-48:325:82//AL008721  
R-OVARC1000060//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING  
DRAFT SEQUENCE./.5.0e-21:297:70//AL033397  
30 R-OVARC1000068//P.falciparum complete gene map of plastid-like DNA (IR-B).//.0.00038:553:58//X95276  
R-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING  
DRAFT SEQUENCE./.5.1e-110:599:93//AL031387  
R-OVARC1000085//DNA encoding component HC5 of human proteasome./.2.7e-65:366:92//E03413  
35 R-nnnnnnnnnnnn//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey se-  
quence./.0.80:285:59//B94391  
R-OVARC1000091  
R-OVARC1000092//CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic clone 2373J20, genomic survey se-  
quence./.1.4e-17:141:85//AQ111520  
R-OVARC 1000106  
40 R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds./.2.6e-  
100:495:97//AF069250  
R-OVARC1000114//Homo sapiens partial XPGC gene, exon 2./.9.5e-49:392:80//X71342  
R-OVARC1000133//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence./.0.00020:243:  
65//U95740  
45 R-OVARC1000145//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence./.  
1.8e-16:370:67//AC005385  
R-OVARC1000148//CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic clone 2386P14, genomic survey  
sequence./.1.1e-05:55:98//AQ240492  
R-OVARC1000151//M.musculus GEG-154 mRNA./.9.8e-21:192:81//X71642  
50 R-OVARC1000168//CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clone 2336F6, genomic survey se-  
quence./.0.050:176:62//AQ042932  
R-OVARC1000191//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING  
DRAFT SEQUENCE, 7 unordered pieces./.3.7e-08:534:58//AC005506  
R-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07;  
55 HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces./.5.2e-111:556:96//AC004604  
R-OVARC1000209//Blacus sp. 16S ribosomal RNA gene, partial sequence./.0.55:165:67//AF003501  
R-OVARC1000212//Mouse DNA for beta-casein./.0.56:225:63//X13484  
R-OVARC1000240//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence./.6.2e-38:193:82//

AC005670  
R-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-25:312:73//  
AF060194  
R-OVARC1000288//Human HepG2 3' region Mbol cDNA, clone hmd1d01m3.//5.4e-07:128:70//D17131  
5 R-OVARC1000302//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//1.7e-10:100:88//  
AC005971  
R-OVARC1000304//Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X52574  
R-OVARC 1000309  
10 R-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
6.5e-83:453:94//AC005236  
R-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//5.0e-  
58:455:81//U19614  
R-OVARC1000335/\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0483I23;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.034:429:60//AC005690  
15 R-OVARC1000347//Mus musculus HRS gene, complete cds.//4.6e-06:339:61//AF020308  
R-OVARC1000384//D. discoideum glycoprotein 24 A and B (GP24A and GP24B) genes, complete cds.//0.48:296:  
62//M27588  
R-OVARC1000408//Homo sapiens DNA from chromosome 19-cosmid R27740 containing MEF2B and RSRFR2  
genes, genomic sequence.//9.4e-39:286:87//AD000812  
20 R-OVARC1000411//CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic clone 2303H10, genomic survey se-  
quence.//1.5e-07:94:84//AQ016720  
R-OVARC1000414//Homo sapiens genomic DNA, 21q region, clone: 149C3X10, genomic survey sequence.//1.8e-  
32:296:75//AG002388  
R-OVARC1000420//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-48:354:77//AC005378  
25 R-OVARC1000427//D. discoideum vegetative specific gene V18 gene for ribosomal protein.//2.5e-09:370:59//  
X15382  
R-OVARC1000431//HS\_2199\_A2\_E02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2199 Col=4 Row=I, genomic survey sequence.//1.3e-34:186:98//AQ093722  
R-OVARC1000437//Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80//L06662  
30 R-OVARC1000440//Homo sapiens BAC clone NH0538D15 from 7q11.23-q21.1, complete sequence.//0.0054:337:  
61//AC006043  
R-OVARC1000442//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey se-  
quence.//1.0e-45:322:86//AQ037381  
R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.1e-77:418:94//AB014583  
35 R-OVARC1000461//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING  
DRAFT SEQUENCE.//0.62:333:59//AL034417  
R-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.1e-  
81:489:91//AF023451  
R-OVARC1000466//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//0.0088:98:  
40 72//AC004526  
R-OVARC1000473//Homo sapiens full-length insert cDNA clone YI53C10.//3.2e-92:317:100//AF085851  
R-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//2.7e-70:502:84//D87671  
R-OVARC1000486//Dictyostelium discoideum FusC (fusC) gene, partial cds.//0.52:411:58//AF019984  
R-OVARC1000496  
45 R-OVARC1000520//Homo sapiens PAC clone DJ412A9 from 22, complete sequence.//3.8e-17:294:71//AC005005  
R-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//  
4.5e-109:547:96//AC005024  
R-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.0e-46:264:93//  
AC004510  
50 R-OVARC1000543//Caenorhabditis elegans cosmid F10C1.//0.00063:417:59//U49831  
R-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3  
gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.5e-39:144:92//AL022069  
R-OVARC1000557//Homo sapiens chromosome 19, cosmid R32469, complete sequence.//1.5e-81:429:96//  
AC005197  
55 R-OVARC1000564//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.83:301:58//  
AC004223  
R-OVARC1000573//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for  
creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na<sup>+</sup>-isocitrate dehydrogenase gamma subunit

(IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lu1 gene and cytochrome C (CCp) pseudogene //2.4e-44:300:88//U52111

5 R-OVARC1000578//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence //6.4e-48:436:78//AF001549

R-OVARC1000588//Homo sapiens chromosome 19, cosmid F19847, complete sequence //2.7e-32:313:78//AC005952

R-OVARC 1000605

10 R-OVARC1000622//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence //6.2e-43:328:83//AC006012

R-OVARC1000640//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces //1.9e-47:514:73//AC005840

R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds //1.6e-29:162:100//AB011162.

15 R-OVARC1000678//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces //0.50:270:60//AC005140

R-nnnnnnnnnnnn//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7 //1.4e-83:549:86//AJ001713

R-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE //3.2e-13:160:76//AL034424

20 R-OVARC1000689//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds //0.90:230:61//U32943

R-OVARC1000700//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence //5.1e-15:133:85//AC005754

R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130\_H\_16, complete sequence //6.9e-48:525:73//AC005585

25 R-OVARC1000730//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence //0.00019:198:63//AQ093513

R-OVARC1000746//P.falciparum complete gene map of plastid-like DNA (IR-B) //0.98:154:65//X95276

R-OVARC1000769//Human coagulation factor XI gene, intron 2, partial, clone pTZ18R //2.0e-30:187:78//M21185

R-OVARC1000771

30 R-OVARC1000781//Sequence 5 from Patent WO9722695 //8.4e-47:401:77//A63552

R-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence //7.8e-111:567:96//AC004542

R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cds //1.3e-17:119:95//L15189

35 R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBNL H171), complete sequence //2.3e-51:482:78//AC005574

R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC //3.6e-105:536:95//Y1771

R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence //2.7e-107:538:96//AC004494

40 R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds //3.6e-114:579:96//AF045584

R-OVARC1000862//M.musculus Fif mRNA //2.3e-20:346:73//X71978

R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence //9.1e-08:427:58//AE001416

R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds //5.6e-34:357:78//U20086

45 R-OVARC1000885//Lycopersicon esculentum alcohol dehydrogenase homolog (GAD3) mRNA, partial cds //0.47:305:60//U21801

R-OVARC 1000886

R-OVARC1000891//HS\_3082\_A2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, genomic survey sequence //1.1e-16:187:79//AQ122500

50 R-OVARC1000897//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence //7.2e-07:476:60//AL020989

R-OVARC1000912

R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces //5.4e-70:509:86//AC004150

55 R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk In NF1 Region, complete sequence //1.6e-77:465:90//AC002471

R-OVARC1000936//HS\_2195\_A2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=24 Row=E, genomic survey sequence //2.4e-76:463:90//AQ191108

R-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE./.0.0028:161:65//Z99716

R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds./.3.5e-62:526:78//AB005549

5 R-OVARC1000948//Hypera postica NADH dehydrogenase subunit 1 (ND1) gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribosomal gene, partial sequence, mitochondrial genes encoding mitochondrial products./.0.018:212:61//U61169

R-OVARC1000959//CIT-HSP-2371K16.TR CIT-HSP Homo sapiens genomic clone 2371K16, genomic survey sequence./.1.1e-45:303:87//AQ111323

10 R-OVARC1000960//Homo sapiens BAC clone GS293C05 from 7q21-q22, complete sequence./.7.5e-44:353:81//AC005021

R-OVARC1000971//H.sapiens DNA for repeat unit locus D18S51(285 bp)./.2.2e-07:223:70//X91255

R-OVARC1000984

15 R-OVARC1000996//Human DNA sequence from clone 272L16 on chromosome 1q32.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Kalinin, BM600) and a novel Rat Ca<sup>2+</sup>/Calmodulin dependent Protein Kinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence./.1.3e-06:179:70//AL023754

R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete sequence./.5.8e-71:332:87//AC003957

20 R-OVARC1001000//HS\_3032\_B1\_G11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, genomic survey sequence./.5.1e-51:257:99//AQ096695

R-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence./.5.6e-92:473:96//AC004190

R-OVARC1001010//RPCI11-10P1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-10P1, genomic survey sequence./.4.1e-05:201:65//B71813

25 R-OVARC1001011//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces./.7.9e-18:219:69//AC005520

R-OVARC1001032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE./.2.7e-89:464:86//AL022345

30 R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence./.1.4e-18:451:64//AC005220

R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds./.1.3e-99:501:96//AF099149

R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096\_G\_20, complete sequence./.9.7e-17:180:78//AC005410

35 R-OVARC1001044

R-OVARC1001051//H.sapiens mRNA for homologue to yeast ribosomal protein L41./.3.7e-15:124:88//Z12962

R-OVARC1001055//Homo sapiens, clone hRPK.15\_A\_1, complete sequence./.2.0e-30:292:76//AC006213

R-OVARC1001062//Sequence 65 from patent US 5691147./.2.6e-54:312:92//I76237

40 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds./.2.3e-95:463:98//AF082657

R-OVARC1001072//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds./.0.92:272:59//U47276

R-OVARC1001074//HS\_2205\_A1\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=G, genomic survey sequence./.1.3e-35:205:94//AQ184530

R-OVARC1001085

45 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))./.4.5e-95:325:98//AJ005897

R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds./.1.0e-73:386:95//AF051782

R-OVARC1001117//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence./.6.1e-37:314:81//AC005272

50 R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBNL H73), complete sequence./.1.5e-44:390:77//AC005372

R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4./.0.81:461:57//AJ235270

55 R-OVARC1001161//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE./.4.6e-08:342:64//AL031680

R-OVARC1001162//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence./.5.9e-48:347:85//B89781

R-OVARC1001167//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces./.

1.3e-28:427:70//AC004963  
R-OVARC1001169//RPCI11-36P6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859  
R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//8.8e-39:301:85//AC002549  
5 R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:83//U67213  
R-OVARC1001180//Homo sapiens 12q24.1 NOVECTOR P443K8 () complete sequence.//9.1e-41:516:72//AC005907  
R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.2e-14:  
10 134:85//AC004796  
R-OVARC1001200//ALS=85 kda insulin-like growth factor binding protein-3 complex acid-labile subunit [baboons, liver, mRNA Partial, 1818 nt].//0.12:345:60//S83462  
R-OVARC1001232//Bovine tyrosine hydroxylase mRNA, complete cds.//0.66:257:59//M36794  
R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, complete sequence.//1.4e-41:284:87//  
15 AC006071  
R-OVARC1001243//HS\_2055\_B2\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, genomic survey sequence.//0.59:83:75//AQ243142  
R-OVARC1001261//Crocodylus porosus mRNA for transthyretin.//0.93:121:66//AJ223148  
R-OVARC1001268  
20 R-OVARC1001270//Plasmodium falciparum MAL3P6, complete sequence.//0.0031:295:62//Z98551  
R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-107:544:97//AC004494  
R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPCI1-199J3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.025:402:59//AC006062  
25 R-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018  
R-nnnnnnnnnnnn//Sequence 13 from patent US 5624818.//5.4e-85:577:84//I41142  
R-OVARC1001329//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402  
30 R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.1, complete sequence.//0.19:256:59//AC004862  
R-OVARC1001339//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.5e-49:366:83//AC004242  
R-OVARC1001341//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818  
35 R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874  
R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261j17 (LBNL H190), complete sequence.//2.8e-46:424:78//AC005350  
40 R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//I34297  
R-OVARC1001360//Homo sapiens chromosome 17, clone hRPK.786\_O\_4, complete sequence.//0.20:335:60//AC005863  
R-OVARC 1001369  
45 R-OVARC1001372//S.scrofa DNA for myogenin 3'flanking region (285 bp).//6.9e-29:249:83//X89210  
R-OVARC1001376//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.1e-50:491:73//AC004491  
R-OVARC1001381//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//9.3e-20:422:  
60//AC005821  
R-OVARC1001391  
50 R-nnnnnnnnnnnn  
R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//9.9e-110:561:95//AB00665  
R-OVARC1001419//CIT-HSP-2362F16.TR CIT-HSP Homo sapiens genomic clone 2362F16, genomic survey sequence.//7.6e-47:242:98//AQ074668  
R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence.//2.3e-20:211:66//  
55 AC005157  
R-OVARC1001436//Human DNA flanking 3' end of transposon L1.1.//0.18:148:66//M80341  
R-OVARC1001442  
R-OVARC1001453//Human PAC clone DJ525N14 from Xq23, complete sequence.//2.3e-19:181:81//AC002086

R-OVARC1001476//CITBI-E1-2517B6.TR CITBI-E1 Homo sapiens genomic clone 2517B6, genomic survey sequence.//0.24:308:59//AQ278655  
R-OVARC1001480//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 753D4, WORKING DRAFT SEQUENCE.//0.99:294:62//AL031676  
5 R-OVARC1001489//E.caballus microsatellite DNA marker (clone ASB32).//0.87:81:71//X93546  
R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//9.3e-116:585:96//AF016507  
R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//2.6e-40:285:86//AC002039  
10 R-OVARC1001525//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:59//AC006036  
R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds.//5.0e-110:566:95//AB016488  
R-OVARC1001547  
15 R-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//5.9e-33:216:92//AF031165  
R-OVARC1001600//Human Chromosome X, complete sequence.//3.0e-22:157:89//AC002418  
R-OVARC1001610//HS\_3070\_A2\_A06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070 Col=12 Row=A, genomic survey sequence.//0.47:107:66//AQ103523  
20 R-OVARC1001611//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//0.17:236:63//AL034423  
R-OVARC1001615//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING DRAFT SEQUENCE.//1.3e-19:248:70//AL031658  
R-OVARC1001668//HS\_3228\_A2\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=24 Row=I, genomic survey sequence.//4.6e-13:156:76//AQ188379  
25 R-OVARC1001702//CITBI-E1-2501P16.TR.1 CITBI-E1 Homo sapiens genomic clone 2501P16, genomic survey sequence.//1.6e-41:217:99//AQ241965  
R-OVARC1001703  
R-OVARC1001711//CITBI-E1-2502N10.TF CITBI-E1 Homo sapiens genomic clone 2502N10, genomic survey sequence.//2.0e-14:220:72//AQ266194  
30 R-OVARC1001726//CIT-HSP-2320O1.TF CIT-HSP Homo sapiens genomic clone 2320O1, genomic survey sequence.//0.021:170:62//AQ038145  
R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (pl).//2.5e-72:422:90//X05276  
R-OVARC1001745//Human DNA sequence from clone 796I11 on chromosome 20q12. Contains ESTs, an STS and GSSs, complete sequence.//7.6e-44:314:84//AL031257  
35 R-nnnnnnnnnnnn//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//1.6e-08:396:60//M23166  
R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//3.5e-108:567:94//U97670  
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds.//6.3e-108:529:97//AB014575  
R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence.//0.24:205:64//Z99279  
40 R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//4.6e-58:558:76//AC005066  
R-OVARC1001795  
R-OVARC1001802//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//1.1e-37:346:78//U89337  
45 R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//3.0e-112:581:95//AL023694  
R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//6.6e-41:345:81//AL031585  
50 R-OVARC1001813//CITBI-E1-2508J18.TR CITBI-E1 Homo sapiens genomic clone 2508J18, genomic survey sequence.//1.6e-72:386:95//AQ263046  
R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence.//4.8e-41:320:83//AC002086  
55 R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.4e-08:527:58//AC004688  
R-OVARC1001846//CIT-HSP-2014F15.TR CIT-HSP Homo sapiens genomic clone 2014F15, genomic survey sequence.//0.0045:165:67//B58905

R-OVARC1001861//*M.musculus* mRNA for pMEM2 protein.//9.5e-28:405:68//X95350  
 R-OVARC1001873//*Homo sapiens* clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611  
 R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,  
 complete sequence.//9.1e-20:206:80//AL031864  
 5 R-OVARC1001880//RPCI11-42I15.TJ RPCI11 *Homo sapiens* genomic clone R-42I15, genomic survey se-  
 quence.//3.9e-50:287:88//AQ052700  
 R-OVARC1001883//*Homo sapiens* chromosome 17, clone hCIT.123\_J\_14, complete sequence.//6.1e-13:457:63//  
 AC003950  
 10 R-OVARC1001900//*Homo sapiens* tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//  
 2.5e-86:346:90//AF061749  
 R-OVARC1001901//*Homo sapiens* testis specific methyl-CpG binding protein MBD2 (MBD2) mRNA, partial cds.//  
 7.2e-89:421:100//AF072246  
 R-OVARC1001911//*Homo sapiens* full-length insert cDNA clone ZD52F10.//8.2e-106:510:98//AF086315  
 15 R-OVARC1001916  
 R-OVARC1001928  
 R-OVARC1001942//*S.cerevisiae* N-acetyltransferase (AAA1) mRNA, complete cds.//0.0013:231:63//M23166  
 R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP329, envelope glycoprotein V3 region  
 (env) gene, partial cds.//0.14:173:64//U58826  
 20 R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//1.3e-09:306:  
 63//M99593  
 R-OVARC1001950//*Homo sapiens* chromosome 17, clone hRPK.112\_H\_10, complete sequence.//8.2e-38:385:  
 75//AC005666  
 R-OVARC1001987  
 25 R-OVARC1001989//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11,  
 WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841  
 R-OVARC1002044//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island,  
 complete sequence.//5.0e-42:298:86//AL031286  
 R-OVARC1002050//*Homo sapiens* mRNA for KIAA0465 protein, partial cds.//1.4e-107:542:96//AB007934  
 30 R-OVARC1002066//*Arabidopsis thaliana* chromosome II BAC F14M4 genomic sequence, complete sequence.//  
 0.23:210:61//AC004411  
 R-OVARC1002082//*Homo sapiens* clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 5.4e-99:546:92//AC006015  
 R-OVARC1002107//Human DNA sequence from PAC 417G15 on chromosome Xq25-Xq26. Contains glycan-3  
 35 precursor (intestinal protein OCI-5) (GTR2-2), pseudogene, ESTs.//4.4e-34:375:74//AL009174  
 R-OVARC1002127  
 R-OVARC1002138//CIT-HSP-2290O18.TF CIT-HSP *Homo sapiens* genomic clone 2290O18, genomic survey se-  
 quence.//2.4e-07:316:62//AQ003988  
 R-OVARC1002143//RPCI11-54M8.TJ RPCI11 *Homo sapiens* genomic clone R-54M8, genomic survey sequence.//  
 40 2.3e-35:220:90//AQ083241  
 R-OVARC1002156  
 R-OVARC1002158//CITBI-E1-2514D4.TF CITBI-E1 *Homo sapiens* genomic clone 2514D4, genomic survey se-  
 quence.//1.6e-12:140:79//AQ265720  
 R-OVARC1002165//CIT-HSP-2307C9.TF CIT-HSP *Homo sapiens* genomic clone 2307C9, genomic survey se-  
 45 quence.//5.0e-59:291:99//AQ020420  
 R-OVARC1002182//*P. falciparum* SD17 gene for knob-associated histidine-rich protein.//0.74:161:65//Y00060  
 R-PLACE100004//*D.discoideum* gene for protein kinase.//0.00081:263:59//Z37981  
 R-PLACE100005//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC8-628 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58//AC005507  
 50 R-PLACE100007//*Homo sapiens* clone 24422 mRNA sequence.//1.2e-14:100:97//AF070557  
 R-PLACE100014//*Homo sapiens* genomic DNA, chromosome 21q22.2, p1 clone: T1212 and T1601, WORKING  
 DRAFT SEQUENCE.//2.8e-44:405:77//D83253  
 R-PLACE100031//*Homo sapiens* clone UWGC:y23c049 from 6p21, complete sequence.//1.8e-24:291:73//  
 AC006162  
 55 R-PLACE100040//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105C5,  
 WORKING DRAFT SEQUENCE.//0.00039:289:61//Z98855  
 R-PLACE100048//Human BAC clone RG210I04, complete sequence.//4.7e-83:518:89//AC002462  
 R-PLACE100050//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING

DRAFT SEQUENCE, 8 unordered pieces./.0.98:73:76//AC005505  
 R-PLACE1000061//Human ribosomal protein L37a mRNA sequence./.5.9e-21:125:98//L22154  
 R-PLACE1000066  
 R-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6  
 5 unordered pieces./.1.2e-87:456:95//AC005848  
 R-PLACE1000081  
 R-PLACE1000094//RPCI11-91K6.TV RPCI11 Homo sapiens genomic clone R-91K6, genomic survey sequence./.  
 2.3e-83:409:98//AQ282619  
 R-PLACE1000133//Homo sapiens chromosome 17, clone hRPK.746\_E\_8, complete sequence./.1.8e-06:420:57//  
 10 AC005358  
 R-PLACE1000142  
 R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds./.1.3e-112:594:94//  
 AF058291  
 R-PLACE1000185  
 15 R-PLACE1000213//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey se-  
 quence./.8.2e-80:410:97//AQ022149  
 R-PLACE1000214//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-09, complete  
 sequence./.1.6e-05:548:59//AL008989  
 R-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING  
 20 DRAFT SEQUENCE./.2.2e-16:118:91//AL032818  
 R-PLACE1000246//X.laevis mRNA for XLCL2 protein./.6.5e-13:66:95//Z14122  
 R-PLACE1000292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING  
 DRAFT SEQUENCE./.6.6e-41:322:84//Z98200  
 R-PLACE1000332//Homo sapiens chromosome 17, clone hCIT.281\_F\_24, complete sequence./.1.8e-16:598:62//  
 25 AC004706  
 R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 from 7q21-q22, complete sequence./.2.3e-11:237:69//  
 AC005326  
 R-PLACE1000374//Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence./.8.7e-09:  
 492:58//AC005278  
 30 R-PLACE1000380//Plasmodium falciparum chromosome 2, section 1 of 73 of the complete sequence./.0.59:354:  
 59//AE001364  
 R-PLACE1000383//Mus musculus myotubularin related protein 1 (Mtmr1) mRNA, complete cds./.0.55:65:84//  
 AF073997  
 R-PLACE1000401//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces./.3.6e-  
 35 17:152:83//AC005015  
 R-PLACE1000406//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence./.  
 0.51:346:58//AB020742  
 R-PLACE1000420//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15,  
 WORKING DRAFT SEQUENCE./.1.5e-25:243:79//AP000009  
 40 R-PLACE1000421//HS\_2251\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2251 Col=24 Row=N, genomic survey sequence./.1.4e-82:430:95//AQ192807  
 R-PLACE1000424//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence./.1.8e-36:483:71//  
 AC002073  
 R-PLACE1000435//Homo sapiens chromosome 21q22.2 cosmid clone Q71A3, complete sequence./.2.6e-37:371:  
 45 76//AF015724  
 R-PLACE1000444//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence./.1.0e-54:429:  
 81//AC005899  
 R-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector  
 pEMBLcos2, complete sequence./.0.66:103:72//AF059580  
 50 R-PLACE1000481//Human DNA sequence from clone 960O17 on chromosome Xp11.21-11.22 Contains EST, CA  
 repeat(DXS991), STS, GSS, complete sequence./.0.019:171:66//AL022166  
 R-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds./.3.2e-17:221:72//  
 U35245  
 R-PLACE1000540//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 55 DRAFT SEQUENCE, 5 unordered pieces./.0.00045:480:60//AC005308  
 R-PLACE1000547//Homo sapiens chromosome 19, cosmid F17987, complete sequence./.9.6e-32:231:85//  
 AC004790  
 R-PLACE1000562//, complete sequence./.1.8e-45:280:92//AC005409

R-PLACE1000564//Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds.//0.0079:180:65//U41302  
R-PLACE1000583//Homo sapiens chromosome 17, clone hRPK.799\_N\_11, complete sequence.//1.5e-37:414:  
74//AC005323  
5 R-nnnnnnnnnnnn//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//1.9e-77:542:82//  
M55542  
R-PLACE1000596//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING  
DRAFT SEQUENCE, 7 unordered pieces.//0.00019:482:59//AC005506  
R-PLACE1000599//Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2,  
10 TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3,  
TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T,  
TCRBV6S5A1N1, TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P,  
TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P,  
TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3).//5.6e-51:369:85//U66059  
15 R-PLACE1000610//HS\_3071\_A1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3071 Col=9 Row=E, genomic survey sequence.//0.051:147:65//AQ103341  
R-PLACE1000636//HS\_3220\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3220 Col=18 Row=J, genomic survey sequence.//0.010:253:64//AQ181157  
R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.6e-99:506:  
20 96//AF102265  
R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and  
LLNLc110F1857Q7 (RZPD Berlin)).//4.5e-101:559:92//AJ005896  
R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//9.1e-10:331:63//S78219  
R-PLACE1000712//Homo sapiens full-length insert cDNA clone ZD76G10.//1.0e-69:345:98//AF086408  
25 R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//1.0:  
174:62//AC002300  
R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence.//1.0e-06:337:60//Z98547  
R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone  
cSRL-15g9, genomic survey sequence.//8.8e-26:236:80//B02791  
30 R-PLACE1000755//HS\_2183\_B1\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2183 Col=21 Row=P, genomic survey sequence.//0.47:151:65//AQ064202  
R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces.//  
7.0e-38:492:74//AC004847  
R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.6e-101:513:96//AB014548  
35 R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete  
cds.//0.078:180:68//U58970  
R-nnnnnnnnnnnn  
R-PLACE1000798//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1.//5.1e-26:348:72//AF039904  
R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//1.4e-26:110:95//  
40 U02081  
R-nnnnnnnnnnnn//Homo sapiens full-length insert cDNA clone ZD55D10.//1.4e-13:93:96//AF086334  
R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxi-  
dase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large  
and small subunits).//2.7e-09:484:59//L04272  
45 R-PLACE1000863  
R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
DRAFT SEQUENCE, 8 unordered pieces.//3.0e-05:274:60//AC005505  
R-PLACE1000931//RPCI11-66P7.TK RPCI11 Homo sapiens genomic clone R-66P7, genomic survey sequence.//  
50 3.4e-73:369:97//AQ237489  
R-PLACE1000948//RPCI11-64K15.TK RPCI11 Homo sapiens genomic clone R-64K15, genomic survey se-  
quence.//6.6e-06:258:62//AQ239337  
R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//8.3e-20:223:76//  
AC005553  
55 R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING  
DRAFT SEQUENCE, 7 unordered pieces.//0.00030:448:59//AC005506  
R-PLACE1000979  
R-PLACE1001000//CIT-HSP-2297I8.TF CIT-HSP Homo sapiens genomic clone 2297I8, genomic survey se-

quence.//7.0e-07:64:95//AQ004997  
R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete cds.//0.0078:215:64//D26607  
R-PLACE1001010  
5 R-PLACE1001015//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.5e-16:452:63//AL022318  
R-PLACE1001024//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE.//0.99:186:63//AL024498  
R-PLACE1001036//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.5e-15:313:68//AC005377  
10 R-PLACE1001062//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.3e-16:119:84//AC003664  
R-PLACE1001076  
R-PLACE1001088//Human DNA sequence from cosmid 203C2, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.97:332:59//Z74696  
15 R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07 :302:62//AC005139  
R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:60//AE001372  
20 R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.9e-06:334:60//Z84480  
R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-31:331:75//AC005412  
25 R-PLACE1001168//HS\_2036\_A1\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=7 Row=O, genomic survey sequence.//0.40:144:63//AQ230662  
R-PLACE1001171  
R-PLACE1001185  
R-PLACE1001238//Human coxVIb gene, last exon and flanking sequence.//3.4e-36:349:76//X58139  
R-PLACE1001241//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.11:258:61//AL008972  
30 R-PLACE1001257//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B4P3; HTGS phase 1, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-46:484:73//AC000016  
R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete sequence.//0.89:119:65//AF045448  
35 R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.//0.99:95:69//AL023839  
R-PLACE1001280//CIT-HSP-2328B24.TF CIT-HSP Homo sapiens genomic clone 2328B24, genomic survey sequence.//5.4e-24:147:76//AQ042129  
R-PLACE1001294//M.musculus GEG-154 mRNA.//1.3e-22:472:65//X71642  
40 R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-22:139:77//AC003682  
R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286  
R-PLACE1001323//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//7.2e-39:308:83//Z84480  
45 R-PLACE1001351//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y39B6, WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399  
R-PLACE1001366//Human Na+/phosphate co-transporter gene, exon 1, partial sequence.//2.2e-46:369:82//D89927  
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-80:431:93//AF009615  
50 R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97//AF055030  
R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86:456:94//AJ001319  
R-PLACE1001387  
R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence.//0.054:148:68//U95355  
R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412  
55 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//8.0e-44:242:95//AF091087  
R-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//0.12:53:84//AC006241

R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na<sup>+</sup>-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq281u1 gene and cytochrome C (CCP) pseudogene.//1.0:250:61//U52111  
 5 R-PLACE1001456//*Borrelia burgdorferi* (section 16 of 70) of the complete genome.//0.0077:173:62//AE001130  
 R-PLACE1001468//HS\_3050\_A2\_D07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey sequence.//0.00023:202:65//AQ133920  
 R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.2e-17:180:80//AC002368  
 10 R-PLACE1001502//RPCI11-24F2.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24F2, genomic survey sequence.//0.15:203:66//B84401  
 R-PLACE1001503//HS\_2183\_A1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic survey sequence.//1.3e-38:181:82//AQ022613  
 15 R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds.//6.4e-56:339:90//AB006969  
 R-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//8.6e-59:304:97//AL031667  
 R-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_L\_16, complete sequence.//2.6e-18:171:82//AC 005669  
 R-PLACE1001551  
 20 R-PLACE1001570//M.capricolum DNA for CONTIG MC188.//0.0043:305:57//Z33135  
 R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.5e-82:408:98//AB020860  
 R-PLACE1001603//Homo sapiens KE05 protein mRNA, complete cds.//1.5e-40:295:84//AF064605  
 R-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//  
 25 2.5e-39:307:82//AC005037  
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//4.9e-41:217:97//AF054174  
 R-PLACE1001632//Human DNA binding protein (HPF2) mRNA, complete cds.//1.4e-08:178:65//M27878  
 R-PLACE1001634//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone H06C16, WORKING DRAFT SEQUENCE.//0.00026:221:62//Z92791  
 30 R-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//2.6e-83:441:95//AC005971  
 R-PLACE1001672//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA26H8.//0.91:115:69//Z79253  
 R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.5e-111:545:97//AF069250  
 35 R-PLACE1001692//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.0e-46:478:75//AC005077  
 R-PLACE1001705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//0.79:91:73//Z99716  
 R-PLACE1001716//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//0.96:172:66//AC002349  
 40 R-PLACE1001720  
 R-PLACE1001729//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.79:280:60//U31120  
 R-PLACE1001739//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.0:109:65//AC005261  
 45 R-PLACE1001740//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//5.3e-11:249:67//AC006027  
 R-PLACE1001745  
 R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//6.0e-05:337:61//AC005509  
 50 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-91:540:89//AF061243  
 R-PLACE1001756//Human BAC clone RG302F04 from 7q31, complete sequence.//0.074:344:62//AC002463  
 R-PLACE1001761  
 R-PLACE1001771//Homo sapiens full-length insert cDNA clone ZD79C11.//4.4e-57:298:96//AF086426  
 R-PLACE1001781//T.thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs-1, clone Tt819.//4.6e-05:282:61//M15711  
 55 R-PLACE1001799//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.015:331:58//AC004710  
 R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//

4.1e-92:463:95//AF058953  
R-PLACE1001821///\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//3.6e-36:281:82//U14567  
R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA, complete cds.//9.1e-26:313:  
73//U37351

5 R-PLACE1001869  
R-PLACE1001897//Mus musculus homeobox protein (D1x5) mRNA, complete cds.//0.0043:207:64//AF033011  
R-PLACE1001912//RPCI11-25F23.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25F23, genomic sur-  
vey sequence.//6.3e-33:248:67//AQ013567

10 R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//5.0e-73:363:98//AF070671  
R-PLACE1001928//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//0.98:248:60//  
AC005245

15 R-PLACE1001983//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y40H7,  
WORKING DRAFT SEQUENCE.//0.12:157:61//AL021389

R-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING  
DRAFT SEQUENCE.//1.4e-44:376:80//AL023755

20 R-PLACE1002046//CITBI-E1-2520J24.TF CITBI-E1 Homo sapiens genomic clone 2520J24, genomic survey se-  
quence.//4.5e-20:144:89//AQ280117

R-PLACE1002052//Human DNA sequence from cosmid U160A4, between markers DXS366 and DXS87 on chro-  
mosome X contains STS.//0.025:362:57//Z80900

25 R-PLACE1002066//Leishmania tarentolae maxicircle DNA fragment.//0.0034:197:62//X02438  
R-PLACE1002072//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//9.7e-06:  
414:60//AC004763

R-PLACE1002073  
R-PLACE1002090//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic se-  
quence, complete sequence.//1.8e-06:278:63//AC002302

30 R-PLACE1002115//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORK-  
ING DRAFT SEQUENCE.//6.0e-12:327:64//AL022344

R-PLACE1002119//Mus musculus IERS (Ier5) mRNA, complete cds.//5.1e-67:442:86//AF079527

35 R-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the  
OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1.  
Contains ESTs, STSs and GSSs, complete sequence.//2.2e-80:403:97//AL022162 R-PLACE1002150//Human  
DNA sequence from PAC 145B12 on chromosome Xq27-Xq28. Contains EST, CA repeat and STS.//0.043:455:  
59//AL008706

R-PLACE1002157//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12  
of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity  
Sodium-Glucose Cotransporter), complete sequence.//9.8e-58:384:79//Z83849

40 R-PLACE1002163//Canis familiaris MHC class IIA DLA-DQA (DQA 1 allele) gene, exon 2, partial cds.//0.82:96:  
70//U44785

R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence.//0.83:196:65//  
AC004456

R-PLACE1002205//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine  
threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked,  
juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.0017:193:61//Z94056

45 R-PLACE1002213//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//8.0e-42:330:81//  
AC004152

R-PLACE1002227//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//2.1e-10:126:  
80//AC003071

R-PLACE1002256//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.7e-  
06:478:57//AC004907

50 R-PLACE1002259//Human DNA sequence from cosmid U75A4 on chromosome X.//6.5e-81:501:88//Z82255  
R-PLACE1002319//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
DRAFT SEQUENCE, 8 unordered pieces.//0.00023:549:58//AC005505

R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//4.9e-94:501:93//AB018271

55 R-PLACE1002395//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//1.4e-69:385:93//  
AC005329

R-PLACE1002399//Human HepG2 3' region cDNA, clone hmd5d06.//2.4e-71:411:92//D16939  
R-PLACE1002433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING  
DRAFT SEQUENCE.//0.85:176:63//AL031984

- R-PLACE1002437//Human BAC clone RG114A06 from 7q31, complete sequence./.0.0040:213:63//AC002542  
 R-PLACE1002438//CITBI-E1-2501M20.TF.1 CITBI-E1 Homo sapiens genomic clone 2501M20, genomic survey sequence./.0.70:247:61//AQ242104  
 R-PLACE1002450//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3./.0.00060:471:59//AJ229041  
 5 R-PLACE1002465//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces./.2.5e-10:98:81//AC004854  
 R-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds./.1.7e-25:199:71//U69262  
 R-PLACE1002477//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE  
 10 LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat./.1.2e-11:382:63//Z92545  
 R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds./.1.1e-  
 53:307:91//AF042273  
 R-PLACE1002499//Plasmodium falciparum MAL3P6, complete sequence./.0.56:270:60//Z98551  
 15 R-PLACE1002500//CIT-HSP-2337C20.TR CIT-HSP Homo sapiens genomic clone 2337C20, genomic survey se-  
 quence./.3.2e-42:297:85//AQ037614  
 R-PLACE1002514//Human DNA Sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING  
 DRAFT SEQUENCE./.7.8e-16:221:73//Z95114  
 R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds./.1.6e-86:582:85//AB018256  
 20 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence./.9.0e-91:453:97//  
 AC004774  
 R-PLACE1002537//Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 5, complete cds./.  
 0.0042:489:60//D16253  
 R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome./.0.034:493:55//L06178  
 25 R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence./.2.5e-44:  
 292:84//AC006084  
 R-PLACE1002583//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete  
 cds./.3.1e-17:517:61//AF045555  
 R-PLACE1002591  
 30 R-PLACE1002598//Caenorhabditis elegans cosmid Y37D8A, complete sequence./.0.080:308:60//AL032626  
 R-PLACE1002604//Human cosmid LL12NC01-88A9, ETV6 gene, exons 6, 7 and 8 and partial cds./.0.0013:176:  
 65//U63313  
 R-PLACE1002625//HS\_2233\_B2\_H04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2233 Col=8 Row=P, genomic survey sequence./.5.2e-13:137:79//AQ146663  
 35 R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds./.5.8e-46:272:94//  
 AF079765  
 R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds./.1.2e-  
 77:390:97//AF068180  
 R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence./.1.3e-35:328:78//AF046656  
 40 R-PLACE1002722//Sequence 1 from patent US 5686597./.1.7e-42:276:89//I73723  
 R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC GSHB-383H3 (Genome Systems Human BAC Library)  
 complete sequence./.0.0098:197:64//AC005185  
 R-PLACE1002772//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence./.6.7e-49:378:  
 82//AC006145  
 45 R-PLACE1002782  
 R-PLACE1002794  
 R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey se-  
 quence./.6.0e-50:250:100//AQ034981  
 R-PLACE1002815//Sequence 2 from patent US 5747660./.2.7e-59:312:84//AR005279  
 50 R-PLACE1002816//Homo sapiens 12q13.1 PAC RPC15-1057I20 (Roswell Park Cancer Institute Human PAC li-  
 brary) complete sequence./.6.3e-59:339:93//AC004466  
 R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9./.1.4e-78:413:95//  
 M27877  
 R-PLACE1002839//Homo sapiens PAC clone DJ0015I23 from 22, complete sequence./.6.5e-25:301:74//  
 55 AC004819  
 R-PLACE1002851//CIT-HSP-2317M9.TR CIT-HSP Homo sapiens genomic clone 2317M9, genomic survey se-  
 quence./.0.0011:210:61//AQ040519  
 R-PLACE1002853//Human interleukin 6 (IL6) gene, 3' flank./.5.8e-06:327:61//J03049

R-PLACE1002881  
R-PLACE1002908//HS\_3064\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=G, genomic survey sequence./.1.9e-09:156:72//AQ142985

5 R-PLACE1002941  
R-PLACE1002962  
R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence./.1.9e-32:314:77//AL022721

10 R-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE./.1.6e-42:343:81//AL023755  
R-PLACE1002993//Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence./.0.56:88:72//AC004921

15 R-PLACE1002996//HS\_2064\_A1\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence./.4.9e-18:117:95//AQ243211  
R-PLACE1003025//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence./.0.26:428:58//AC006145  
R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence./.1.3e-95:465:98//AC005920

20 R-PLACE1003044  
R-PLACE1003092//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence./.3.6e-05:358:60//AL010266  
R-PLACE1003100//HS\_2244\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=O, genomic survey sequence./.2.3e-42:288:86//AQ084224

25 R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces./.0.00066:233:61//AC004885  
R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence./.0.019:429:57//AL034558  
R-PLACE1003145  
R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence./.3.2e-05:390:58//AC004616  
R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence./.2.4e-06:390:60//AB015479

30 R-PLACE1003176  
R-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces./.4.0e-78:406:81//AC005095  
R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence./.0.016:411:57//Z98551  
R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces./.0.00084:288:61//AC005139

35 R-PLACE1003238//Homo sapiens full-length insert cDNA clone ZD79H11./.7.6e-114:567:96//AF086432  
R-PLACE1003249//Human Chromosome X, complete sequence./.1.3e-45:317:85//AC002416  
R-PLACE1003256//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence./.1.0e-45:328:85//AC004099  
R-PLACE1003258  
R-PLACE1003296//Diphoropria sp. 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence./.0.050:228:59//U39952  
R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, 2, and-9./.1.7e-91:458:96//M27877

40 R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 22q13-q13.33. Contains a gene for the presumptive isolog of Rat RTP60 (nuclear pore complex protein Npap60). Contains ESTs, complete sequence./.4.3e-34:370:71//Z82243  
R-PLACE1003342//CIT-HSP-2311D21.TF CIT-HSP Homo sapiens genomic clone 2311D21, genomic survey sequence./.1.0:159:68//AQ020460

45 R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./.1.1e-05:330:61//AC004153  
R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds./.3.4e-98:469:98//U92715  
R-PLACE1003361

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R-PLACE1003366//Homo sapiens CAG repeated sequence./.0.018:319:61//AJ006805  
R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence./.0.050:155:63//B20174  
5 R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence./.1.2e-62:434:  
83//AC004771  
R-PLACE1003375//Dictyostelium discoideum golvesin (gol) gene, complete cds./.0.042:263:57//U89350  
R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment  
10/10./.1.7e-83:429:96//AB020878  
10 R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence./.2.4e-13:175:76//  
AC005695  
R-PLACE1003420//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence./.2.1e-05:340:61//  
AC005587  
15 R-PLACE1003454//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, complete  
sequence./.0.47:411:58//AL009014  
R-PLACE1003478//M.capricolum DNA for CONTIG MC175./.0.51:253:59//Z33125  
R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence./.4.6e-37:319:  
81//AC006080  
20 R-PLACE1003516//CIT-HSP-2295M19.TF CIT-HSP Homo sapiens genomic clone 2295M19, genomic survey se-  
quence./.1.0e-40:251:90//AQ007480  
R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal  
protein homologue pseudogene L23a./.2.7e-29:163:89//AF064859  
25 R-PLACE1003521//HS\_3252\_A2\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3252 Col=10 Row=M, genomic survey sequence./.0.00017:274:60//AQ221562  
R-PLACE1003528//HS\_2041\_B1\_B07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2041 Col=13 Row=D, genomic survey sequence./.6.6e-40:219:83//AQ230483  
30 R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs  
(Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A61, 2 and 3./.8.3e-05:300:61//  
J01404  
R-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING  
35 DRAFT SEQUENCE./.2.7e-87:450:96//AL031297  
R-PLACE1003566  
R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete sequence./.4.7e-20:148:78//  
AC003965  
R-PLACE1003583//Human DNA sequence from PAC 388N15 on chromosome Xq21.1./.3.5e-18:287:68//Z99571  
35 R-PLACE1003584  
R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence./.2.5e-10:153:73//AF061032  
R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence./.6.9e-07:240:65//AC002066  
R-PLACE1003596//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y87G2,  
WORKING DRAFT SEQUENCE./.0.13:393:60//AL022597  
40 R-PLACE1003602//Homo sapiens mRNA expressed in placenta./.2.4e-95:576:88//D83200  
R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequence./.2.9e-19:302:71//  
AC002081  
R-nnnnnnnnnnnnn  
45 R-PLACE1003618//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191E19, WORKING  
DRAFT SEQUENCE./.8.3e-57:469:80//AL034451  
R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
DRAFT SEQUENCE, 4 unordered pieces./.2.1e-05:339:62//AC004688  
R-PLACE1003638//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING  
50 DRAFT SEQUENCE./.2.5e-38:279:84//AL022312  
R-PLACE1003669//HS\_3054\_A2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3054 Col=14 Row=I, genomic survey sequence./.0.014:265:61//AQ132713  
R-PLACE1003704//HS\_3213\_A1\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3213 Col=23 Row=G, genomic survey sequence./.0.80:195:61//AQ176784  
55 R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequence./.0.018:152:61//  
AC002067  
R-PLACE1003711//Human endothelial nitric oxide synthase gene, complete cds./.1.7e-61:366:89//D26607  
R-PLACE1003723//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one  
exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence./.2.7e-

44:505:73//AL022336  
R-PLACE1003738//H.sapiens DNA sequence./.0.93:185:60//Z22357  
R-PLACE1003760//Human globin gene./.5.9e-97:538:91//M69023  
R-PLACE1003762//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence./.4.6e-13:134:79//  
5 AC003070  
R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence./.5.4e-12:189:  
71//AC005919  
R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence./.1.7e-119:619:95//  
10 AC004160  
R-PLACE1003783  
R-PLACE1003784//Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence./.5.6e-15:  
204:74//AC004659  
R-PLACE1003795//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey se-  
quence./.7.0e-37:234:89//AQ114933  
15 R-PLACE1003833//Homo sapiens full-length insert cDNA clone ZE15C06./.4.4e-59:313:95//AF086558  
R-PLACE1003850  
R-PLACE1003858  
R-nnnnnnnnnnnnn  
R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 In DGCR Region, complete se-  
20 quence./.8.7e-33:285:81//AC000072  
R-nnnnnnnnnnnnn  
R-PLACE1003886  
R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence./.0.73:127:65//  
AC004069  
25 R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds./.1.9e-05:239:59//L78810  
R-PLACE1003903//Homo sapiens full-length insert cDNA clone ZD78D11./.8.1e-74:369:97//AF086422  
R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete  
cds./.0.56:247:61//U73520  
R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete sequence./.0.67:213:63//Z99281  
30 R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs./.8.7e-49:  
342:85//Z74022  
R-PLACE1003936//H.sapiens gene for ventricular myosin light chain 2./.2.6e-09:394:61//Z15030  
R-PLACE1003968//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-62, complete  
35 sequence./.1.3e-07:245:65//AL010247  
R-PLACE1004104  
R-PLACE1004114//Human PAC clone RG212D03, complete sequence./.5.0e-07:336:61//AC002485  
R-PLACE1004118//HS\_3092\_B1\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3092 Col=1 Row=D, genomic survey sequence./.0.80:207:60//AQ128151  
R-PLACE1004128//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds./.1.8e-  
40 06:193:66//AF022085  
R-PLACE1004149//HS\_2253\_A2\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2253 Col=22 Row=K, genomic survey sequence./.2.4e-59:315:95//AQ129711  
R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC  
Library) containing Arylsulfatase D and E genes, complete sequence./.8.3e-53:299:76//AC005295  
45 R-PLACE1004161  
R-PLACE1004183//Homo sapiens for TOM1-like protein./.1.3e-80:434:93//AJ010071  
R-PLACE1004197//RPCI11-69N15.TK RPCI11 Homo sapiens genomic clone R-69N15, genomic survey se-  
quence./.0.0078:170:65//AQ265515  
R-PLACE1004203//Homo sapiens semaphorin L (SEMAL) mRNA, complete cds./.3.4e-105:501:98//AF030698  
50 R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic  
marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence./.6.1e-65:373:86//  
AL021326  
R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence./.0.011:383:  
61//AC006031  
55 R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete  
sequence./.3.4e-09:576:59//AC004470  
R-PLACE1004258//HS\_3034\_A1\_B12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3034 Col=23 Row=C, genomic survey sequence./.1.4e-35:359:77//AQ128936

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R-PLACE1004270//CITBI-E1-2504K14.TR CITBI-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence.//2.7e-06:150:74//AQ261108  
R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//0.025:116:72//AC005234  
R-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//4.4e-106:581:91//AF084830  
R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.59:231:60//AC005308  
R-FLACE1004289//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//5.8e-31:340:75//AC005920  
R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.4e-90:572:86//AC005095  
R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//1.9e-113:590:94//Y11588  
R-PLACE1004336//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//2.3e-65:292:82//AL033383  
R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//2.4e-70:379:93//AF100153  
R-PLACE1004376//CIT-HSP-2287M8.TF CIT-HSP Homo sapiens genomic clone 2287M8, genomic survey sequence.//0.47:173:61//AQ000837  
R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic clone 2316J11, genomic survey sequence.//0.035:109:69//AQ037817  
R-PLACE1004388//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-82, complete sequence.//4.2e-06:381:60//AL010149  
R-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.20:270:60//AC005027  
R-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//1.3e-96:516:94//AC005532  
R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, complete sequence.//5.8e-10:279:65//AL031296  
R-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.9e-88:516:88//U49283  
R-PLACE1004451//HS\_2258\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=L, genomic survey sequence.//0.82:172:61//AQ221189  
R-PLACE1004460  
R-PLACE1004467//Syrian hamster carbamoylphosphate synthetase-aspartate transcarbamylasedihydroorotate (CAD) gene, exons 1 and 2.//1.2e-24:311:62//M31621  
R-PLACE1004471//Homo Sapiens Chromosome X clone bWXD75, complete sequence.//2.1e-34:333:70//AC004389  
R-PLACE1004473  
R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial A+T region.//1.0e-08:485:60//U11584  
R-PLACE1004506  
R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//0.0094:543:56//AE001427  
R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.00011:343:59//AC003071  
R-PLACE1004518  
R-PLACE1004548//Homo sapiens Xp22 BAC GS-551O19 (Genome Systems Human BAC library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride channel 4 gene, complete sequence.//4.9e-40:245:80//AC003666  
R-PLACE1004550  
R-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.7e-82:532:86//X75931  
R-PLACE1004629//Homo sapiens chromosome 7 clone UWGC:g3586a230 from 7p14-15, complete sequence.//0.015:437:59//AC004800  
R-PLACE1004645//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.033:76:75//AQ110136  
R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq28, complete sequence.//2.0e-23:237:79//AF036876  
R-PLACE1004658//Homo sapiens Chromosome 12p13.3 BAC RPCI11-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.1e-09:94:87//AC005343  
R-nnnnnnnnnnnn//RPCI11-79G23.TV RPCI11 Homo sapiens genomic clone R-79G23, genomic survey se

quence.//2.2e-81:433:94//AQ283692  
R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//2.7e-24:263:74//U07561  
R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.1e-89:513:91//  
5 AF035606  
R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//1.3e-96:498:95//AB020860  
R-PLACE1004686  
10 R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 2/11.//2.1e-33:290:80//AB020859  
R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9A, complete sequence.//1.0:195:60//AL021448  
R-PLACE1004716//CITBI-E1-2519C14.TR CITBI-E1 Homo sapiens genomic clone 2519C14, genomic survey se-  
quenc.//5.0e-43:245:93//AQ276965  
R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
15 DRAFT SEQUENCE, 9 unordered pieces.//0.0022:360:60//AC005507  
R-PLACE1004736  
R-PLACE1004740  
R-nnnnnnnnnnnn//Homo sapiens ubiquitin-protein ligase E3-alpha (UBR1) mRNA, partial cds.//5.4e-105:575:92//  
AF061556  
20 R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//9.0e-26:317:76//  
AC002523  
R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//8.5e-88:437:96//AF084367  
R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15,  
WORKING DRAFT SEQUENCE.//0.050:138:65//AP000010  
25 R-PLACE1004793//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR.//5.1e-58:313:80//U60269  
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds.//5.8e-98:580:88//AB011178  
R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:64//AC005140  
30 R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//3.5e-  
107:358:99//AF069250  
R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//3.8e-61:353:89//  
AC004126  
R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3  
35 unorderd pieces.//5.7e-42:364:79//AC004666  
R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bmx gene, complete sequence.//2.7e-14:156:79//AC003669  
R-PLACE1004836//HS\_2270\_A2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2270 Col=20 Row=O, genomic survey sequence.//8.6e-51:267:96//AQ164110  
40 R-PLACE1004838//CIT-HSP-2343E10.TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey se-  
quence.//0.071:168:63//AQ058544  
R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//I92820  
R-PLACE1004868//Human Chromosome X clone bWXD342, complete sequence.//0.57:344:59//AC004072  
45 R-PLACE1004885//HS\_3235\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193  
R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alterna-  
tively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin,  
subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs,  
complete sequence.//2.0e-44:334:84//AL022577  
50 R-PLACE1004902  
R-nnnnnnnnnnnn//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//7.7e-58:377:  
87//Z82209  
R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//  
0.00084:373:60//AC004605  
55 R-PLACE1004930//Homo sapiens MDC-3.13 isoform 1 mRNA, complete cds.//2.0e-100:532:93//AF099936  
R-PLACE1004934//Homo sapiens clone RG062N11, WORKING DRAFT SEQUENCE, 2 unorderd pieces.//  
0.00030:198:66//AC005683  
R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds.//1.3e-13:367:61//AF020788

R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, complete sequence.//0.97:116:  
71//Z84494

R-PLACE1004972

R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970

5 R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308

R-PLACE1004985//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING  
DRAFT SEQUENCE.//2.5e-10:410:60//AL033522

10 R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.7e-56:158:99//  
AC004925

R-PLACE1005027

R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//  
AC005775

15 R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SE-  
QUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867

R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2  
(Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene.  
Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584

20 R-PLACE1005077//H.sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556

R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293\_K\_20, complete sequence.//2.1e-42:384:  
69//AC005495

R-PLACE1005086//RPCI11-30H10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30H10, genomic survey  
sequence.//0.13:112:67//B87788

25 R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401

R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//  
AC004476

30 R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:232:84//U85195

R-PLACE1005111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 566H6, WORKING  
DRAFT SEQUENCE.//3.0e-18:174:74//AL031845

R-PLACE1005128

R-PLACE1005146

R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140

35 R-nnnnnnnnnnnn//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018

R-PLACE1005181//HS\_2182\_B2\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2182 Col=10 Row=D, genomic survey sequence.//4.9e-05:193:65//AQ030787

R-PLACE1005187//Arabidopsis thaliana chromosome II BAC T14A4 genomic sequence, complete sequence.//  
0.00073:264:60//AC006161

40 R-PLACE1005206//Homo sapiens full-length insert cDNA YN66A06.//6.3e-64:343:93//AF075043

R-PLACE1005232//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 25J6, WORKING  
DRAFT SEQUENCE.//1.3e-34:286:81//Z84476

R-PLACE1005243

R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132

45 R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15:166:78//AC005067

R-PLACE1005277//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey se-  
quence.//2.5e-34:358:74//AQ265720

R-PLACE1005287//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING  
DRAFT SEQUENCE.//4.1e-07:495:60//AL031744

50 R-PLACE1005305//HS\_3180\_B2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3180 Col=4 Row=H, genomic survey sequence.//1.1e-42:308:85//AQ169443

R-PLACE1005308

R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered  
pieces.//0.00048:320:60//AC000383

R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-103:537:94//AB007960

55 R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//2.2e-94:536:91//  
AC004794

R-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
5.3e-32:313:79//AC000380

R-PLACE1005373//Homo sapiens BAC129, complete sequence./.8.8e-10:229:68//U85195  
R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence./.3.0e-44:434:77//  
AC005291  
R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence./.8.8e-105:529:96//AC003991  
5 R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequence./.4.7e-39:302:82//  
AC002477  
R-PLACE1005467//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING  
DRAFT SEQUENCE./.1.1e-40:328:81//Z93014  
R-PLACE1005471//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1  
10 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Ami-  
notransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)  
pseudogene. Contains ESTs, STSs and GSSs, complete sequence./.6.4e-68:409:90//AL022310  
R-PLACE1005477//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING  
DRAFT SEQUENCE./.0.020:216:66//AL023693  
15 R-PLACE1005480//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence./.  
2.8e-44:327:70//AC005392  
R-PLACE1005481//Homo sapiens-chromosome 17, clone hRPC.1164\_O\_3, complete sequence./.4.2e-23:284:  
74//AC004703  
R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4./.0.19:468:60//AF031631  
20 R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds./.1.6e-55:277:98//AF071185  
R-PLACE1005526//Human mRNA for alpha-1 type II collagen./.0.10:227:63//X16468  
R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SE-  
QUENCE./.2.3e-76:395:96//AP000038  
R-PLACE1005530//C.familiaris CA repeat sequence (isolate )./0.023:90:75//X86184  
25 R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence./.2.0e-09:235:  
64//AL025928  
R-PLACE1005554//Homo sapiens chromosome 17, clone hRPC.215\_P\_18, complete sequence./.0.069:305:60//  
AC005969  
R-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence./.4.3e-105:587:  
30 91//AC004707  
R-PLACE1005574//Human BAC 367D17 from chromosome 18, complete sequence./.1.5e-17:274:67//AC003971  
R-PLACE1005584//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence./.2.7e-15:191:  
77//AC004991  
R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence./.6.4e-90:453:96//  
35 AC004126  
R-PLACE1005603//Homo sapiens cosmid clone U169D2 from Xp22.1-22.2, complete sequence./.0.69:322:61//  
U72788  
R-PLACE1005611//Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds./.0.059:473:56//U42599  
R-PLACE1005623//Homo sapiens full-length insert cDNA clone ZD76B03./.1.6e-113:575:95//AF086405  
40 R-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1  
ordered pieces./.5.6e-79:270:94//AC005840  
R-PLACE1005639//Human BAC clone RG022J17 from 7q21, complete sequence./.8.2e-56:441:83//AC002382  
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds./.3.2e-110:585:93//  
AF083255  
45 R-PLACE1005656//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence./.8.6e-08:505:  
58//AC005701  
R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and  
polymorphic CA repeat./.3.2e-27:307:72//Z82203  
R-PLACE1005698/344B22.TV CIT978SKA1 Homo sapiens genomic clone A-344B22, genomic survey se-  
50 quence./.0.030:91:70//B15144  
R-PLACE1005727//Human variable number tandem repeat (VNTR) region, allele 17R1 3' to collagen type II  
(COL2A1) gene./.5.2e-10:587:59//L10171  
R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds./.0.0039:239:58//L78810  
R-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds./.2.2e-21:270:72//U15635  
55 R-PLACE1005755//Caenorhabditis elegans cosmid M03F4./.6.9e-08:219:64//U64601  
R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds./.1.0e-45:268:87//D42087  
R-PLACE1005799//Human X chromosome mRNA for CCG1 protein inv. in cell proliferation./.0.030:91:78//X07024  
R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence./.1.4e-69:391:92//

AC004827  
R-PLACE1005803  
R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete sequence./.1.8e-21:175:75//  
AC002530

5 R-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1  
ordered pieces./.2.9e-56:333:91//AC004150  
R-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING  
DRAFT SEQUENCE./.0.020:513:55//AL031745  
R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta./.1.8e-10:182:69//Y00763 R-PLACE1005850

10 R-PLACE1005851//Homo sapiens clone DJ0789I05, WORKING DRAFT SEQUENCE, 2 unordered pieces./.5.5e-  
06:318:63//AC004887  
R-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor./.6.7e-28:366:72//X75931  
R-PLACE1005884//Human DNA sequence from cosmid V526F1, between markers DDX366 and DDX87 on chro-  
mosome X contains STS./.1.0e-06:306:64//Z70281

15 R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING  
DRAFT SEQUENCE, 5 unordered pieces./.0.0094:449:59//AC005139  
R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic clone 2509N21,-genomic survey se-  
quence./.4.8e-84:494:89//AQ261347  
R-PLACE1005923//RPCI11-65N9.TJ RPCI11 Homo sapiens genomic clone R-65N9, genomic survey sequence./.  
20 8.3e-97:520:93//AQ237243  
R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS,  
complete sequence./.5.2e-67:578:78//AL022719  
R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete sequence./.0.0035:176:62//AL032654  
R-PLACE1005934

25 R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence./.  
0.00021:272:62//AF069716  
R-PLACE1005951  
R-PLACE1005953//Caenorhabditis elegans cosmid F09E5./.1.3e-07:349:60//U37429  
R-PLACE1005955//Human HepG2 3' region MboI cDNA, clone hmd1d01m3./.8.3e-08:128:70//D17131

30 R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, com-  
plete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial  
RNAs./.7.0e-09:549:59//AF044863  
R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds./.1.1e-51:394:81//AB002086  
R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE,  
35 51 ordered pieces./.4.4e-63:369:91//AC005866  
R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10sp13./.5.9e-27:299:74//U15177  
R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequence./.3.5e-07:164:67//AF046375  
R-PLACE1006011//Mus musculus poly-(ADPribosyl)-transferase homolog PARP mRNA, complete cds./.1.1e-32:  
266:83//AF072521

40 R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31e In DGCR Region, complete se-  
quence./.1.8e-17:164:82//AC000077  
R-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA./.2.0e-49:557:72//U01139  
R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine./.4.3e-13:128:81//X99906  
R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces./.3.3e-  
45 18:220:74//AC004885  
R-PLACE1006119//Plasmodium berghei (STRAIN ANKA) gamma-GCS gene, complete CDS./.0.0050:271:63//  
AJ005122  
R-PLACE1006129//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete  
sequence./.0.43:178:65//AC005454  
50 R-PLACE1006139//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence./.7.5e-13:222:68//  
AC004849  
R-PLACE1006143//Plasmodium falciparum MAL3P6, complete sequence./.0.00019:455:59//Z98551  
R-PLACE1006157//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
DRAFT SEQUENCE./.0.00018:351:60//AL034557

55 R-PLACE1006159//Homo sapiens chromosome 10 clone LA10NC01\_124\_D\_3 map 10q25.1, WORKING DRAFT  
SEQUENCE, 1 ordered pieces./.1.0e-113:586:96//AC006103  
R-PLACE1006164//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemo-  
chromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds./.1.0e-

28:342:75//U91328  
R-PLACE1006167//Homo sapiens full-length insert cDNA clone ZE14E04.//4.6e-77:426:93//AF086555  
R-nnnnnnnnnnnn//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82//X14972  
R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//1.6e-116:597:95//AF091433  
5 R-PLACE1006195//Homo sapiens chromosome 19, fosmid 39554, complete sequence.//8.8e-11:148:74//  
AC004410  
R-PLACE1006196  
R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence.//8.4e-44:332:85//AC000398  
R-PLACE1006223//Human DNA sequence from cosmid U74C11, between markers DXS6791 and DXS8038 on  
10 chromosome X contains ESTs.//0.041:215:61//Z73362  
R-PLACE1006225//Caenorhabditis elegans cosmid Y69H2, complete sequence.//9.7e-13:358:63//Z98877  
R-PLACE1006236//Plasmodium falciparum MAL3P4, complete sequence.//0.00019:538:58//AL008970  
R-nnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//3.1e-96:497:95//  
AC004142  
15 R-PLACE1006246//Homo sapiens clone NH0144M13, WORKING DRAFT SEQUENCE, 1 unordered pieces.//  
0.029:499:56//AC006034  
R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//9.2e-96:499:95//AB014548  
R-PLACE1006262//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete se-  
quence.//0.00043:160:66//AC004087  
20 R-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING  
DRAFT SEQUENCE.//3.5e-120:611:96//AL031320  
R-PLACE1006318  
R-PLACE1006325//Plasmodium falciparum MAL3P8, complete sequence.//1.0:426:57//AL034560  
R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq21.//0.96:173:66//AL008987  
25 R-PLACE1006357//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.9e-07:491:58//X95276  
R-PLACE1006360//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.25:484:  
56//AE001398  
R-PLACE1006368//Caenorhabditis elegans cosmid Y38H6C, complete sequence.//1.0:240:59//AL031630  
R-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//3.7e-101:  
30 574:91//AC004232  
R-PLACE1006382  
R-PLACE1006385//Mus musculus intersectin-EH binding protein Ibp2 mRNA, partial cds.//1.4e-50:350:86//  
AF057286  
R-PLACE1006412//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//  
35 5.1e-51:339:82//AC004854  
R-PLACE1006414//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC li-  
brary) complete sequence.//1.6e-38:297:84//AC004804  
R-PLACE1006438//Homo sapiens full-length insert cDNA YH73H06.//7.6e-73:422:90//AF074985  
R-PLACE1006445//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING  
40 DRAFT SEQUENCE.//3.0e-07:376:61//AL031726  
R-PLACE1006469  
R-PLACE1006470//Mouse B1 repetitive sequence DNA.//1.0:96:66//M24152  
R-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING  
DRAFT SEQUENCE.//3.0e-101:535:94//AL021977  
45 R-PLACE1006492//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//0.78:44:95//  
AC005972  
R-PLACE1006506//R.norvegicus BSP gene.//1.0:206:60//X86100  
R-PLACE1006521//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey se-  
quence.//9.0e-17:414:61//B75158  
50 R-PLACE1006531//Plasmodium falciparum coronin gene, isolate 3D7.//0.98:186:63//AJ002197  
R-PLACE1006534//Anopheles gambiae complete mitochondrial genome.//0.051:412:61//L20934  
R-PLACE1006540//Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.//7.5e-41:470:70//  
AC004209  
R-PLACE1006552//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3,  
55 WORKING DRAFT SEQUENCE.//0.57:355:57//Z98865  
R-PLACE1006598//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING  
DRAFT SEQUENCE, 2 unordered pieces.//0.016:291:58//AC004710  
R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//

2.9e-116:590:95//U97670  
R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence//2.2e-45:209:  
88//AC004050  
R-PLACE1006626//C. elegans cosmid K12H4//1.2e-16:344:64//L14331  
5 R-PLACE1006629//Homo sapiens chromosome 19, cosmid F20900, complete sequence//2.8e-25:343:70//  
AC006128  
R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey se-  
quence//0.00020:201:62//B90038  
R-PLACE1006673//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces//1.4e-  
10 42:309:84//AC004882  
R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence//6.4e-09:454:  
59//AC006024  
R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS, com-  
plete sequence//0.56:226:63//AL022154  
15 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//6.0e-101:486:98//AF038172  
R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence//1.4e-68:381:93//  
AC005626  
R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//6.2e-72:397:92//AF070622  
R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promoter and partial cds//1.6e-11:420:61//  
20 U20984  
R-PLACE1006782//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3,  
WORKING DRAFT SEQUENCE//0.60:321:58//Z98865  
R-PLACE1006792//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence//2.9e-40:379:  
77//AC005599  
25 R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence//6.2e-07:291:63//  
AC005083  
R-PLACE1006800//HS\_2270\_B1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2270 Col=3 Row=H, genomic survey sequence//4.1e-76:367:99//AQ085793  
R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
30 DRAFT SEQUENCE, 9 unordered pieces//0.00058:354:59//AC005507  
R-PLACE1006815//HS\_3028\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3028 Col=7 Row=D, genomic survey sequence//1.5e-33:251:77//AQ120174  
R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome  
35 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments//1.4e-76:544:84/  
Z86062  
R-PLACE1006829  
R-PLACE1006860  
R-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING  
40 DRAFT SEQUENCE//3.2e-107:549:95//AL033378  
R-PLACE1006878//Homo sapiens full-length insert cDNA clone ZB55G05//1.4e-46:241:97//AF086155  
R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence//1.3e-38:  
283:85//AC004232  
R-nnnnnnnnnnnnn  
R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and  
45 polymorphic CA repeat//4.1e-15:477:62//Z82203  
R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library)  
complete sequence//1.3e-42:305:87//AC005184  
R-PLACE1006932  
R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X//0.0014:114:74//Z86061  
50 R-nnnnnnnnnnnnn//Mouse mRNA for germ cell specific protein APG-1, complete cds//9.5e-85:590:83//D49482  
R-PLACE1006961//Homo sapiens chromosome 17, clone hRPK.349\_A\_8, complete sequence//6.7e-42:295:86//  
AC005544  
R-PLACE1006962//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete se-  
quence//1.1e-19:302:71//AC002349  
55 R-PLACE1006966//HS\_2219\_B2\_C02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2219 Col=4 Row=F, genomic survey sequencer//0.019:180:63//AQ145873  
R-PLACE1006989  
R-PLACE1007014

R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces./.1.6e-23:362:70//AC005845  
R-PLACE1007045//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE./.2.3e-90:584:86//AL023693  
5 R-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces./.2.4e-108:550:96//AC004895  
R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence./.1.8e-103:552:93//AL021368  
R-PLACE1007105//Mus musculus muskelin mRNA, complete cds./.2.7e-32:379:73//U72194  
R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces./.0.14:422:57//AC004688  
10 R-PLACE1007112//Cynips cornifex cyt b gene./.0.020:427:58//AJ228479  
R-PLACE1007132//Homo sapiens full-length insert cDNA YH77E09./.5.7e-107:535:96//AF074987  
R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 unordered pieces./.0.36:408:58//AC005050  
R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA./.0.99:63:73//AF009283  
20 R-PLACE1007226  
R-PLACE1007238  
R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds./.2.0e-91:534:89//D50495  
R-PLACE1007242//CITBI-E1-2512M9.TF CITBI-E1 Homo sapiens genomic clone 2512M9, genomic survey sequence./.1.3e-05:117:76//AQ279454  
R-PLACE1007243//*Prototheca wickerhamii* 263-11 complete mitochondrial DNA./.0.21:284:58//U02970  
R-PLACE1007257//Homo sapiens mRNA for dia-12c protein./.6.9e-113:607:93//Y15908  
R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence./.4.4e-10:135:74//AC006080  
30 R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence./.1.7e-36:435:72//AF069291  
R-PLACE1007282//*B.garinii* (strain TIs1) p83/100 gene (partial)./.0.95:183:60//X81533  
R-PLACE1007286//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence./.6.1e-55:519:76//B75158  
35 R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island./.0.75:180:62//Z97195  
R-PLACE1007317//*Drosophila dasyncnemia* 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence./.0.59:236:59//U94253  
40 R-PLACE1007342  
R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds./.3.7e-65:367:91//AF096870  
R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces./.1.0e-06:385:62//AC005507  
45 R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces./.0.10:309:59//AC004709  
R-PLACE1007386//*Reclinomonas americana* mitochondrial DNA, complete genome./.0.0012:403:58//AF007261  
R-PLACE1007402//HS\_2055\_A2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=6 Row=G, genomic survey sequence./.0.0046:88:79//AQ234824  
50 R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence./.7.6e-112:590:94//AF093771  
R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence./.0.96:98:70//AC005594  
R-PLACE1007450//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE./.1.7e-39:308:82//Z98304  
55 R-PLACE1007452//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence./.2.6e-59:389:82//AC004081  
R-PLACE1007460  
R-PLACE1007478//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC li-

brary) complete sequence.//7.0e-08:335:60//AC004241  
 R-PLACE1007484  
 R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//2.5e-05:421:61//AF072373  
 5 R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence.//2.3e-09:577:57//AL034559  
 R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.2e-79:387:  
 96//AC004231  
 R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and  
 10 R32804, complete sequence.//3.4e-09:148:73//AC003682  
 R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//4.7e-38:  
 297:82//AC004381  
 R-PLACE1007544  
 R-PLACE1007547//Human laminin alpha 4 chain (LAMA4\*-1) mRNA, complete cds.//4.0e-17:108:97//U77706  
 R-PLACE1007557//Human BAC clone RG343P13 from 7q31, complete sequence.//2.2e-45:390:77//AC002465  
 15 R-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING  
 DRAFT SEQUENCE.//1.0e-56:302:95//AL031665  
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence.//1.5e-102:554:93//AF038179  
 R-PLACE1007618  
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence.//1.4e-103:537:94//AF038176  
 20 R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1  
 ordered pieces.//3.3e-76:289:94//AC005840  
 R-PLACE1007645//Homo sapiens full-length insert cDNA clone ZD76G10.//0.0080:96:77//AF086408  
 R-PLACE1007649//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey se-  
 quence.//1.1e-82:412:97//AQ022149  
 25 R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0041:  
 470:57//AE001367  
 R-PLACE1007688  
 R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence.//1.3e-22:162:  
 91//AC002044  
 30 R-PLACE1007697  
 R-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING  
 DRAFT SEQUENCE.//4.4e-121:624:95//AL031662  
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.8e-73:374:96//AF061243  
 R-PLACE1007725//Caenorhabditis elegans cosmid F38A5.//0.070:186:60//U70854  
 35 R-PLACE1007729//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase  
 and envelope genes, partial cds, and 3'LTR.//3.8e-53:415:81//U60269  
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.1e-92:556:89//AB014585  
 R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence.//4.0e-43:302:77//AF015169  
 R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence.//1.0e-06:533:59//AL034560  
 40 R-PLACE1007746//T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and  
 NADH dehydrogenase subunits 4 and 5, complete cds.//0.28:386:58//M14820  
 R-PLACE1007791//D.discoideum gene for protein kinase.//0.17:263:60//Z37981  
 R-PLACE1007807//Human DNA sequence from clone 878O8 on chromosome Xq21.1-21.33. Contains an EST,  
 STSs, a GSS and genomic marker DXS472, complete sequence.//1.1e-72:324:88//AL031116  
 45 R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete sequence.//2.2e-14:325:67//  
 AF017104  
 R-PLACE1007829//Human BAC clone GS165I04 from 7q21, complete sequence.//0.00052:455:61//AC002379  
 R-PLACE1007843//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.0050:447:57//X95275  
 50 R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15,  
 WORKING DRAFT SEQUENCE.//2.2e-111:570:95//AP000010  
 R-PLACE1007852//HS\_3028\_B2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3028 Col=8 Row=L, genomic survey sequence.//1.3e-12:209:71//AQ131021  
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//6.6e-110:574:94//AB018309  
 R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the  
 55 OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete  
 sequence.//1.6e-43:551:70//AL022162  
 R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.6e-22:  
 222:78//AC005754

R-PLACE1007897//HS\_3113\_B2\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3113 Col=8 Row=J, genomic survey sequencer.//2.9e-72:381:95//AQ186905  
R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//8.8e-88:460:95//AB007956

5 R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING DRAFT SEQUENCE.//4.9e-23:172:78//AC003095  
R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//1.7e-27:303:75//AC006157  
R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//3.9e-102:513:95//  
10 AF084530  
R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.2e-87:  
465:93//AF079529  
R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//4.8e-72:556:81//  
U13262  
15 R-PLACE1007990//E.tenella antigen LPMC61 mRNA, partial cds.//0.043:273:63//M30933  
R-PLACE1008000//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING  
DRAFT SEQUENCE.//8.8e-10:453:62//AL034346  
R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//9.0e-  
114:563:96//AC005628

20 R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//2.6e-44:509:  
72//L31840  
R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), complete sequence.//0.32:137:  
66//AC005592  
R-PLACE1008080//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//  
25 0.082:292:59//AC006232  
R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//5.4e-27:260:76//  
AC005036  
R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type II  
(COL2A1) gene.//2.2e-07:444:59//L10157  
30 R-PLACE1008122//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.9e-11:384:  
63//AC005919  
R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//  
3.0e-10:189:66//AC004955  
R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06.//7.4e-47:320:86//D16939  
35 R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-  
32:410:70//D14849  
R-PLACE1008181//Caenorhabditis elegans cosmid C31H2.//0.055:358:60//U41748  
R-PLACE1008198  
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102  
40 R-PLACE1008209//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING  
DRAFT SEQUENCE.//4.6e-16:250:71//AL034549  
R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688  
R-PLACE1008244//P.falciparum P.195 gene.//0.11:212:66//A04562  
45 R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611  
R-nnnnnnnnnnnn  
R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//  
1.5e-05:104:76//AC005272  
R-PLACE1008309//Human 'at'-rich region adjacent to alpha satellite DNA.//0.70:138:63//M80308  
50 R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence.//  
0.00061:150:68//AC005886  
R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//4.8e-74:252:98//  
AC005176  
R-PLACE100833//Genomic sequence from Human 13, complete sequence.//1.0:176:65//AC001226  
55 R-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, 3' UTR.//2.5e-98:556:90//  
AF036145  
R-PLACE1008368//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.2e-05:375:62//B36336

R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466:61//AP000011  
R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence.//1.0e-46:282:82//AC005244  
5 R-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529:94//AL034417  
R-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//0.18:379:58//AC004604  
R-nnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds.//1.6e-101:521:95//D86326  
10 R-PLACE1008405//Human cosmidCRI-JC2015 at D10S289 in 10sp13.//6.8e-22:328:71//U15177  
R-PLACE1008424  
R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11//7.5e-101:505:96//AB020864  
15 R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.2e-11:118:78//AL022576  
R-PLACE1008437//H.sapiens genomic DNA (PAC 838L14) from chromosome 11, WORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335  
R-PLACE1008455  
20 R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.2e-109:588:93//AC004526  
R-PLACE1008465//CIT978SK-A-28A11.TVE CIT978SK Homo sapiens genomic clone A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696  
R-PLACE1008488  
25 R-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778  
R-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//8.5e-96:510:93//AF045555  
R-PLACE1008532  
30 R-PLACE1008533  
R-PLACE1008568//HS\_3218\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey sequence.//0.0042:295:62//AQ214623  
R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence.//5.0e-26:254:66//AC003074  
35 R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//4.0e-78:498:86//AC006120  
R-nnnnnnnnnnnn  
R-PLACE1008626//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297  
R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:335:71//Y12836  
40 R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.55:326:58//AC004826  
R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence.//0.13:440:55//AG011096  
R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//1.3e-58:356:82//AC004001  
45 R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333  
R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742  
R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406  
50 R-PLACE1008715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147  
R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP.Homo sapiens genomic clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841  
55 R-PLACE1008757//Homo sapiens 12q24.2 PAC RPCI4-765H13 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.99:211:61//AC005864  
R-PLACE1008790//Rattus norvegicus clone1 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.052:108:68//U00762

R-PLACE1008798//Homo sapiens full-length insert cDNA clone YZ86C05.//7.7e-58:285:100//AF086088  
R-PLACE1008807//CIT-HSP-2366O14.TR CIT-HSP Homo sapiens genomic clone 2366O14, genomic survey sequence.//3.5e-35:223:89//AQ079210  
R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//2.3e-97:499:95//  
5 AF030933  
R-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//9.7e-45:394:78//AF032668  
R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 un-  
ordered pieces.//2.9e-28:207:87//AC004581  
R-nnnnnnnnnnnn//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey se-  
10 quence.//8.9e-30:166:97//B93289  
R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//3.5e-76:404:95//  
AC005058  
R-PLACE1008887//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-  
37:585:67//AC004932  
15 R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494\_G\_17, complete sequence.//0.0022:409:60//  
AC005820  
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.2e-55:344:89//AB018308  
R-PLACE1008925//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4,  
20 WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860  
R-PLACE1008934  
R-PLACE1008941//Homo sapiens chromosome 17, clone hRPK.293\_K\_20, complete sequence.//9.8e-84:429:  
92//AC005495  
R-PLACE1008947  
R-PLACE1009020  
25 R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like pro-  
tease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.3e-82:434:95//AL031117  
R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.1-22.3. Contains STSs,  
GSSs and a putative CpG island, complete sequence.//0.00010:297:58//AL031391  
R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//2.9e-06:160:  
30 70//AC004707  
R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last  
coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene  
downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//1.3e-16:  
339:66//AL023694  
35 R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023  
R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting protein X, short form, complete CDS.//  
0.00075:79:83//AJ005074  
R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-  
13:212:73//AC004783  
40 R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence.//0.49:221:61//Z70206  
R-PLACE1009099  
R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete se-  
quence.//5.1e-17:301:66//AC004025  
45 R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140  
R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//7.5e-06:426:58//Z98551  
R-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//2.3e-  
118:614:95//AJ011929  
50 R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SE-  
QUENCE.//1.4e-107:584:93//AP000031  
R-PLACE1009158//Homo sapiens full-length insert cDNA clone YP10D03.//1.9e-105:539:95//AF085876  
R-PLACE1009166//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//2.8e-44:360:71//  
AC005972  
R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046  
55 R-PLACE1009174//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.1e-17:140:81//  
AC004925  
R-PLACE1009183//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5')  
two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and

STSs, complete sequence.//1.9e-46:572:69//Z84480  
 R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC004070  
 R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:487:58//AL034560  
 R-PLACE1009200//H.sapiens mRNA for sortilin.//1.0e-31:195:92//X98248  
 5 R-PLACE1009230//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//  
 1.8e-75:364:85//AC005392  
 R-PLACE1009246//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mR-  
 NA, complete cds.//6.6e-44:525:71//U22818  
 R-PLACE1009308  
 10 R-PLACE1009319//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence.//0.00010:132:75//AC004801  
 R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//3.3e-87:576:  
 85//AC006120  
 R-PLACE1009335//Borrelia burgdorferi (section 62 of 70) of the complete genome.//0.32:315:60//AE001176  
 15 R-PLACE1009338//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 DRAFT SEQUENCE, 14 unordered pieces.//6.8e-05:411:59//AC005140  
 R-PLACE1009368//Homo sapiens PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280:  
 61//AC004989  
 R-PLACE1009375//D. yakuba mitochondrial DNA for origin of replication, small ribosomal RNA , transfer RNAs  
 20 tRNA-fMet, tRNA-GIn, tRNA-Ile and tRNA-Val.//1.1e-08:444:60//X05915  
 R-PLACE1009388  
 R-PLACE1009398//Homo sapiens BAC clone GS011E15 from 5q31, complete sequencer.//0.065:279:61//  
 AC002427  
 R-nnnnnnnnnnnnnn//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-  
 25 06:253:64//AC005038  
 R-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//9.8e-112:561:  
 96//AC005919  
 R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS,  
 30 GSS, complete sequence.//2.2e-21:126:79//AL031120 R-PLACE1009443//Homo sapiens nucleolar protein Nop30  
 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91//  
 AF064598  
 R-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L36151  
 R-PLACE1009459  
 R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-  
 35 101:540:94//AC004531  
 R-PLACE1009477//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.4e-46:284:91//AC006213  
 R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581:  
 92//U91321  
 R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome-22q12.3-13.1. Contains part  
 40 of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown  
 gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//0.74:  
 301:61//Z94160  
 R-PLACE1009539//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING  
 DRAFT SEQUENCE.//5.7e-29:357:74//AL031427  
 45 R-PLACE1009542//CIT-HSP-2166P10.TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey  
 sequence.//2.6e-10:145:75//B89614  
 R-PLACE1009571//RPCI11-61J16.TK RPCI11 Homo sapiens genomic clone R-61J16, genomic survey se-  
 quence.//0.016:68:80//AQ202146  
 R-PLACE1009581  
 50 R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006  
 R-PLACE1009596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING  
 DRAFT SEQUENCE.//1.2e-29:314:76//Z98051  
 R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone  
 55 cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230  
 R-PLACE1009613//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete  
 sequence.//3.6e-08:434:59//AL010266  
 R-PLACE1009621//Sequence 50 from patent US 5691147.//1.5e-20:235:73//I76222  
 R-PLACE1009622//CIT-HSP-2023D13.TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey

sequence.//0.72:176:62//B81271  
R-PLACE1009637//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276  
R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAI project).//0.013:521:  
5 58//AL021811  
R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159  
R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075  
R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534  
R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-103:542:94//AC006011  
R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//4.6e-85:518:88//AC000109  
10 R-PLACE1009731//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the  
HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE  
pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs,  
complete sequence.//0.0033:215:65//AL022398  
R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:598:95//AF046024  
15 R-PLACE1009794  
R-nnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-  
quione Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene  
Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene  
20 similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs,  
complete sequence.//7.5e-88:191:96//AL030996  
R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6q21. Contains an unknown  
gene, ESTs and STSs, complete sequence.//8.7e-19:226:69//Z98172  
R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence.//2.1e-  
25 29:230:76//AG002672  
R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//0.99:203:  
61//AC004945  
R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//5.3e-  
91:577:88//AC006116  
R-nnnnnnnnnnnn  
30 R-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//4.7e-81:385:84//  
M63005  
R-PLACE1009924//HS\_3151\_B1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3151 Col=19 Row=D, genomic survey sequence.//5.5e-47:240:99//AQ167412  
R-PLACE1009925//CIT978SK-A-931F6.TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey  
35 sequence.//0.00010:159:68//B51673  
R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308  
R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//  
AC002483  
40 R-PLACE1009971//Homo sapiens full-length insert cDNA clone ZD38E12.//3.7e-11:152:75//AF086247  
R-PLACE1009992  
R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0019:  
305:61//AE001367  
R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete  
45 sequence.//1.8e-43:462:76//AC005874  
R-PLACE1010023//HS\_30I8\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00013:198:63//AQ093513  
R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel  
50 genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial  
genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete se-  
quence.//7.4e-115:581:96//AL031775  
R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//1.9e-05:136:74//X84692  
R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 2328B12, genomic survey se-  
quence.//2.6e-60:324:94//AQ042094  
55 R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//4.6e-87:543:88//AF065482  
R-PLACE1010076/\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0473M13;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.3e-08:489:58//AC005699  
R-PLACE1010083

R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence.//0.14:400:59/B10583  
 R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:562:87//X64411  
 R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic spacer region, mitochondrial sequence.//1.5e-08:357:60//AF039556  
 R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.//4.0e-09:510:59//AE001374  
 R-PLACE1010106//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304  
 R-PLACE1010134  
 R-PLACE1010148//HS\_3128\_A1\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, genomic survey sequence.//0.17:281:61//AQ140790  
 R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds.//3.1e-45:351:81//D38417  
 R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.6e-06:207:66//AC004928  
 R-PLACE101019411HS\_2232\_B1\_H10\_MR CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=2232 Col=19 Row=P, genomic survey sequence.//2.4e-08:134:74//AQ185425  
 R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//0.00035:383:61//AL031585  
 R-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL033377  
 R-PLACE1010261  
 R-PLACE1010270//H.sapiens CpG island DNA genomic Mse1 fragment, clone 85a6, reverse read cpg85a61rt1a.//0.068:171:63//Z63482  
 R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X59280  
 R-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.7e-91:522:90//AC004464  
 R-PLACE1010321  
 R-PLACE1010324//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149  
 R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//7.9e-35:328:79//AC000024  
 R-PLACE1010341//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.3e-31:418:66//AC004971  
 R-PLACE1010362  
 R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77098  
 R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//1.4e-105:543:95//AC004675  
 R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62//AC004137  
 R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8.6e-79:556:83//AF003927  
 R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081  
 R-PLACE1010492//HS\_3169\_B2\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892  
 R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082  
 R-nnnnnnnnnnnnn  
 R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929  
 R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein var1.//1.7e-05:271:65//X02893  
 R-PLACE1010580  
 R-PLACE1010599  
 R-PLACE1010616//Human BAC clone RG343P13 from 7q31, complete sequence.//3.0e-13:151:75//AC002465  
 R-PLACE1010622//Arabidopsis thaliana BAC F1104.//0.00031:366:60//AF096370  
 R-PLACE1010624//Homo sapiens chromosome 7q22 sequence, complete sequence.//8.2e-34:322:79//AF053356  
 R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-97:515:94//AC004846

R-PLACE1010629//HS\_3003\_A2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey sequence./.5.6e-60:321:95//AQ130493  
R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence./.0.051:372:59//AE001382  
5 R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds./.2.6e-92:497:93//AB011102  
R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 2008K15, genomic survey sequence./.5.7e-27:160:95//B57089  
R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequence./.9.4e-09:151:73//Z81467  
10 R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 2314C3, genomic survey sequence./.1.3e-90:459:96//AQ028536  
R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds./.5.3e-08:478:58//U49822  
15 R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds./.3.8e-55:300:95//AF092564  
R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence./.3.4e-89:507:90//Z95400  
R-PLACE1010743  
20 R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence./.3.0e-103:511:97//AC005921  
R-PLACE1010771  
R-PLACE1010786  
R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces./.1.8e-43:545:71//AC005682  
25 R-PLACE1010802//Phoebis agarithe large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs./.1.9e-09:492:59//AF044862  
R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence./.0.041:415:59//AC002524  
30 R-PLACE1010833  
R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./.0.0022:512:55//AC004153  
R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11//4.9e-85:507:90//AB020868  
35 R-PLACE1010870//RPCI11-59K21:TK RPCI11 Homo sapiens genomic clone R-59K21, genomic survey sequence./.8.2e-85:422:97//AQ195697  
R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds./.7.0e-100:501:96//AB011182  
R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces./.0.10:162:61//AC002489  
40 R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces./.0.00032:409:59//AC005505  
R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region./.3.2e-07:180:71//AB018488  
R-PLACE1010916//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE./.0.041:205:60//AL034557  
45 R-PLACE1010917  
R-PLACE1010925//HS\_2027\_B2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic survey sequence./.1.6e-46:404:77//AQ247031  
R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds./.4.2e-65:402:89//AB011126  
R-nnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds./.1.9e-80:441:93//AF064243  
50 R-PLACE1010944  
R-PLACE1010947//D.discoideum rasG gene./.0.00044:181:65//Z11533  
R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces./.3.0e-51:518:74//AC005077  
R-PLACE1010960//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE./.0.022:292:63//AL033522  
55 R-PLACE1010965//Human mariner1 transposase gene, complete consensus sequence./.1.0e-64:444:84//U52077  
R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4./.0.59:345:61//

AJ235272  
R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242  
R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248  
5 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153  
R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains KloTho, ESTs.//4.7e-29:280:73//Z84483  
R-PLACE1011056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985  
10 R-PLACE1011057//CIT-HSP-2014F10.TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896  
R-PLACE1011090//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//0.12:489:59//AC005509  
R-PLACE1011109//Homo sapiens chromosome Y, clone 486, O, 2, complete sequence.//8.4e-43:427:76//  
15 AC002531  
R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-14).//1.7e-29:179:94//Y16709  
R-PLACE1011133//HS-1058-B1-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//44006  
20 R-PLACE1011143//H.sapiens CpG island DNA genomic Mse1 fragment, clone 127a4, forward read cpg127a4.ft1a.//1.0:127:67//Z56550  
R-PLACE1011160//Homo sapiens HRIHFB2038 mRNA, partial cds.//2.4e-95:534:91//AB015333  
R-PLACE1011165//Human Cosmid g5129s232 from 7q31.3, complete sequence.//0.47:355:58//AC003968  
R-PLACE1011185//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.3e-  
25 26:403:70//AC004820  
R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//K00908  
R-PLACE1011219//HS\_3036\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey sequence.//2.6e-39:253:88//AQ104587  
30 R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.32:279:60//AE000659  
R-PLACE1011229//HS\_3002\_B1\_E10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey sequence.//9.3e-3l:317:74//AQ303626  
R-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.2e-109:571:94//  
35 AC005014  
R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.00027:337:61//M97514  
R-PLACE1011291  
R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80//M68887  
40 R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661  
R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.3.0e-10:511:59//AE001398  
R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344  
45 R-PLACE1011340//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//0.67:290:58//AC002530  
R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310  
R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140  
R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:  
50 282:81//Z74022  
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102  
R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013  
R-PLACE1011465  
55 R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//7.9e-103:515:96//AB018255  
R-PLACE1011492//A-837A4.TP CIT978SK Homo sapiens genomic clone A-837A4, genomic survey sequence.//6.5e-37:234:82//B14085  
R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171\_I\_10, complete sequence.//0.99:267:60//

AC004687  
R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence././/2.0e-116:591:96//AC004968  
R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
DRAFT SEQUENCE, 4 unordered pieces././/1.2e-13:566:59//AC004688  
5 R-PLACE1011567//Plasmodium-falciparum MAL3P6, complete sequence././/0.62:358:61//Z98551  
R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence././/8.7e-45:400:78//  
AC003973  
R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence././/2.2e-59:338:93//  
AC004477  
10 R-PLACE1011635//C.pasteurianum pfl gene and act gene././/0.71:288:60//X93463  
R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds././/0.023:232:60//U02205  
R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence././/1.4e-21:432:67//  
AC005620  
R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence././/7.8e-72:414:91//AF070535  
15 R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence././/5.1e-27:174:79//  
AC002477  
R-PLACE1011664//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone. 460D19, WORKING  
DRAFT SEQUENCE././/7.4e-05:238:65//AL031905  
R-PLACE1011675//CIT-HSP-2370M16.TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey se-  
20 quence././/1.3e-27:233:81//AQ108283  
R-PLACE1011682//H.sapiens HLA-DMB gene././/2.3e-22:390:67//X76776  
R-PLACE1011719//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Li-  
brary) complete sequence././/3.1e-24:409:66//AC004806  
R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic  
25 acid././/0.13:143:65//AF026526  
R-PLACE1011729//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING  
DRAFT SEQUENCE././/1.1e-15:157:82//AL022345  
R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces././/1.5e-  
38:314:81//AC005089  
30 R-PLACE1011762//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence././/1.9e-35:538:68//  
AC002383  
R-PLACE1011778//CIT-HSP-2326C17.TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey se-  
quince././/2.8e-58:346:91//AQ028782  
R-PLACE1011783//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING  
35 DRAFT SEQUENCE././/4.6e-38:288:84//Z86090  
R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS,  
complete sequence././/4.1e-104:524:97//AL031321  
R-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence././/2.1e-100:511:95//  
AC004478  
40 R-PLACE1011875  
R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11././/0.0011:195:64//L04193  
R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the  
HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE  
45 pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs,  
complete sequence././/0.010:110:74//AL022398  
R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence././/3.5e-10:152:74//  
AF042090  
R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds././/7.0e-98:546:92//AF059617  
R-PLACE1011962//CIT-HSP-2294L24.TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey se-  
50 quence././/0.31:131:63//AQ006352  
R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence././/2.5e-08:393:63//  
AC002994  
R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence././/  
9.6e-09:463:62//AB016889  
55 R-PLACE1011995//Human Down Syndrome region of chromosome 21, clone A12H1-2H4././/2.7e-39:294:82//  
U44738  
R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds././/2.5e-104:540:95//AB018256  
R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence././/4.9e-10:439:63//AC004000

R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 3.//1.0:151:66//L78722  
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.5e-103:524:95//AF091080  
 R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequence.//0.94:372:57//AC005191  
 R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//3.0e-55:299:86//  
 5 AC006236  
 R-PLACE2000021//CIT-HSP-2343C18.TR CIT-HSP Homo sapiens genomic clone 2343C18, genomic survey se-  
 quence.//4.5e-54:295:94//AQ058140  
 R-PLACE2000033//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//6.5e-38:298:82//X69907  
 R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.3e-  
 10 34:200:79//AC005628  
 R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//1.8e-49:274:89//  
 AC003083  
 R-PLACE2000047//CIT-HSP-2373C2.TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey se-  
 quence.//1.8e-48:389:79//AQ112243  
 15 R-PLACE2000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING  
 DRAFT SEQUENCE.//0.0027:95:76//AL022315  
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2.9e-39:429:72//AB011147  
 R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//  
 5.9e-40:310:84//AC004832  
 20 R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1.9e-109:550:95//AF027219  
 R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SE-  
 QUENCE, 39 unordered pieces.//1.6e-106:553:95//AC005910  
 R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part  
 25 of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-  
 38:285:84//AL031730  
 R-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING  
 DRAFT SEQUENCE.//4.3e-113:559:97//AL031848  
 R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricel light chain, exon 1.//0.00041:347:61//  
 X16325  
 30 R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 microsatellite.//0.50:165:63//U63067  
 R-PLACE2000132  
 R-PLACE2000136//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-30, complete  
 sequence.//0.0032:310:61//AL008974  
 R-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING  
 35 DRAFT SEQUENCE.//1.1e-111:566:96//AL020995  
 R-PLACE2000164  
 R-PLACE2000170///\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.9e-40:390:76//AC005598  
 R-PLACE2000172  
 40 R-PLACE2000176  
 R-PLACE2000187//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING  
 DRAFT SEQUENCE.//8.7e-45:298:87//AL008718  
 R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end.//5.6e-88:495:92//L02897  
 R-PLACE2000223  
 45 R-PLACE2000235//HS\_3159\_B1\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3159 Col=11 Row=D, genomic survey sequence.//1.8e-88:454:96//AQ179271  
 R-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58  
 50 unordered pieces.//9.1e-41:282:86//AC005902  
 R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs  
 and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//8.3e-35:305:80//Z97181  
 R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//3.5e-18:325:  
 67//AC002394  
 R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287:85//  
 AC003043  
 55 R-PLACE2000305//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING  
 DRAFT SEQUENCE.//1.2e-43:295:85//Z93015  
 R-PLACE2000317//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-  
 threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNC-

TION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-05:284:65//Z92542  
R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.5e-26:334:70//AC006147

5 R-PLACE2000342//Fugu rubripes cosmid 258N02 containing IGFII, TH, NAP2 genes.//4.0e-05:254:64//AL021880  
R-PLACE2000347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//1.6e-82:504:88//AL022147  
R-PLACE2000359//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 40E16, WORKING DRAFT SEQUENCE.//2.0e-36:314:80//AL031963

10 R-PLACE2000366//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//2.0e-48:389:80//AL031291  
R-PLACE2000371  
R-PLACE2000373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 324M8, WORKING DRAFT SEQUENCE.//0.61:231:61//AL008734

15 R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence.//3.5e-11:287:67//AC004917  
R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//6.8e-108:553:96//AL031432  
R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.9e-26:326:73//AC005059

20 R-PLACE2000399  
R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//6.5e-84:434:96//AC005216  
R-PLACE2000411//P.clarkii mRNA; repeat region (ID 2R).//0.47:104:70//Z54273  
R-PLACE2000419

25 R-PLACE2000425//Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.9e-40:447:74//AF003528  
R-PLACE2000427  
R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence.//3.5e-40:286:85//AC000379  
R-PLACE2000435

30 R-PLACE2000438//Homo sapiens full-length insert cDNA clone ZE04D01.//2.2e-107:523:98//AF086521  
R-PLACE2000450 4.1e-42:328:79//AG006257  
R-PLACE2000455

R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete-sequence.//5.1e-116:570:97//AC005740

35 R-PLACE2000465//Human BAC clone RG191D16, complete sequence.//6.3e-37:408:75//AC002460  
R-PLACE2000477//M.musculus tex264 mRNA (3'region).//7.5e-06:117:76//X80427  
R-PLACE3000004

R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a CpG island.//5.8e-34:308:78//Z82976

40 R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-36:273:87//Y17267  
R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//2.3e-10:181:71//AC004648  
R-PLACE3000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.2e-48:495:74//AL022156

45 R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion Region, complete sequence.//3.4e-39:283:85//AC000026  
R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//9.2e-23:171:76//AC005200  
R-PLACE3000136//U.arctos microsatellite DNA, clone UarMU23.//0.00052:171:65//Y09645

50 R-PLACE3000142//HS\_3037\_82\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey sequence.//0.88:121:66//AQ097023  
R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds.//3.3e-23:472:66//AB001735  
R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//3.5e-11:176:73//Z49237

55 R-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//6.9e-106:549:94//AC005277  
R-PLACE3000156//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//7.0e-38:545:70//AC002383

R-PLACE3000157  
R-PLACE3000158//, complete sequence./.1.4e-33:283:81//AC005500  
R-PLACE3000160  
5 R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence./.5.2e-43:229:85//  
AC006130  
R-PLACE3000194  
R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence./.7.2e-61:394:89//  
AC005291  
10 R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for  
neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-  
acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1  
receptor-associated kinase (IRAK) genes, complete cds, and Xq28u2 gene./.0.23:309:57//U52112 R-  
PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey se-  
quence./.1.1e-15:156:81//B54637  
15 R-PLACE3000208//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING  
DRAFT SEQUENCE./.1.3e-16:139:87//AL031594  
R-PLACE3000218//HS\_3185\_B1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3185 Col=1 Row=D, genomic survey sequence./.3.5e-07:120:75//AQ155720  
20 R-PLACE3000220//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence./.2.4e-44:363:80//  
AC004167  
R-PLACE3000226//Caenorhabditis elegans cosmid M01G5./.0.88:95:77//AF078786  
R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and  
lactoferrin (lactoferrin) gene, partial cds, complete sequence./.5.3e-69:536:81//U95626  
25 R-PLACE3000242//Sequence 1 from patent US 5599918./.3.2e-62:546:78//I35489  
R-PLACE3000244//M.musculus mRNA for 200 kD protein./.1.7e-45:404:75//X80169  
R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds./.7.5e-28:174:94//AB002307  
R-PLACE3000271//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
DRAFT SEQUENCE./.3.9e-54:492:77//AL034379  
30 R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence./.5.4e-12:176:69//  
AC004081  
R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence./.5.7e-114:555:97//  
AC005328  
R-PLACE3000310//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467L1, WORKING  
DRAFT SEQUENCE./.6.2e-51:314:84//Z98884  
35 R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds./.2.5e-  
44:289:90//U93037  
R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3./.5.9e-20:153:88//M21006  
R-PLACE3000331//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces./.  
1.1e-43:230:84//AC005480  
40 R-PLACE3000339  
R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Park Cancer Institute Human PAC  
Library) complete sequence./.2.5e-111:550:97//AC006055  
R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and  
GSSs, complete sequence./.1.5e-44:314:78//AL022323  
45 R-PLACE3000352//HS\_3095\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3095 Col=17 Row=J, genomic survey sequence./.8.5e-73:356:99//AQ123142  
R-PLACE3000353//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y22F5,  
WORKING DRAFT SEQUENCE./.0.21:194:63//Z99712  
50 R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7./.0.26:360:60//AJ002197  
R-PLACE3000363  
R-PLACE3000365//Human BAC clone RG343P13 from 7q31, complete sequence./.4.6e-52:487:76//AC002465  
R-PLACE3000373//HS\_3202\_B1\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3202 Col=9 Row=N, genomic survey sequence./.2.4e-75:437:90//AQ252699  
55 R-PLACE3000388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING  
DRAFT SEQUENCE./.6.4e-61:515:81//AL008722  
R-PLACE3000399//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces./.  
0.00098:444:60//AC005231  
R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING

DRAFT SEQUENCE, 7 unordered pieces./.0.78:155:66//AC005506  
 R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces./.8.0e-47:223:81//AC006023  
 5 R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence./.1.0:179:63//AC000003  
 R-PLACE3000405//Homo sapiens chromosome 7qtelo BAC F6, complete sequence./.2.4e-44:466:74//AF104455  
 R-PLACE3000406//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING  
 DRAFT SEQUENCE./.7.7e-49:471:75//AL008718  
 R-PLACE3000413  
 10 R-PLACE3000416//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SE-  
 QUENCE./.5.4e-42:416:77//AJ009612  
 R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal  
 protein L29 pseudogene, ESTs and STSs./.1.1e-41:366:78//AL008627  
 R-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING  
 DRAFT SEQUENCE./.3.8e-98:549:92//AL031284  
 15 R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds./.1.9e-82:440:92//  
 U43899  
 R-PLACE3000477  
 R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to heymann nephritis antigen  
 gp330./.6.6e-17:344:68//Z11995  
 20 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds./.2.7e-83:433:95//AB018352  
 R-PLACE4000034//cSRSL-51C5-u cSRSL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone  
 cSRSL-51C5, genomic survey sequence./.0.54:116:66//B04984  
 R-PLACE4000049//Human BAC clone GS165I04 from 7q21, complete sequence./.0.29:313:59//AC002379  
 R-PLACE4000052//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
 25 DRAFT SEQUENCE./.0.0058:466:57//AL034557  
 R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence./.0.98:246:61//AF053356  
 R-PLACE4000089//RPCI11-15I1.TUB RPCI-11 Homo sapiens genomic clone RPCI-11-15I1, genomic survey se-  
 quence./.3.2e-07:284:60//B82414  
 R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING  
 30 DRAFT SEQUENCE, 7 unordered pieces./.2.4e-07:429:60//AC005506  
 R-PLACE4000100  
 R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds./.9.3e-100:419:91//AF055010  
 R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence./.9.6e-45:284:  
 90//AC003007  
 35 R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500./.1.6e-19:118:100//  
 AB007969  
 R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence./.8.9e-17:208:73//  
 AC005034  
 R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a  
 40 pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde  
 dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence./.3.7e-43:281:90//AL021939  
 R-PLACE4000192  
 R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces./.5.4e-44:280:82//AC005631  
 45 R-PLACE4000233//Homo sapiens full-length insert cDNA YH59G06./.1.8e-79:414:97//AF074981  
 R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence./.5.7e-59:558:  
 76//AC005821  
 R-PLACE4000250//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey se-  
 quence./.1.7e-44:313:84//AQ037381  
 50 R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence./.1.5e-39:311:83//  
 AC005920  
 R-PLACE4000261//H.sapiens BF1P-g1H03np gene for immunoglobulin heavy chain variable region./.0.33:197:  
 61//Z80410  
 R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence./.1.4e-31:327:  
 68//AC005510  
 55 R-PLACE4000270//Homo sapiens DNA for amyloid precursor protein, complete cds./.2.3e-32:345:74//D87675  
 R-PLACE4000300//Sequence 61 from patent US 5744300./.0.0017:51:98//AR003339  
 R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete

sequence.//8.2e-41:295:85//Z99495  
 R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence.//1.3e-32:404:75//U73640  
 R-PLACE4000326  
 R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//0.32:135:68//  
 AC005587  
 R-PLACE4000367//H.sapiens gene encoding RING finger protein.//0.61:146:67//Y07829  
 R-PLACE4000369//HS\_3181\_A1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3181 Col=3 Row=C, genomic survey sequence.//7.1e-80:424:94//AQ173222  
 R-PLACE4000379//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING  
 5 DRAFT SEQUENCE.//1.7e-05:160:65//AL022312  
 R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.4e-  
 10 47:351:81//AC004913  
 R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown  
 15 gene, ESTs, STSs and GSSs, complete sequence.//8.5e-88:541:88//AL034377  
 R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT  
 SEQUENCE, 17 unordered pieces.//2.7e-17:143:83//AC000406  
 R-PLACE4000411  
 R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//  
 20 0.028:91:78//AC005628  
 R-PLACE4000465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING  
 DRAFT SEQUENCE.//1.6e-43:532:71//AL022156  
 R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//4.1e-06:  
 25 357:61//AE001427  
 R-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC  
 Library) complete sequence.//2.7e-37:416:74//AC005865  
 R-PLACE4000522  
 R-PLACE4000548//Homo sapiens 12p13.3 PAC RPCI5-1096D14 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence.//0.0020:383:60//AC005342  
 R-PLACE4000558//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC li-  
 30 brary) complete sequence.//2.9e-44:465:75//AC002996  
 R-THYRO1000026//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 37E16, WORKING  
 DRAFT SEQUENCE.//2.2e-43:354:82//Z83844  
 R-THYRO1000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.022:  
 35 327:60//AE001422  
 R-THYRO1000035//HS\_3018\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3018 Col=20 Row=L, genomic survey sequence.//2.3e-36:228:91//AQ092318  
 R-THYRO1000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//1.0:367:56//AC004157  
 R-THYRO1000070//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.1/1e-44:284:89//U14573  
 R-THYRO1000072//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//6.6e-33:150:83//U14567  
 40 R-THYRO1000085  
 R-THYRO1000092//Homo sapiens chromosome 7qtelo BAC F6, complete sequence.//3.3e-36:301:78//AF104455  
 R-THYRO1000107//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING  
 DRAFT SEQUENCE.//1.4e-35:282:82//AL033528  
 R-THYRO1000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//4.0e-  
 45 32:351:65//AC002300  
 R-THYRO1000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//6.6e-77:507:  
 85//U91318  
 R-THYRO1000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1  
 50 ordered pieces.//0.66:334:59//AC005840  
 R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//2.3e-88:449:96//AF087142  
 R-THYRO1000132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING  
 DRAFT SEQUENCE.//1.1e-40:298:84//Z95114  
 R-THYRO1000156//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//3.4e-37:425:  
 55 73//AC005703  
 R-THYRO1000163//RPCI11-1B20.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1B20, genomic survey  
 sequence.//8.4e-38:276:84//B63536  
 R-THYRO1000173//Human DNA sequence from PAC 323B6 on chromosome X contains ESTs CpG island.//1.1e-

70:553:81//Z83841  
R-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE./.6.7e-41:345:81//AL031732  
5 R-THYRO1000187//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta./.1.3e-43:356:80//U18271  
R-THYRO1000190//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence./.2.6e-40:386:77//AC004139  
R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease./.1.1e-108:535:97//AJ005698  
R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds./.1.4e-113:559:97//AB014552  
10 R-THYRO1000206//Rat PMSG-induced ovarian mRNA, 3'sequence, N4./.4.0e-43:318:86//D84482  
R-THYRO1000221//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence./.2.7e-44:452:76//AC002115  
R-THYRO1000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal location, complete sequence./.4.8e-58:447:81//AC000039  
15 R-THYRO 1000242  
R-THYRO1000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence./.3.4e-56:300:84//Z95152  
20 R-THYRO1000270  
R-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE./.4.8e-113:584:96//AL031664  
R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds./.1.1e-98:566:91//AB016068  
25 R-THYRO1000320//HS\_2033\_B1\_A07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=13 Row=B, genomic survey sequence./.0.97:211:63//AQ233366  
R-THYRO1000327//Sequence 1 from patent US 5541298./.2.8e-52:289:93//I24058  
R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds./.1.1e-111:559:96//AB018333  
R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds./.4.6e-47:317:87//U29091  
30 R-THYRO1000368//HS\_3049\_A1\_E12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=23 Row=l, genomic survey sequence./.7.0e-11:111:83//AQ126777  
R-nnnnnnnnnnnnn  
R-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence./.2.4e-101:545:93//AC006019  
R-THYRO1000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces./.1.6e-46:233:88//AC006078  
35 R-THYRO1000395//Mouse MIPP mRNA for a placenta-expressed gene./.2.3e-57:395:85//X58523  
R-THYRO 1000401  
3.3e-111:546:97//AF051907  
R-THYRO1000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces./.2.7e-44:289:89//AC005231  
40 R-THYRO1000452//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence./.6.7e-27:222:82//AC005668  
R-THYRO1000471//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE./.2.4e-36:369:76//AL021391  
45 R-THYRO1000484//Homo sapiens clone DJ1099N07, complete sequence./.1.6e-43:288:81//AC004962  
R-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence./.1.6e-95:512:94//AC005740  
R-THYRO1000501//HS \_2208\_A1\_G11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence./.0.0063:189:63//AQ091586  
50 R-THYRO1000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds./.0.19:468:60//AF000987  
R-THYRO1000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence./.0.20:214:58//AC004798  
R-THYRO1000558  
R-THYRO 1000569  
55 R-THYRO1000570//Homo sapiens full-length insert cDNA clone ZD76G10./.4.3e-41:209:100//AF086408  
R-nmmmmnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds./.8.2e-107:533:97//AF075587  
R-THYRO 000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPolB) mRNA, nuclear gene encoding mitochondrial protein, partial cds./.0.36:170:67//AF006072

R-THYRO1000602//Homo sapiens DNA for amyloid precursor protein, complete cds././/2.2e-53:289:92//D87675  
R-THYRO 1000605  
R-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence././/1.3e-31:261:82//  
AC005546

5 R-THYRO1000637//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence././/4.0e-06:249:63//AL022323  
R-THYRO1000641//P.falciparum glutamic acid-rich protein gnen, complete cds././/3.1e-08:244:68//J03998  
R-THYRO1000658//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence././/3.9e-49:282:93//U14572  
R-nnnnnnnnnnnnnn

10 R-THYRO1000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence././/1.9e-20:215:77//AL031005  
R-THYRO1000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence././/1.2e-06:227:  
64//AC004069

15 R-THYRO1000684  
R-THYRO1000699  
R-THYRO1000712  
R-THYRO1000734//Human BAC clone RG191D16, complete sequence././/3.7e-14:468:64//AC002460  
R-THYRO1000748//Homo sapiens cosmid 123E15, complete sequence././/2.6e-11:182:73//AF024533  
R-THYRO1000756//Sequence 21 from patent US 5552281././/1.4e-15:106:98//I25660

20 R-THYRO1000777//Plasmodium falciparum MAL3P2, complete sequence././/1.0:175:66//AL034558  
R-THYRO1000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey se-  
quence././/1.2e-81:391:99//AQ038226  
R-THYRO1000787//Homo sapiens chromosome Y, clone 264,M,20, complete sequence././/9.4e-07:494:58//  
AC004617

25 R-THYRO1000793  
R-THYRO1000796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING  
DRAFT SEQUENCE././/1.7e-42:379:79//Z93014  
R-THYRO1000805//Human Chromosome 11 pac pDJ610i20, WORKING DRAFT SEQUENCE, 18 unordered piec-  
es././/4.7e-40:362:76//AC002555

30 R-THYRO1000815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING  
DRAFT SEQUENCE././/4.0e-58:295:92//Z82199  
R-THYRO1000829//Sequence 7 from patent US 5716622././/0.97:362:61//I87788  
R-THYRO1000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angel-  
man Syndrome region, complete sequence././/3.3e-57:522:76//AC004738

35 R-THYRO1000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE,  
9 unordered pieces././/4.2e-17:291:69//AC005849  
R-THYRO1000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs,  
complete sequence././/1.1e-41:419:75//AL031592

40 R-THYRO1000865//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORK-  
ING DRAFT SEQUENCE././/9.0e-47:294:84//AL034549  
R-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380F5, WORKING  
DRAFT SEQUENCE././/3.7e-111:569:96//AL031719  
R-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces././/  
1.0e-97:554:92//AC006015

45 R-THYRO1000926//Homo sapiens CAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds././/9.6e-109:  
566:94//AF079529  
R-THYRO1000934//Homo sapiens full-length insert cDNA clone ZD69A10././/1.6e-104:539:95//AF086378  
R-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57I14, WORKING DRAFT SEQUENCE, 29 un-  
ordered pieces././/8.9e-61:479:81//AC004229

50 R-THYRO1000952//Human autoimmune thyroid disease-related antigen mRNA././/5.3e-16:116:93//M28639  
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds././/3.2e-59:321:95//  
AF047440  
R-THYRO1000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence././/1.9e-44:396:79//  
AC006126

55 R-THYRO1000983//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence././/0.99:71:78//  
AC005562  
R-THYRO1000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene,  
WORKING DRAFT SEQUENCE, 11 unordered pieces././/6.7e-42:320:84//AC006078

R-THYRO1000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466  
 R-THYRO1001003//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//2.5e-39:310:83//AQ253727  
 5 R-THYRO1001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z84466  
 R-THYRO1001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 2007J14, genomic survey sequence.//5.1e-26:143:100//B56677  
 10 R-THYRO1001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882  
 R-THYRO1001093  
 R-THYRO1001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complete sequence.//0.47:102:73//AC005070  
 R-THYRO1001120  
 15 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//8.9e-81:429:94//AJ006417  
 R-THYRO1001133//CIT-HSP-2381I10.TR CIT-HSP Homo sapiens genomic clone 2381I10, genomic survey sequence.//4.7e-12:237:67//AQ111077  
 R-THYRO1001134  
 20 R-THYRO1001142//H.sapiens CpG island DNA genomic Mse1 fragment, clone 81d1, reverse read cpg81d1.rt1a.//0.95:214:60//Z56037  
 R-THYRO1001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6e-26:262:77//B04145  
 R-THYRO1001177  
 25 R-THYRO1001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973  
 R-THYRO 1001204  
 R-THYRO1001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581  
 R-THYRO1001262//Homo sapiens, clone hRPK.16\_A\_1, complete sequence.//8.7e-53:442:79//AC006227  
 30 R-THYRO1001271//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630  
 R-THYRO 1001290  
 R-THYRO1001313//H.sapiens CpG island DNA genomic Mse1 fragment, clone 195h3, forward read cpg195h3.fl1b.//0.046:126:66//Z57783  
 35 R-THYRO1001320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207  
 R-THYRO100132//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558  
 R-nnnnnnnnnnnnnn  
 R-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288  
 R-THYRO1001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92/B05884  
 40 R-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//1.8e-109:584:94//AC005660  
 R-THYRO1001374  
 R-THYRO1001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953  
 45 R-THYRO1001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//8.7e-38:307:82//AC002377  
 R-THYRO1001405  
 R-THYRO1001406//RPCI11-69F22.TK RPCI1 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297  
 50 R-THYRO1001411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123  
 R-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553  
 55 R-THYRO1001434//Microcentus caryae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877  
 R-THYRO1001458//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578

R-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-99:517:95//AC006001  
R-THYRO1001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085  
5 R-THYRO10001534//HS\_2242\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326  
R-THYRO1001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//0.42:323:60//AL023876  
R-THYRO1001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-10:42:370:78//AC005077  
R-THYRO1001559//Homo sapiens 12q24.2 PAC RPCI5-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868  
R-THYRO1001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308  
15 R-THYRO1001573//M.avium rpsL gene.//0.98:131:66//X80120  
R-THYRO1001584//A.longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653  
R-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808  
R-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//4.4e-13:320:  
20 67//AC005919  
R-THYRO1001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249  
R-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:  
448:92//AJ002190  
R-THYRO1001637//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 688G8, WORKING  
25 DRAFT SEQUENCE.//5.4e-41:381:78//AL031671  
R-THYRO1001656//HS\_2201\_B2\_A08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence.//0.096:162:63//AQ293168  
R-THYRO1001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:  
62//U22954  
30 R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//4.8e-110:562:95//  
AJ225089  
R-THYRO1001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence.//1.5e-17:224:68//AQ042426  
R-THYRO1001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072  
35 R-THYRO1001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011  
R-THYRO1001721//, complete sequence.//1.3e-101:571:92//AC005500  
R-nnnnnnnnnnnnn  
R-THYRO1001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//1.1e-15:  
193:70//AC004777  
40 R-THYRO1001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3.//0.54:260:61//M88244  
R-THYRO1001772//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156  
R-THYRO1001793  
R-THYRO1001809//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING  
45 DRAFT SEQUENCE.//2.5e-43:486:74//AL031728  
R-THYRO1001854//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//5.0e-41:245:87//  
AC005696  
R-THYRO1001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence.//4.4e-12:419:61//  
AC005137  
50 R-THYRO1001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCR Region, complete sequence.//8.1e-35:340:78//AC000075  
R-VESEN1000122//Homo sapiens Luman mRNA, complete cds.//1.3e-23:138:98//AF009368  
R-Y79AA1000013  
55 R-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//9.9e-112:551:97//  
AC006027  
R-Y79AA1000037//CIT-HSP-2334F3.TR CIT-HSP Homo sapiens genomic clone 2334F3, genomic survey sequence.//0.16:308:60//AQ036673  
R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.1e-

56:314:88//AC002300  
R-Y79AA1000065//Human carboxylesterase gene, exon 5.//0.64:203:63//D21079  
R-Y79AA1000131///\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0548N01;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169:79//AC004795  
5 R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,  
complete sequence.//1.1e-106:474:98//AL031864  
R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey  
sequence.//1.0e-10:78:97//B68074  
10 R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//  
6.5e-59:386:90//AC004854  
R-Y79AA1000230//Cytauxzoon felis 18S ribosomal RNA.//1.0:167:62//L19080  
R-Y79AA1000231//HS\_3009\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3009 Col=5 Row=O, genomic survey sequence.//6.4e-52:348:88//AQ090225  
15 R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127:65//D10558  
R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN  
1 like gene and ESTs, complete sequence.//4.7e-40:300:84//Z98047  
R-Y79AA1000313//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 con-  
tains Klotho ESTs and CpG island.//5.0e-14:136:83//Z92540  
20 R-Y79AA1000328  
R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189:65//X54107  
R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611  
R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300:81//X84692  
25 R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl  
pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//5.7e-45:403:  
80//AL022163  
R-Y79AA1000368  
R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16B12, genomic survey  
sequence.//0.10:171:65//B88000  
30 R-Y79AA1000410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING  
DRAFT SEQUENCE.//4.1e-50:361:83//Z93097  
R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite  
surface protein 2, and adenylosuccinate lyase genes, complete cds.//0.071:474:57//AF033037  
R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence.//1.8e-86:221:90//AC005033  
35 R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//2.1e-14:179:  
72//AC004057  
R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.5e-  
43:321:83//AC005282  
R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//0.0012:275:59/  
40 AC006143  
R-Y79AA1000540//Z.diploperennis repetitive DNA (clone ZEAR 260).//0.0017:258:62//X53609  
R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X14972  
R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete sequence.//0.96:224:61//AC002325  
R-Y79AA1000627//Homo sapiens full-length insert cDNA ZA77G02.//6.3e-100:533:94//AF075117  
45 R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7, genomic survey sequence.//  
4.6e-88:429:98//AQ268433  
R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//2.7e-112:586:  
95//AF093670  
R-Y79AA1000748  
50 R-Y79AA1000752  
R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey se-  
quence.//5.3e-45:316:86//AQ005014  
R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-17:107:100//D87433  
R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
55 DRAFT SEQUENCE, 8 unordered pieces.//0.00034:520:55//AC005505  
R-Y79AA1000794//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 989H11, WORKING  
DRAFT SEQUENCE.//0.015:322:60//Z83851  
R-Y79AA1000800//M.musculus tex264 mRNA (3'region).//1.1e-06:104:78//X80427

R-nnnnnnnnnnnnn//CIT-HSP-2295G6.TF CIT-HSP Homo sapiens genomic clone 2295G6, genomic survey sequence.//0.67:152:62//AQ007605  
 R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//3.1e-26:423:68//U73642  
 R-Y79AA1000824//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING  
 5 DRAFT SEQUENCE.//1.1e-08:449:61//Z97832  
 R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds.//1.0:101:69//  
 AF083344  
 R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds.//0.40:386:59//U85647  
 R-Y79AA1000962//CIT-HSP-2298N11.TR CIT-HSP Homo sapiens genomic clone 2298N11, genomic survey se-  
 10 quence.//0.00019:253:65//AQ013111  
 R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete  
 cds.//1.7e-58:446:80//U38253  
 R-Y79AA1000969  
 R-Y79AA1000976//CIT-HSP-2350C4.TF CIT-HSP Homo sapiens genomic clone 2350C4, genomic survey se-  
 15 quence.//3.3e-60:295:100//AQ061422  
 R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:348:76//U05823  
 R-Y79AA1001023  
 R-Y79AA1001041  
 R-Y79AA1001048  
 20 R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//1.2e-  
 60:537:78//AC004626  
 R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.3e-41:405:77//  
 AC005031  
 R-Y79AA1001077  
 25 R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence.//2.0e-09:534:59//AC004801  
 R-Y79AA1001105//Staphylococcus epidermidis trimethoprim resistance plasmid pSK639//0.0072:309:63//U40259  
 R-Y79AA1001145//RPCI11-59N12.TK RPCI11 Homo sapiens genomic clone R-59N12, genomic survey se-  
 quence.//3.7e-07:256:64//AQ200068  
 30 R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15,  
 WORKING DRAFT SEQUENCE.//0.55:223:61//AP000012  
 R-Y79AA1001177//Human gene for Gi3 alpha protein, intron 7 through exon 9, variant U6 gene, and snRNP E  
 protein pseudogene LH87.//7.0e-09:203:69//X54048  
 R-Y79AA1001185  
 35 R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Li-  
 brary) complete sequence.//2.1e-32:277:81//AC005912  
 R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.98:325:59//U47924  
 R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence.//  
 0.0034:378:59//AB018112  
 40 R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.19:  
 106:72//AC004988  
 R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and  
 IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//3.4e-109:549:95//AJ005892  
 R-Y79AA1001281  
 45 R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y17126  
 R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymerase pseudogene, partial cds.//  
 0.0070:284:58//U45372  
 R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.//0.11:125:70//  
 AL025355  
 50 R-Y79AA1001384//W.makrui mitochondrial CYTB and tRNA genes.//0.070:209:65//X66594  
 R-Y79AA1001391//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING  
 DRAFT SEQUENCE.//0.80:163:62//AL031745  
 R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.99:241:  
 63//AC004221  
 55 R-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library)  
 complete sequence.//0.25:81:80//AC005924  
 R-Y79AA1001493  
 R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,

complete sequence.//1.3e-35:207:95//AL034430  
R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.7e-44:285:  
81//D14336  
R-nnnnnnnnnnnn//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a  
5 putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574  
R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151  
R-Y79AA1001555  
R-Y79AA1001585  
R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X; contains STS.//6.6e-19:241:76//  
10 Z94722  
R-Y79AA1001603//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72f8, forward read cpg72f8.ft1a.//  
3.3e-21:131:96//Z62766  
R-Y79AA1001613  
R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromo-  
15 some X.//6.3e-08:338:63//Z82975  
R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15,  
WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008  
R-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743  
R-nnnnnnnnnnnn//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//  
20 0.013:64:89//AQ052792  
R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178  
R-Y79AA1001705  
R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139  
R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:  
25 57//AE001402  
R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING  
DRAFT SEQUENCE.//2.8e-05:329:61//Z98044  
R-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//2.3e-90:557:89//U74297  
R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the  
30 SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2  
and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//  
2.1e-34:306:78//Z95152  
R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I14369  
R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//  
35 0.0089:527:58//AB016874  
R-Y79AA1001874  
R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X89650  
R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alterna-  
40 tively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin,  
subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs,  
complete sequence.//1.0:138:68//AL022577  
R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.71:153:67//X04465  
R-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 172B20, WORKING  
45 DRAFT SEQUENCE.//1.0:178:64//AL022319  
R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.3e-  
49:377:81//AC005011  
R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-32:174:99//L77612  
R-Y79AA1002103//CIT-HSP-2328I21.TR CIT-HSP Homo sapiens genomic clone 2328I21, genomic survey se-  
50 quence.//1.9e-44:245:96//AQ044502  
R-Y79AA1002115//CITBI-E1-2514F10.TF CITBI-E1 Homo sapiens genomic clone 2514F10, genomic survey se-  
quence.//1.8e-24:249:78//AQ265752  
R-Y79AA1002125//RPCI11-15J6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15J6, genomic survey se-  
quence.//8.5e-21:147:91//B75354  
R-Y79AA1002139  
55 R-Y79AA1002204  
R-nnnnnnnnnnnn//Human ankyrin G (ANK-3) mRNA, complete cds.//0.040:319:59//U13616  
R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4).//0.99:106:65//X65415  
R-Y79AA1002210

R-Y79AA1002211//H.sapiens NGAL gene./.1.0:311:59//X99133  
R-Y79AA1002220//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
DRAFT SEQUENCE./.5.9e-07:535:57//AL034557  
R-Y79AA1002229  
5 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds./.6.1e-117:564:98//AB014592  
R-Y79AA1002246  
R-Y79AAI002258//Homo sapiens mRNA for HIP3, complete cds./.1.3e-92:453:97//AB013384  
R-Y79AA1002298//HS\_3071\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3071 Col=16 Row=J, genomic survey sequence./.1.9e-56:384:87//AQ171331  
10 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds./.2.5e-108:403:99//AB014534  
R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173I12 map 10q25, complete sequence./.  
1.1e-07:368:61//AC005887  
R-Y79AA1002351  
R-Y79AA1002361//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65b9, reverse read cpg65b9.rt1a./.  
15 0.57:59:79//Z62206  
R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence./.2.0e-98:385:99//  
AC005920  
R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence./.5.4e-59:490:  
76//AC004662  
20 R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete se-  
quence./.6.3e-08:103:80//AC004087  
R-Y79AA1002431  
R-nnnnnnnnnnnn//Mouse transcriptional control element./.0.064:84:71//M17284  
R-Y79AA1002472//Homo sapiens chromosome 19, BAC CTY-B-393i15 (BC301323), complete sequence./.1.6e-  
25 103:525:96//AC006116  
R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence./.9.7e-38:302:  
83//AC006238  
R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

## 30 Homology Search Result Data 4.

[0307] The result of the homology search of the Human Unigene using the clone sequence of 5'-end.

[0308] Data include

35 the name of clone,  
title of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the Accession No. of the top hit data, as in the order separated by //.

40 [0309] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069  
F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:  
L40157  
45 F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668  
F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078  
F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247  
F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharo-  
myces cerevisiae]//0.00019:192:65//Hs.7900:W22411  
50 F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759  
F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910  
F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734  
F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:  
342:61//Hs.14207:U86453  
55 F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8e-169:791:98//Hs.27197:  
AB018340  
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200  
F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//

Hs.135552:AI215187  
F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//2.1e-07:265:63//Hs.85313:  
AF071309

5 F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079  
F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [H.sapiens]//  
1.3e-18:111:96//Hs.163863:W28729

F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125:68//Hs.78909:U07802  
F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:AI240133  
F-HEMBA1000201//Human In1 mRNA, complete cds//6.5e-75:440:92//Hs.155626:U04847

10 F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529  
F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//Hs.8136:U81984  
F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, complete cds//1.3e-05:311:  
64//Hs.81248:U63289

F-HEMBA1000231  
15 F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377  
F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703  
F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460  
F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562  
F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568

20 F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186  
F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406  
F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664  
F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:AI206095

F-HEMBA1000303  
25 F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946  
F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:AI124898  
F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965  
F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//Hs.79299:D86961  
F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317:80//Hs.  
30 99189:X84712

F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frames//0.020:334:59//Hs.23094:M19503  
F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61//Hs.78344:AF001548  
F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802

35 F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:78//Hs.154326:D42087  
F-HEMBA1000366//ESTs//0.025 :56:87//Hs.141629:H74010  
F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433:58//Hs.159899:AC004853  
F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878  
F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320

40 F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15//2.3e-141:712:95//Hs.22900:AC004520  
F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//Hs.139088:AF070533  
F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.2e-26:351:70//Hs.138992:C14008  
F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915  
F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:AI079253  
F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:A1032875

45 F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//7.6e-31:616:66//Hs.  
159897:AB007970  
F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034  
F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398  
F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.37953:X66893

50 F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:AI032875  
F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590  
F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853  
F-HEMBA1000469  
F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//  
0.15:253:58//Hs.104640:AF000561  
F-HEMBA1000490//Homo sapiens kinectin mRNA, complete cds//0.71:539:56//Hs.82709:Z22551  
F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970  
F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312:77//Hs.5247:AF029750

F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)//1.3e-08:57:100//Hs.155095:  
D13666  
F-HEMBA1000505//Homo sapiens KE04p mRNA, complete cds//1.0:197:62//Hs.131962:AF064093  
F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646  
5 F-HEMBA1000518  
F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:AI281881  
F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//2.9e-16:132:  
84//Hs.155871:AA533783  
F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//2.1e-25:192:  
10 87//Hs.22383:R51067  
F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H.sapiens]//2.4e-57:288:97//Hs.116022:  
AA455706  
F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:153:88//Hs.113283:AF018080  
F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809  
15 F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.088:581:57//Hs.65436:U24389  
F-HEMBA1000545//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//7.8e-106:731:83//Hs.139107:  
K00629  
F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//Hs.77495:D87684  
F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729  
20 F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8e-64:665:72//Hs.137168:  
AB018303  
F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:AI338977  
F-HEMBA1000568//EST//0.12:270:61//Hs.134833 :AI091046  
25 F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchored protein p137//3.8e-19:409:62//Hs.119283:Z48042  
F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681  
F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy chain [C.elegans]//7.7e-41:217:96//  
Hs.55084:AA479162  
F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-44:228:97//Hs.155218:  
AJ007509  
30 F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H.sapiens]//1.7e-27:463:65//Hs.13794:AA203241  
F-HEMBA1000594//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.0e-68:574:  
79//Hs.159176:U92019  
F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:AI092535  
35 F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7e-120:561:99//Hs.5003:AB007925  
F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68//Hs.153563:AF011333  
F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//7.4e-22:166:84//Hs.26252:  
AA643235  
F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1e-138:639:99//Hs.60103:  
AB014590  
40 F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174  
F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582  
F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:AI123912  
F-HEMBA1000673//H.sapiens mRNA for translin associated protein X//1.7e-47:366:79//Hs.96247:X95073  
F-HEMBA1000682//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878  
45 F-HEMBA1000686  
F-HEMBA1000702  
F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309  
F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:AI039850  
F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630  
50 F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:AI281881  
F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491  
F-HEMBA1000747  
F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:AI091568  
F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:H52716  
55 F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239  
F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803  
F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535216  
F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300

F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536  
 F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542  
 F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367  
 F-HEMBA1000843  
 5 F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X69962  
 F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572  
 F-HEMBA1000867  
 F-HEMBA1000869//ESTs//5.1 e-33:166:77//Hs.141186:R99609  
 F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237  
 10 F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047  
 F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660  
 F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154  
 F-HEMBA1000910//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z98046  
 15 F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537  
 F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142  
 F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:  
 20 AB011119  
 F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens]//9.4e-10:77:93//Hs.111445:H00596  
 F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens]//0.0039:54:92//Hs.58338:  
 25 AA609476  
 F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide-synthetase, phosphoribosylaminoimidazole synthetase//0.93:132:66//Hs.82285:X54199  
 F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//0.080:128:71//Hs.118972:AA761369  
 F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161  
 30 F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI127903  
 F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775  
 F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314  
 F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.3e-05:424:59//Hs.  
 35 159564:AF061936  
 F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.0036:389:60//Hs.  
 127338:AB007961  
 F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132  
 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895  
 F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835  
 40 F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.  
 46468:U45984  
 F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529  
 F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:  
 AB007937  
 45 F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572  
 F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238  
 F-HEMBA1001022  
 F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.  
 159897:AB007970  
 50 F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142  
 F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515  
 F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881  
 F-HEMBA1001052//EST//0.94:149:67//Hs.31216:AI017971  
 F-HEMBA1001059//N-ACETYLGLACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159479:  
 55 U06088  
 F-HEMBA1001060//ESTs//6.8e-14:150:78//Hs.24821:AA044813  
 F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420  
 F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//

Hs.147802:R71297  
F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172

5 F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248  
F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284  
F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017  
F-HEMBA1001099  
F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4-61:341:85//Hs.5247:AF029750

10 F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497  
F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940  
F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917  
F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747

15 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341  
F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582  
F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457  
F-HEMBA1041174//ESTs//1.4e-63:363:92//Hs.132798:AA922226  
F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//5.0e-54:555:71//Hs.55165:  
20 AA573499  
F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463  
P-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717  
F-HEMBA1001226//ESTs/1.9e-11:407:65//Hs.157977:AI369694  
F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748

25 F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058  
F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046  
F-HEMBA1001265  
F-HEMBA1001281  
F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155

30 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-30:530:64//Hs.154050:  
AC004131  
F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741  
F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs.155464:AF088219  
F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:AI129590

35 F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.  
120847:AA731201  
F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873  
F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301  
F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:  
40 L20861  
F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC  
REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108734:AI073427  
F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013  
F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569

45 F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//3.6e-105:  
516:97//Hs.9006:AF057358  
F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794  
F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074  
F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156

50 F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353  
F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-132:643:97//Hs.  
124217:AA020848  
F-HEMBA1001388  
F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660  
55 F-HEMBA1001398  
F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117  
F-HEMBA1001407//ESTs//10.53:390:57//Hs.150447:AI017798  
F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108

F-HEMBA1001413  
 F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605  
 F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040  
 F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726  
 5 F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-74:469:  
 80//Hs.1361:M55053  
 F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031  
 F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//6.8e-47:550:71//Hs.55165:  
 AA573499  
 10 F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIPA1) mRNA, complete cds//0.82:312:58//Hs.  
 7019:AB005666  
 F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107  
 F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412  
 F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:88//Hs.40100:AB002390  
 15 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489:99//Hs.14409:  
 AB011144  
 F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451  
 F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219  
 F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054  
 20 F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-105:773:82//Hs.23094:  
 M19503  
 F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902  
 F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869  
 F-HEMBA1001526  
 25 F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476  
 F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580  
 F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652  
 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//  
 Hs.91589:M36205  
 30 F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814  
 F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:  
 AJ012449  
 F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184  
 F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228  
 35 F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988  
 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918  
 F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210  
 F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400  
 F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870  
 40 F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//  
 0.038:198:64//Hs.34579:AI338536  
 F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899  
 F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204  
 F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560  
 45 F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283  
 F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121  
 F-HEMBA1001661  
 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:  
 669:99//Hs.107254:AC005943  
 50 F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-57:447:79//Hs.  
 158095:AB007953  
 F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788  
 F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060  
 F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760  
 55 F-HEMBA1001709//EST//0.85:131:65//Hs.131451:AI023995  
 F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:AI302836  
 F-HEMBA1001712//EST//0.26:214:59//Hs.159088:AI383114  
 F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus nor-

vegicus]]/3.0e-30:195:92//Hs.132948:AA194452  
 F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554  
 F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101524:U58197  
 F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363  
 5 F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415  
 F-HEMBA1001744//EST//8.7e-77:420:92//Hs.133226:AI052250  
 F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37:300:62//Hs.10887:AB013924  
 F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328  
 F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//0.76:218:60//Hs.135553:  
 10 N41598  
 F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//Hs.98776:AC005622  
 F-HEMBA1001784//Homo sapiens mRNA for KJAA0474 protein, complete cds//6.4e-09:265:67//Hs.158232:  
 AB007943  
 F-HEMBA1001791  
 15 F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570  
 F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817  
 F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.8e-07:439:59//Hs.266:U06233  
 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//2.-5e-175:809:98//Hs.  
 20 118164:AB007969  
 F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305  
 F-HEMBA1001815  
 F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//4.9e-80:842:70//Hs.  
 158174:U66561  
 F-HEMBA1001820//EST//0.057:214:62//Hs.148715:A1223845  
 25 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//6.7e-42:510:65//Hs.66392:  
 AF064244  
 F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//5.2e-13:253:68//Hs.85313:  
 AF071309  
 F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//Hs.6151:D87078  
 30 F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.155243:N70293  
 F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:68//Hs.6833:AB002324  
 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.8e-185:865:98//Hs.78946:  
 AB014517  
 F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121  
 35 F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE  
 PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:AI141922  
 F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:367:95//Hs.15423:T84036  
 F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//5.4e-86:835:76//Hs.  
 158095:AB007953  
 40 F-HEMBA1001896  
 F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//0.43:114:71//Hs.6133:U94346  
 F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633  
 F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:  
 200:62//Hs.9573:AF027302  
 45 F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511  
 F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141  
 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:  
 855:99//Hs.154934:AF000145  
 F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295  
 50 F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221  
 F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882  
 F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943  
 F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360  
 F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.30:85:69//  
 55 Hs.25674:AF072242  
 F-HEMBA1001962//ESTs//0.0012:289:59//Hs.125492:AA938930  
 F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708  
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/

Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178  
 F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732  
 F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100  
 5 F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581  
 F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//9.8e-09:294:63//  
 Hs.99936:X14487  
 F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803 :W63582  
 10 F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867:  
 M93426  
 F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907  
 F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827  
 F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057  
 15 F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-26:  
 223:81//Hs.105292:AA504776  
 F-HEMBA1002084  
 F-HEMBA1002092  
 F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds//5.6e-21:  
 124:96//Hs.101842:L32832  
 20 F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09:434:62//Hs.135102:AI190276  
 F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973  
 F-HEMBA1002119  
 F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802  
 F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393  
 25 F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:D86980  
 F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:62//Hs.23741:AB018263  
 F-HEMBA1002151  
 F-HEMBA1002153//EST//10.014:328:60//Hs.149115:AI244695  
 30 F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-49:303:79//Hs.  
 158241:AB007976  
 F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:67//Hs.929:M57965  
 F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:AJ007590  
 F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:AF088219  
 35 F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:AF026245  
 F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141  
 F-HEMBA1002189//EST//5.1 e-24:193:81//Hs.163161:AA778363  
 F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.27:382:59//Hs.21992:AB014589  
 F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs.  
 159897:AB007970  
 40 F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696  
 F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767  
 F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.59906:  
 AA001281  
 F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs.  
 45 67619:AB007957  
 F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394  
 F-HEMBA1002237//EST//0.044:1 37:66//Hs.144448:AA812455  
 F-HEMBA1002241  
 F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887  
 50 F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.1e-152:731:97//Hs.  
 159564:AF061936  
 F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420  
 F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//1.0:395:60//  
 Hs.150926:AF017445  
 55 F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404  
 F-HEMBA1002321//Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds//0.17:338:60//  
 Hs.77729:AB010710  
 F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982

- F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087  
 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314  
 F-HEMBA10023481//EST//1.0e-19:285:70/Ms.121860:AA776692  
 F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996  
 5 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:  
 872:99//Hs.119023:AF092563  
 F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216  
 F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144  
 F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954  
 10 F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE  
 BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141  
 F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U79289  
 F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:  
 111:67//Hs.162154:AA528561  
 15 F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121:  
 W26490  
 F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160  
 F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, com-  
 20 plete cds//0.00024:240:64//Hs.113286:U77783  
 F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912  
 F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508  
 F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:83//Hs.6189:AB011133  
 F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235  
 F-HEMBA1002495  
 25 F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161  
 F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173  
 F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080  
 F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.Oe-159:738:98//Hs.  
 6764:AJ011972  
 30 F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795  
 F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951  
 F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-46:238:87//Hs.  
 10458:AF088219  
 F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:98//Hs.68900:AF016903  
 35 F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:U31875  
 F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:57//Hs.20912:AB012162  
 F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205  
 F-HEMBA1002561//Humanclone 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:U90905  
 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-142:457:99//Hs.  
 40 151411:AF075587  
 F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//2.8e-30:156:  
 100//Hs.32170:AB015132  
 F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159  
 F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363  
 45 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:  
 AB011169  
 F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013  
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:  
 AB018351  
 50 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334  
 F-HEMBA1002629//Human density enhanced phosphatase 1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:  
 U10886  
 F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390  
 F-HEMBA1002651  
 55 F-HEMBA1002659//Human vascular endothelial growth factor related protein VRP mRNA, complete cds//0.74:  
 223:60//Hs.79141:U43142  
 F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094:  
 M19503

F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497  
 F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368  
 F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)//0.00096:418:61//Hs.1323:S42457  
 5 F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.8e-11:541:601//Hs.124161:AF065164  
 F-HEMBA10026961//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647:AC004221  
 10 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924  
 F-HEMBA1002712  
 F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800  
 F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521  
 15 F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811:AB007867  
 F-HEMBA1002742//EST//0.97:138:60//Hs.160545:71596  
 F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372  
 F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786  
 20 F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817  
 F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126  
 F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947  
 F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:  
 25 59//Hs.128208:U63809  
 F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392  
 F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326  
 F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756  
 F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938  
 30 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185  
 F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744  
 F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119  
 F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:M279904  
 35 F-HEMBA1002833  
 F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550  
 F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823  
 F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME  
 II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730  
 40 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AE79429  
 F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679  
 F-HEMBA1002921  
 F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001  
 F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915  
 45 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148  
 F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:GenBank Accession Number  
 M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053  
 F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703  
 50 F-HEMBA1002944//Human putative endothelin receptor type B-like protein mRNA, complete cds//0.83:326:58//  
 Hs.27747:U87460  
 F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.26762:AA913925  
 F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099  
 F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092  
 55 F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828  
 F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219  
 F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)  
 //1.5e-37:247:89//Hs.188:L20971

F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.7e-05:797:  
 58//Hs.50758:AF092564  
 F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525  
 F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs.155464:AF088219  
 5 F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486  
 F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:330:78//Hs.113283:AF018080  
 F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.159425:AJ001454  
 F-HEMBA1003037//EST//0.53:59:74//Hs.148011:M268003  
 F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:337:95//Hs.I05907:AA186514  
 10 F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//3.2e-  
 166:777:98//Hs.44097:AF054182  
 F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438  
 F-HEMBA1003067  
 F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.5e-15:611:  
 15 59//Hs.124161:AF065164  
 F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865  
 F-HEMBA1003078//CYTOCHROME P450 1VF3//2.0e-29:452:67//Hs.106242:AB002454  
 F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461  
 F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881  
 20 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721  
 F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.musculus]//0.98:216:61//Hs.97865:  
 AA405872  
 F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721  
 F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802  
 25 F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575  
 F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314  
 F-HEMBA1003136  
 F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279  
 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670  
 30 F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.I41874:  
 AB014588  
 F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740  
 F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs.  
 II8831:AA211895  
 35 F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523  
 F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135  
 F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412  
 F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:154:85//Hs.113283:AF018080  
 F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765  
 40 F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784  
 F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310  
 F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012  
 F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.00054:432:58//Hs.I32206:  
 AF039694  
 45 F-HEMBA1003250  
 F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64//Hs.  
 49585:AF075292  
 F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991  
 F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020  
 50 F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864  
 F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867  
 F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds//2.9e-  
 146:539:97//Hs.13225:AF038662  
 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.6e-167:799:98//Hs.12836:  
 AB011109  
 F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912  
 F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160  
 F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.I05486:AA521012

F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189:865:99//Hs.124224:AB001872  
 F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:X99459  
 F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254  
 5 F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328  
 F-HEMBA1003330  
 F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:78//Hs.146395:AB002329  
 F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092  
 10 F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159  
 F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819  
 F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637  
 F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017  
 F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552  
 15 F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488  
 F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813  
 F-HEMBA1003403//Adducin 2 (beta) {alternative products }//5.0e-05:445:61//Hs.90951:U43959  
 F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309  
 F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-20 05:541:58//Hs.89709:L35546  
 F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962  
 F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:686:99//Hs.25812:AF058696  
 F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60//Hs.47822:AB002378  
 F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08:775:58//Hs.3847:U59632  
 25 F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578  
 F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16:321:60//Hs.13999:AB014600  
 F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443  
 F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:78//Hs.22271:D26067  
 F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811  
 30 F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5.0e-75:736:73//Hs.505:U07559  
 F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311  
 F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6e-33:562:64//Hs.81469:U01833  
 F-HEMBA1003556  
 F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122  
 35 F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327  
 F-HEMBA1003569//Human metastasis-associated mta1 mRNA, complete cds//2.0e-58:455:66//Hs.101448:U35113  
 F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972  
 F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546  
 40 F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:108:99//Hs.18420:AA599232  
 F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:92//Hs.57937:W68285  
 F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405  
 F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827  
 45 F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916  
 F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782  
 F-HEMBA1003617//Homo sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344  
 F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//50 4.4e-16:161:78//Hs.111323:AF077954  
 F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750  
 F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159  
 F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591  
 55 F-HEMBA1003640//ESTs//1.1e-11:267:661//Hs.34359:AI122791  
 F-HEMBA1003645  
 F-HEMBA1003646  
 F-HEMBA1003656

F-HEMBA1003662  
F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381  
F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906  
F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204  
5 F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//1.6e-100:478:98//Hs.118866:AI017072  
F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691  
F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187  
F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254:62//Hs.32316:AB011116  
10 F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995  
F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760  
F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//Hs.91916:AF035317  
F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921  
F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839  
15 F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102:753:81//Hs.23094:M19503  
F-HEMBA1003742//Homo sapiens chromosome 19, cosmid R31180//0.16:242:62//Hs.153325:AC005390  
F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946  
20 F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//Hs.8136:U81984  
F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920  
F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//1.7e-24:224:81//Hs.18171:AA524327  
F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172  
F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064  
25 F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.13:222:61//Hs.89230:AF031815  
F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239  
F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:M88108  
F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721  
30 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3e-85:586:87//Hs.6051:AB014516  
F-HEMBA1003836//EST//6.8e-06:98:74//Hs.I45447:AI204220  
F-HEMBA1003838//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//3.8e-40:151:88//Hs.139007:H74314  
F-HEMBA1003856//ESTs//8.6e-53286:95//Hs.116645:AI005167  
35 F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66//Hs.21355:AB002367  
F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.3e-30:580:63//Hs.27621:U52840  
F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.89563:D32002  
F-HEMBA1003880  
40 F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2e-18:302:67//Hs.23711:AB018295  
F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGEN-IC REGION [S.cerevisiae]//1.2e-49:295:92//Hs.114673:W72675  
F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236  
F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.081:345:58//Hs.78494:AB011097  
45 F-HEMBA1003926//EST//2.5e-32:253 :83//Hs.132635:AI032875  
F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:69//Hs.154668:AB002389  
F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562  
F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]//0.0029:222:61//Hs.I44236:W52380  
F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055  
50 F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:66//Hs.2076:M29580  
F-HEMBA1003958//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//2.1e-44:243:76//Hs.91146:N73230  
F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567  
F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI138965  
55 F-HEMBA1003978  
F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009  
F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456  
F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//

0.022:349:58//Hs.104640:AF000561  
 F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468  
 F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493  
 F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573  
 5 F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:AI379721  
 F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.2e-51:359:84//Hs.I5519:  
 AB018315  
 F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:AI239930  
 F-HEMBA1004042//EST//0.00088:272:6I//Hs.155763:AI312281  
 10 F-HEMBA1004045//EST//2.7e-20:408:66//Hs.I62529:AA584160  
 F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M60315  
 F-HEMBA1004049//ESTs//8.1e-68:430:86/Jhs.146307:AA584638  
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457:58//Hs.82837:L13435  
 F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.5e-46:199:80//Hs.  
 15 46328:D87942  
 F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426  
 F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107  
 F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M28713  
 F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.3e-39:335:79//Hs.  
 20 46468:U45984  
 F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610:61//Hs.80712:D86957  
 F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064  
 F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:AI419759  
 F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.00055:343:62//Hs.5923:X82260  
 25 F-HEMBA1004143  
 F-HEMBA1004146  
 F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI186056  
 F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.8e-15:591:60//Hs.159277:  
 AB018341  
 30 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649:97//Hs.59988:AF067855  
 F-HEMBA1004199  
 F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:AI375427  
 F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.2e-35:205:94//Hs.  
 10092:AI189282  
 35 F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040  
 F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748  
 F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514  
 F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans]//0.012:156:67//Hs.I63588:AI073878  
 F-HEMBA1004238  
 40 F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571  
 F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522  
 F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds//1.1e-28:295:72//Hs.  
 56205:U96876  
 F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553:60//Hs.83634:U52112  
 45 F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.9e-73:490:77//Hs.141874:  
 AB014588  
 F-HEMBA1004272  
 F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444  
 F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118:65//Hs.155313:AB002331  
 50 F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.0:364:56//Hs.118738:AB018343  
 F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.9e-187:868:  
 99//Hs.101766:AF022795  
 F-HEMBA1004289  
 F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484  
 55 F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:AI270047  
 F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:AI336314  
 F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452:65//Hs.69740:U09367  
 F-HEMBA1004323//EST//0.44:134:64//Hs.145464:AI204532

F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.017:209:64//Hs.43627:U35612  
 F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062  
 F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888  
 5 F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.49:80:73//Hs.139648:AB014606  
 F-HEMBA1004341  
 F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//2.7e-39:270:86//Hs.80686:D89667  
 F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3e-46:190:92//Hs.27424:U75968  
 10 F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.3022:D85376  
 F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928  
 F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800  
 F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019  
 15 F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250  
 F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818  
 F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199  
 F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin. [H.sapiens]/1.4e-20:144:  
 20 88//HS.121076:AI246426  
 F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype includ-  
 ed)//4.8e-18:248:72//Hs.69747:M35531  
 F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219  
 F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080  
 F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606  
 25 F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984  
 F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450  
 F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600  
 F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431  
 F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-89:758:76//Hs.23094:M19503  
 30 F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans]/1.4e-61:296:99//Hs.114622:AA693492  
 F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:  
 265:61//Hs.43543:AF042800  
 F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:X53416  
 F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381  
 35 F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552  
 F-HEMBA1004554  
 F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331  
 F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802  
 F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]/1.2e-17:334:67//Hs.24536:  
 40 AA479825  
 F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1 e-35:337:78//Hs.78160:AF010238  
 F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661  
 F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds//0.42:186:  
 66//Hs.84136:1170370  
 45 F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-  
 16:297:68//Hs.106008:AA147606  
 F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198  
 F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178  
 F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416  
 50 F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891  
 F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780  
 F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522  
 F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083  
 F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796  
 55 F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582  
 F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141  
 F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252  
 F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.64:313:61//Hs.118578:X80821

F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892  
 F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515  
 F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019  
 F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903  
 5 F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874:  
 AA524909  
 F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515  
 F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004  
 10 F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503  
 F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813  
 F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504  
 F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:  
 AB006626  
 15 F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.153563:AF011333  
 F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082  
 F-HEMBA1004758//Homosapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:  
 L39060  
 F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.155657:M61120  
 20 F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-115:909:78//Hs.23094:  
 M19503  
 F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139  
 F-HEMBA1004771  
 25 F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//  
 Hs.62004:AF039235  
 F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106  
 F-HEMBA1004795  
 F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952  
 F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971  
 30 F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:  
 171:92//Hs.134510:L01042  
 F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646  
 F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481  
 F-HEMBA1004847//ESTs//2.1 e-09:66:98//Hs.158161:AA312511  
 35 F-HEMBA1004850//EST//0.033:253:64//Hs.158782:A376601  
 F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150  
 F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:  
 AA446987  
 F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077  
 40 F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633  
 F-HEMBA1004889//Growth arrest-specific II//0.20:146:68//Hs.65029:L13698  
 F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304  
 F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106  
 F-HEMBA1004918//EST//0.78:122:61//Hs.145491:AI254348  
 45 F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172  
 F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947  
 F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959  
 F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//  
 0.11:182:65//Hs.105932:U89331  
 50 F-HEMBA1004934  
 F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981  
 F-HEMBA1004954//ESTs//0.0i4:404:60//Hs.11177:AA417813  
 F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478  
 F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274  
 55 F-HEMBA1004972  
 F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:  
 AB007914  
 F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946

F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013  
 F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750  
 F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589  
 F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026  
 5 F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429  
 F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356  
 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:  
 AB014548  
 F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560  
 10 F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III  
 [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237  
 F-HEMBA1005039//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627  
 F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs.  
 15 100602:AF010193  
 F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802  
 F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462  
 F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//  
 20 1.5e-59:411:85//Hs.129727:AF035587  
 F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381  
 F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid  
 dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785  
 F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:  
 25 631:59//Hs.27910:AF049105  
 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:  
 AF080561  
 F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916  
 F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304  
 F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106  
 F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875  
 30 F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021  
 F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216  
 F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914  
 F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197  
 F-HEMBA1005202  
 35 F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436  
 F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547  
 F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081  
 F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302  
 F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399:79//Hs.  
 40 129735:AF010144  
 F-HEMBA1005244//ESTs//2.5e-14:85:10011Hs.128744:AI191922  
 F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896  
 F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705:98//Hs.72660:  
 AB011157  
 45 F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380  
 F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777  
 F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//Hs.12451:U97018  
 F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232  
 F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs.155464:AF088219  
 50 F-HEMBA1005311  
 F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516  
 F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615  
 F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117  
 F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310:63//Hs.111597:U68723  
 55 F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:97//Hs.29361:AJ007581  
 F-HEMBA1005353//EST//5.4e-09:2-22:68//Hs.119508:AA485732  
 F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88//Hs.151689:U09414  
 F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572:73//Hs.43265:

AF071787  
F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905  
F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs.154069:U06452  
5 F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI93053  
F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA80448  
F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans]//1.0e-130:620:98//Hs.108990:N25951  
10 F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans]//7.7e-151:727:97//Hs.17118:AI033807  
F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513  
F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347  
F-HEMBA1005411  
15 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248  
F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323  
F-HEMBA1005443//Zinc finger protein 157 (ZFP157) mRNA//9.0e-34:259:72//Hs.89897:U28687  
F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783  
20 F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107  
F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:L37368  
F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481:92//Hs.23094:M19503  
F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219  
25 F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:AF039694  
F-HEMBA1005497//Glucocorticoid receptor alpha { alternative products}//8.7e-41:588:69//Hs.102761:U25029  
F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318:73//Hs.159530:AC004957  
30 F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635  
F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911  
F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353  
F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220  
35 F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56//Hs.143551:AF048693  
F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575  
F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:AF057280  
F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs.155464:AF088219  
40 F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs.17035:AI080471  
F-HEMBA1005530  
F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376  
45 F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461  
F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903  
F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257  
F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507  
50 F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:AB007932  
F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873  
F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538  
F-HEMBA1005582  
55 F-HEMBA1005583  
F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381  
F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS//0.54:439:591:Hs.2137:D49357  
F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323

F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609  
 F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982  
 F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:  
 AF057280  
 5 F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//1.8e-89:454:96//Hs.19400:  
 AA662845  
 F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535  
 F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734  
 F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199  
 10 F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956  
 F-HEMBA1005666  
 F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:  
 AB011142  
 F-HEMBA1005679//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629  
 15 F-HEMBA1005680  
 F-HEMBA1005685  
 F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-  
 71:497:85//Hs.26988:U66406  
 F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678  
 20 F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143  
 F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltrans-  
 ferase, geranyltransferase)//2.6e-20:151:88//Hs.77393:D14697  
 F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754  
 F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024  
 25 F-HEMBA1005755//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627  
 F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219  
 F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141  
 F-HEMBA10058131//ESTs//0.012:209:63//Hs.113365:R77747  
 30 F-HEMBA1005815//Human calpain-like protease (htr-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346  
 F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577  
 F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788  
 F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9e-42:690:66//Hs.23094:M19503  
 F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//Hs.79706:U53204  
 F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150  
 35 F-HEMBA1005884//Homosapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.  
 158095:AB007953  
 F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097  
 F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.  
 46468:U45984  
 40 F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766  
 F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081  
 F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//  
 2.0e-46:434:78//Hs.125231:AF068006  
 F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]//1.2e-46:228:100//Hs.  
 45 152178:AI224880  
 F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588  
 F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883  
 F-HEMBA1005963  
 F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.  
 50 26285:AF082516  
 F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530  
 F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526  
 F-HEMBA1006002  
 F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151  
 55 F-HEMBA1006031  
 F-HEMBA1006035  
 F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080  
 F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.41186:R99609

F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.43321:AI139422  
 F-HEMBA1006081  
 F-HEMBA1006090//EST//1.2e-12:340:62//Hs.61195:AI418788  
 F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313  
 5 F-HEMBA1006100//ESTs//7.1 e-22:273:73//Hs.144407:AA737799  
 F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741  
 F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968  
 F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222  
 F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372  
 10 F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734  
 F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881  
 F-HEMBA1006155  
 F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575  
 F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627  
 15 F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117  
 F-HEMBA1006198//ESTs//0.017:133 :67//Hs.142168:AA292540  
 F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98//Hs.109268:AF070557  
 F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.7647:M94046  
 F-HEMBA1006252  
 20 F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706  
 F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158:69//Hs.159277:  
 AB018341  
 F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631  
 F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140  
 25 F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770  
 F-HEMBA1006283  
 F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964  
 F-HEMBA1006291  
 F-HEMBA1006293  
 30 F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//  
 Hs.46465:U45285  
 F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637:68//Hs.37656:AB011174  
 F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350  
 F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789  
 35 F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142  
 F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.  
 22767:N99220  
 F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287  
 F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107:X59244  
 40 F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026  
 F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422:59//Hs.  
 80667:AF010233  
 F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:  
 265:61//Hs.8813:AF032922  
 45 F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531  
 F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503  
 F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477  
 F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881  
 F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830  
 50 F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835  
 F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264  
 F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194  
 F-HEMBA1006445  
 F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889  
 55 F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124:AF019369  
 F-HEMBA1006467  
 F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:AI091453  
 F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Bornavirus]//1.1e-13:346:63//Hs.31257:

AA875998  
F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081  
F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532  
F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897  
5 F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.28621:AA910431  
F-HEMBA1006492  
F-HEMBA1006494//ESTs//8.5e -24:299:72//Hs.153413:AI248625  
F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389  
F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072  
10 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:  
AB014566  
F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483:97//  
Hs.94811:AA011185  
F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002  
15 F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI160081  
F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:  
654:98//Hs21301:AF093419  
F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638  
F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898  
20 F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425  
F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136  
F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.44372:AI346522  
F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479  
25 F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778  
F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219  
F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB018295  
F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862  
F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875  
30 F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC  
REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:AI391502  
F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI343331  
F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589  
F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:  
92//Hs.109818:AA411185  
35 F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:  
AA505003  
F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196:  
U40282  
F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:  
40 452:96//Hs.159574:AA190615  
F-HEMBA1006653  
F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189  
F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317  
45 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065  
F-HEMBA1006676  
F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575  
F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145  
F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198  
F-HEMBA1006708  
50 F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545  
F-HEMBA1006717//ESTs//12.6e-31:286:78//Hs.55573:W37226  
F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105  
F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087  
55 F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//  
2.0e-92:817:78//Hs.129727:AF035587  
F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576:56//Hs.149323:AB002325  
F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs141073:W72720  
F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657

F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250  
 F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798  
 F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503  
 F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298  
 5 F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III [C.elegans]//4.8e-110:523:98//Hs.125790:AA287723  
 F-HEMBA1006821//EST//5.1e-ll:246:66//Hs.150542:AI051551  
 F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624  
 F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970  
 10 F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327  
 F-HEMBA1006865  
 F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938  
 15 F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214  
 F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592  
 F-HEMBA1006914//EST//0.065 :366:6211Hs.162914:AA666199  
 F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989  
 F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154764:U16258  
 20 F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539  
 F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712  
 F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382  
 F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644:  
 AJ010841  
 25 F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6940:Z48633  
 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740:94//Hs.  
 14934:AF004828  
 F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase//1.9e-79:447:89//  
 Hs.75268:X74570  
 30 F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968  
 F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723  
 F-HEMBA1007002  
 F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282  
 F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827:  
 35 70//Hs.43003:AF035812  
 F-HEMBA1007045  
 F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659  
 F-HEMBA1007052  
 F-HEMBA1007062  
 40 F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212  
 F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845  
 F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:91//Hs.80510:  
 M74002  
 F-HEMBA1007080  
 45 F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:61//Hs.1974:M92432  
 F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541:  
 57//Hs.3828:U49260  
 F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595  
 F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354  
 50 F-HEMBA1007121//ESTs//3.Se-69:335:98//Hs.140519:AA643182  
 F-HEMBA1007129  
 F-HEMBA1007147//ESTs//3.2e-07:235:641//Hs.124813:W46172  
 F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136  
 F-HEMBA1007151  
 55 F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318:97//Hs.22396:AF062085  
 F-HEMBA1007178//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-  
 39:248:90//Hs.157148:AA311921  
 F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965

F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:98//Hs.3363:D86987  
 F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252  
 F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6e-177:839:98//Hs.27197:  
 5 AB018340  
 F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs.  
 82314:M31642  
 F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:U53204  
 F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:6411Hs.12432:AF070575  
 10 F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//0.99:239:60//Hs.111749:  
 U13695  
 F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836  
 F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:H06475  
 15 F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529  
 F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637  
 F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062  
 F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74615  
 F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506  
 F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634  
 20 F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241  
 F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens]//3.5e-09:144:76//Hs.20597:  
 W58370  
 F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130  
 F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006  
 25 F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561  
 F-HEMBB100005//ESTs//1.6e-07:337:60//Hs.126718:AA916568  
 F-HEMBB100008//H.sapiens mRNA for translin associated protein X//1.1e-43:370:78//Hs.96247:X95073  
 F-HEMBB100018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs.  
 83428:M58603  
 30 F-HEMBB1000024//EST//5.4e-07:137:70//Hs.125389:AA878307  
 F-HEMBB1000025//EST//0.99:362:58//Hs.121221:AA757392  
 F-HEMBB1000030//H.sapiens mRNA for cylcin II//1.3e-10:525:62//Hs.3232:Z46788  
 F-HEMBB1000036  
 F-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450:  
 35 98//Hs.20815:AF084928  
 F-HEMBB1000039//EST//0.0034:97:73//Hs.141684:W35358  
 F-HEMBB1000044//ESTs//0.0048:218:63//Hs.123161:AA807319  
 F-HEMBB1000048//EST//0.00025:222:62//Hs.122474:AA765131  
 F-HEMBB1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717  
 40 F-HEMBB1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3e-54:259:88//Hs.23094:M19503  
 F-HEMBB1000055//ESTs//0.0017:289:62//Hs.125755:AA286923  
 F-HEMBB1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs.93121:AB018304  
 F-HEMBB1000083  
 F-HEMBB1000089//EST//0.0016:192:661//Hs.137093:AA917621  
 45 F-HEMBB1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645  
 F-HEMBB1000103//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs.103948:K00627  
 F-HEMBB1000113//EST//4.6e-23:221:76//Hs.142065:AA173763  
 F-HEMBB1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521  
 F-HEMBB1000136//ESTs112.3e-101:507:96//Hs.12659:AA195207  
 50 F-HEMBB1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044  
 F-HEMBB1000144//EST//4.5e-52:298:91//Hs.149580:AI281881  
 F-HEMBB1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:X92715  
 F-HEMBB1000175//EST//1.0:101:65//Hs.162898:AA659646  
 F-HEMBB1000198//EST//0.99:179:56//Hs.116880:AA662457  
 55 F-HEMBB1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4e-15:139:82//Hs.101414:  
 AB011129  
 F-HEMBB1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277  
 F-HEMBB1000218//EST//0.11:136:63//Hs.134683:AI092013

F-HEMBB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962  
 F-HEMBB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612  
 F-HEMBB1000244//ESTs//3.2e-15:139:81//HS.134549:AI078483  
 F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:981/Hs.  
 5 151411:AF075587  
 F-HEMBB1000258//EST//0.0091:325:60//Hs.97533:AA435884  
 F-HEMBB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4e-33:100:100//Hs.27424:U75968  
 F-HEMBB1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.0019:373:60//Hs.  
 10 16533:D87930  
 F-HEMBB1000272//ESTs//1.3e-93:440:99//Hs.I09224:N46684  
 F-HEMBB1000274//ESTs//0.41:221:65//Hs.71990:AA151796  
 F-HEMBB1000284//EST//0.00024:108:73//Hs.100725:F13689  
 F-HEMBB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574  
 F-HEMBB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.00092:252:65//Hs.41153:  
 15 AB018326  
 F-HEMBB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787  
 F-HEMBB1000318//EST//0.014:184:61//Hs.155758:AI311870  
 F-HEMBB1000335//EST//0.99:187:63//Hs.137424:AA243729  
 F-HEMBB1000336//EST//1.0:209:63//Hs.150410:AI003611  
 20 F-HEMBB1000337//EST//0.086:133:66//Hs.128207:AA972330  
 F-HEMBB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127  
 F-HEMBB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:7611Hs.155464:AF088219  
 F-HEMBB1000341  
 F-HEMBB1000343//EST//0.66:163:63//Hs.150822:AI302729  
 25 F-HEMBB1000354//ESTs//7.e-61:292:100//Hs.152266:AA926874  
 F-HEMBB1000369//ESTs, Highly similar to t-BOP [M.musculus]//10.013:157:64//Hs.129982:AI420970  
 F-HEMBB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934  
 F-HEMBB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348  
 F-HEMBB1000391//ESTs//0.033:237:64//Hs.135289:AI092963  
 30 F-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4e-165:762:98//Hs.16184:AJ001642  
 F-HEMBB1000402//EST//0.013:291:59//Hs.149191:AI246155  
 F-HEMBB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194  
 F-HEMBB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925  
 F-HEMBB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.  
 35 129735AF010144  
 F-HEMBB1000438//ESTs//0.073:446:58//Hs.134632:AI223429  
 F-HEMBB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627  
 F-HEMBB1000449//EST//5.5e-21:356:671//Hs.157848:AI362501  
 F-HEMBB1000455//ESTs//0.092:147:65//Hs.106446:N93227  
 40 F-HEMBB1000472  
 F-HEMBB1000480//EST//0.98:83:71//Hs.146462:AI124898  
 F-HEMBB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206  
 F-HEMBB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560  
 F-HEMBB1000491  
 45 F-HEMBB1000493//ESTs//0.019:103:69//Hs.138358:T66178  
 F-HEMBB1000510//Glucocorticoid receptor alpha {alternative products} //1.6e-46:409:77//Hs.102761:U25029  
 F-HEMBB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413  
 F-HEMBB1000523//ESTs//0.69:332:59//Hg.106845:W19543  
 F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:  
 50 96//Hs.36131:Y11710  
 F-HEMBB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//7.7e-31:  
 554:67//Hs.157142:U85996  
 F-HEMBB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.  
 158095:AB007953  
 F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.0e-33:537:65//Hs.5444:  
 55 AB018293  
 F-HEMBB1000564  
 F-HEMBB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001

F-HEMBB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238  
 F-HEMBB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164,  
 DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533  
 F-HEMBB10005891//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091  
 5 F-HEMBB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990  
 F-HEMBB1000592//EST//0.0038:51:88//Hs.148022:AI269323  
 F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//Hs.3386:AF053356  
 F-HEMBB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589  
 F-HEMBB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809  
 10 F-HEMBB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864  
 F-HEMBB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI346481  
 F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349  
 F-HEMBB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075  
 F-HEMBB1000638//EST//0.0076:92:75//Hs.125496:AA883735  
 15 F-HEMBB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830  
 F-HEMBB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778  
 F-HEMBB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531  
 F-HEMBB1000665//EST//0.44:152:63//Hs.149534:AI280924  
 F-HEMBB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2e-79:280:85//Hs.23094:M19503  
 20 F-HEMBB1000673//ESTs//0.99:177:59//Hs.149864:N80474  
 F-HEMBB1000684//Protein kinase, interferon-inducible double stranded RNA dependent//2.6e-31:220:87//Hs.  
 73821:M35663  
 F-HEMBB1000693//Homo sapiens neuroanl mRNA, complete cds//5.3e-120:575:97//Hs.158300:AF040723  
 F-HEMBB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125  
 25 F-HEMBB1000706//EST//8.6e-14:373:61//Hs.138281:RS5703  
 F-HEMBB1000709//EST//0.99:110:651//Hs.162437:AA577510  
 F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56741  
 F-HEMBB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216  
 F-HEMBB1000738//EST//5.9e-13:259:64//Hs.159699:AI417328  
 30 F-HEMBB1000749//EST//3.1e-42:271:871//Hs.162197:AA535216  
 F-HEMBB1000763  
 F-HEMBB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:  
 72//Hs.38178:AA921830  
 F-HEMBB1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5 e-116:580:97//Hs.5009:AA081390  
 35 F-HEMBB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//Hs.86201:U78876  
 F-HEMBB1000789//Homosapiens mRNA for KIAA0677 protein, complete cds//3.0e-65:672:71//Hs.155983:  
 AB014577  
 F-HEMBB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI133727  
 F-HEMBB1000794//ESTs//0.00098:289:59//Hs.138782:N73572  
 40 F-HEMBB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI298375  
 F-HEMBB1000810//ESTs//0.038:92:71//Hs.148763:AA66887  
 F-HEMBB1000821//EST//0.94:129:62//Hs.162299:AA555154  
 F-HEMBB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421  
 F-HEMBB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI283069  
 45 F-HEMBB1000827  
 F-HEMBB1000831  
 F-HEMBB1000835//EST//4.3e-27:201:851//Hs.141451:N29915  
 F-HEMBB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948  
 F-HEMBB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-135:875:85//Hs.23094:  
 50 M19503  
 F-HEMBB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:61//Hs.311:U00238  
 F-HEMBB1000870//EST//0.00091:246:62//Hs.126502:AA913831  
 F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//Hs.128434:AF085351  
 F-HEMBB1000883//ESTs//0.42:107:67//Hs.154173:AI379823  
 55 F-HEMBB1000887  
 F-HEMBB1000888//ESTs//1.0:137:67//Hs.8121:AA521290  
 F-HEMBB1000890//ESTs//1.0:116:65//Hs.7105:T23433  
 F-HEMBB1000893//EST//0.0079:408:58//Hs.146504:AI129834

F-HEMBB1000908//EST//9.2e-21:205:79//Hs.132635:AI032875  
 F-HEMBB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//Hs.7938:D86984  
 F-HEMBB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049  
 F-HEMBB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI095468  
 5 F-HEMBB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089  
 F-HEMBB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593  
 F-HEMBB1000947  
 F-HEMBB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9.3e-48:572:72//Hs.2379:U23942  
 F-HEMBB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938  
 10 F-HEMBB1000975//ESTs//0.78:180:66//Hs.104789:AA417124  
 F-HEMBB1000981  
 F-HEMBB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs.122967:AF059569  
 F-HEMBB1000991//EST//0.12:125:66//Hs.22945:R43713  
 15 F-HEMBB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055  
 F-HEMBB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193:62//Hs.119004:AB014565  
 F-HEMBB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025  
 F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384:67//Hs.108604:  
 20 AC002310  
 F-HEMBB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991  
 F-HEMBB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247  
 F-HEMBB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61//Hs.129982:AI420970  
 F-HEMBB1001037//EST//0.0057:192:66//Hs.149987:AI291177  
 25 F-HEMBB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721  
 F-HEMBB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687:X96586  
 F-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149:96//Hs.15832:AB014518  
 F-HEMBB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs.155464:AF088219  
 30 F-HEMBB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942  
 F-HEMBB1001063  
 F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736:95//Hs.12953:AF034803  
 F-HEMBB1001096//EST//0.017:154:66//Hs.130403:AA909272  
 F-HEMBB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293  
 35 F-HEMBB1001105//Human BRCA2 region, mRNA sequence  
 CG016//0.30:84:75//Hs.112434:U50529  
 F-HEMBB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:R06800  
 F-HEMBB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062  
 40 F-HEMBB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139  
 F-HEMBB1001119  
 F-HEMBB1001126  
 F-HEMBB1001133//H.sapiens mRNA for translin associated protein X//1.2e-28:739:61//Hs.96247:X95073  
 F-HEMBB1001137  
 45 F-HEMBB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:69//Hs.146395:AB002329  
 F-HEMBB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854  
 F-HEMBB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716  
 F-HEMBB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863  
 F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334  
 50 F-HEMBB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183  
 F-HEMBB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129  
 F-HEMBB1001199  
 F-HEMBB1001208//ESTs//0.12:120:69//Hs.130093:AA928802  
 55 F-HEMBB1001209//EST//0.00028:215:65//Hs.118276:W15258  
 F-HEMBB1001210//EST//2.9e-05:297:60//Hs.88840:AA281452  
 F-HEMBB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157  
 F-HEMBB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.

158241:AB007976  
F-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]/6.7e-103:477:  
100//Hs.127835:AI378790

5 F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754  
F-HEMBB1001249//EST//0.26:203:63//Hs.140791:AA935909  
F-HEMBB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219  
F-HEMBB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977  
F-HEMBB1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//6.1e-24:146:  
78//Hs.51187:U82828

10 F-HEMBB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI359248  
F-HEMBB1001282//GA-binding protein transcription factor, beta subunit 2 (47kD)//0.39:531:57//Hs.78915:  
U13045  
F-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III  
[Caenorhabditis elegans]//4.9e-10:91:89//Hs.16606:W81021

15 F-HEMBB1001289//ESTs//6.4e-100:467:99//Hs.151720:AI287890  
F-HEMBB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]/1.3e-135:654:98//Hs.  
124217:AA020848  
F-HEMBB1001302  
F-HEMBB1001304//ESTs//0.98:109:68//Hs.138972:AA047725

20 F-HEMBB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339  
F-HEMBB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219  
F-HEMBB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503  
F-HEMBB1001326//ESTs//0.00030:257:63//Hs.62208:H12380  
F-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:87//Hs.43071:AA206222

25 F-HEMBB1001335  
F-HEMBB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:  
AB011135  
F-HEMBB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694  
F-HEMBB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878

30 F-HEMBB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:  
AB011142  
F-HEMBB1001356//EST//0.32:292:59//Hs.135771:AI005648  
F-HEMBB1001364  
F-HEMBB1001366//EST//7.8e-24:367:69//Hs.138765:N70347

35 F-HEMBB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219  
F-HEMBB1001369//EST//0.17:211:63//Hs.120066:AA707973  
F-HEMBB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:  
AB011099  
F-HEMBB1001384

40 F-HEMBB1001387//ESTs//0.61:215:60//Hs.145915:AI342230  
F-HEMBB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503  
F-HEMBB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:  
AF065988  
F-HEMBB1001424//EST//0.20:307:58//Hs.135336:AI049827

45 F-HEMBB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174  
F-HEMBB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]//5.5e-153:729:96//Hs.  
21679:AF034175  
F-HEMBB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345  
F-HEMBB1001443

50 F-HEMBB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:  
58//Hs.5462:AF007216  
F-HEMBB1001454//ESTs//1.4e-46:279:93//HS.104866:AA426038  
F-HEMBB1001458//EST//1.7e-09:106:83//Hs.141422:N20920  
F-HEMBB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220

55 F-HEMBB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740  
F-HEMBB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:  
AB018303  
F-HEMBB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088

F-HEMBB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.  
46328:D87942

F-HEMBB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815

F-HEMBB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735

5 F-HEMBB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093

F-HEMBB1001536//ESTs//0.0047:120:68//Hs.144858:R67748

F-HEMBB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-  
20:297:73//Hs.42457:AA523306

10 F-HEMBB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//  
Hs.102877:U41315

F-HEMBB1001562//ESTs//0.95:161:61//Hs.145075:AI208240

F-HEMBB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.  
15 158095:AB007953

F-HEMBB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080

F-HEMBB1001585

F-HEMBB1001586//EST//0.84:132:64//Hs.145264:AI218708

F-HEMBB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U79289

F-HEMBB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414

20 F-HEMBB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680

F-HEMBB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314

F-HEMBB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713

F-HEMBB1001635//ESTs//0.92:282:60//Hs.126980:AA934077

F-HEMBB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172

25 F-HEMBB1001641//EST//0.11:53:81//Hs.112445:AA594279

F-HEMBB1001653//EST//0.91:124:64//Hs.144213:T40480

F-HEMBB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:473:63//Hs.54481:  
D86407

F-HEMBB1001668//ESTs//0.94:83:69//Hs.146202:AI252519

30 F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:  
AB014546

F-HEMBB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:100//Hs.106104:AA599496

F-HEMBB1001685//EST//2.2e-05:112:73//Hs.130984:AI015430

F-HEMBB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664

35 F-HEMBB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398

F-HEMBB1001706

F-HEMBB1001707//EST//0.091:241:60//Hs.136830:AA769219

F-HEMBB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064

40 F-HEMBB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219

F-HEMBB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485:97//Hs.120581:W25578

F-HEMBB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244

F-HEMBB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.  
129735:AF010144

F-HEMBB1001753//ESTs//0.00013:35:100//Hs.139643:H06263

45 F-HEMBB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077

F-HEMBB1001760//ESTs//6.5e-06:503:58//Hs.21766:AI357639

F-HEMBB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.  
158241:AB007976

F-HEMBB1001785//EST//0.16:262:60//Hs.162526:AA584102

50 F-HEMBB1001797//ESTs//0.37:201:63//Hs.91559:AA806370

F-HEMBB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951

F-HEMBB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.  
92381:AB007956

F-HEMBB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017

55 F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//7.6e-  
164:763:98//Hs.159396:AF056209

F-HEMBB1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190

F-HEMBB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067

F-HEMBB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370

F-HEMBB1001850//EST//0.0035:204:61//Hs.7311:T23858  
 F-HEMBB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:82//Hs.155464:AF088219  
 F-HEMBB1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752  
 F-HEMBB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371  
 5 F-HEMBB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503  
 F-HEMBB1001872  
 F-HEMBB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923:Y12478  
 F-HEMBB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//0.32:346:60//Hs.  
 10 100555:X98743  
 F-HEMBB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868  
 F-HEMBB1001899//ESTs//0.17:242:62//Hs.136969:AA830918  
 F-HEMBB1001905  
 F-HEMBB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155  
 15 F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//1.2e-83:672:  
 81//Hs.82210:U47742  
 F-HEMBB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62//Hs.159777:Z19955  
 F-HEMBB1001911  
 F-HEMBB1001915//ESTs//0.92:136:71//Hs.144465:R68882  
 F-HEMBB1001921//EST//2.0e-19:398:67//Hs.44789:N36113  
 20 F-HEMBB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245  
 F-HEMBB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398  
 F-HEMBB1001930//EST//0.043:157:63//Hs.161927:AA483904  
 F-HEMBB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087  
 F-HEMBB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875  
 25 F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390  
 F-HEMBB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669  
 F-HEMBB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101  
 F-HEMBB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070  
 F-HEMBB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418  
 30 F-HEMBB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:  
 70//Hs.1361:M55053  
 F-HEMBB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969  
 F-HEMBB1001973//Myelin oligodendrocyte glycoprotein {alternative products} //2.1e-48:426:78//Hs.53217:  
 Z48051  
 35 F-HEMBB1001983  
 F-HEMBB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051  
 F-HEMBB1001990//ESTs//0.25:171:64//Hs.7961:AA401205  
 F-HEMBB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103  
 F-HEMBB1001997//EST//5.3e-33:294:76//Hs.161041:H82636  
 40 F-HEMBB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964  
 F-HEMBB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093  
 F-HEMBB1002009//ESTs//0.066:441:58//Hs.125313:AI201685  
 F-HEMBB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951  
 F-HEMBB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699  
 45 F-HEMBB1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:217:60//Hs.3487:AA425553  
 F-HEMBB1002044  
 F-HEMBB1002045  
 F-HEMBB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256  
 F-HEMBB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661  
 50 F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:  
 AB014512  
 F-HEMBB1002069  
 F-HEMBB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239  
 F-HEMBB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625  
 55 F-HEMBB1002115//EST//0.0083:244:64//Hs.125353:AA877080  
 F-HEMBB1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027  
 F-HEMBB1002139//ESTs//0.64:145:71//Hs.157821:AI362013  
 F-HEMBB1002142//ESTs//0.013:311:59//Hs.150037:AI292214

F-HEMBB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254  
 F-HEMBB1002189//EST//0.26:81:70//Hs.147726:AI220208  
 F-HEMBB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.16:608:58//Hs.4:X03350  
 F-HEMBB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//Hs.301:U18934  
 5 F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:405:67//Hs.104115:X52332  
 F-HEMBB1002218//EST//0.015:241:61//Hs.105298:AA489813  
 F-HEMBB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:AF088219  
 F-HEMBB1002247  
 10 F-HEMBB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//  
 6.8e-47:418:77//Hs.125231:AF068006  
 F-HEMBB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:77//Hs.154872:  
 AB011166  
 F-HEMBB1002255//ESTs//0.017:255:61//Hs.126786:U74314  
 F-HEMBB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete cds//0.17:511:57//  
 15 Hs.58169:AF017790  
 F-HEMBB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998  
 F-HEMBB1002300  
 F-HEMBB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-14:228:72//Hs.  
 46468:U45984  
 20 F-HEMBB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083  
 F-HEMBB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:96//Hs.105837:AA536054  
 F-HEMBB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188  
 F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:98//Hs.42644:  
 AJ010841  
 25 F-HEMBB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991  
 F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:  
 U00943  
 F-HEMBB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838  
 F-HEMBB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796  
 30 F-HEMBB1002381  
 F-HEMBB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566  
 F-HEMBB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784  
 F-HEMBB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456  
 35 F-HEMBB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.0e-32:371:73//Hs.  
 159897:AB007970  
 F-HEMBB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.54486:X54150  
 F-HEMBB1002442  
 F-HEMBB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:77//Hs.154326:D42087  
 F-HEMBB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101  
 40 F-HEMBB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274  
 F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-89:493:92//Hs.159605:U43885  
 F-HEMBB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds//0.019:228:63//  
 Hs.74304:AF001691  
 F-HEMBB1002492//EST//0.24:149:62//Hs.146790:AI149051  
 45 F-HEMBB1002495//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//1.3e-22:331:71//Hs.30:  
 M89796  
 F-HEMBB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494  
 F-HEMBB1002509//ESTs//0.017:220:63//Hs.155263:AI273725  
 F-HEMBB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354  
 50 F-HEMBB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-50:580:72//Hs.23094:M19503  
 F-HEMBB1002522//EST//0.010:172:62//Hs.147224:AI205719  
 F-HEMBB1002531  
 F-HEMBB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs.155464:AF088219  
 F-HEMBB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102  
 55 F-HEMBB1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648  
 F-HEMBB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191  
 F-HEMBB1002579//EST//1.0:77:68//Hs.147935:AI250286  
 F-HEMBB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095

F-HEMBB1002590//ESTs//0.64:132:63//Hs.155688:AI003657  
 F-HEMBB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336  
 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-152:710:98//Hs.129826:  
 AF089749  
 5 F-HEMBB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817  
 F-HEMBB1002603//EST//0.10:144:63//Hs.158180:AI367945  
 F-HEMBB1002607//ESTs//0.024:345:62//Hs.143304:AI084058  
 F-HEMBB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323  
 F-HEMBB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711  
 10 F-HEMBB1002614//ESTs//0.0048:136:71//Hs.106280:R13901  
 F-HEMBB1002617//EST//0.034:320:59//Hs.41223:H89127  
 F-HEMBB1002623//ESTs//0.88:222:60//Hs.129920:AA167217  
 F-HEMBB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs.151051:U07620  
 F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811  
 15 F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680  
 F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679  
 F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124  
 F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674  
 F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504  
 20 F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992  
 F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds//  
 0.059:297:62//Hs.158341:AF023614  
 F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588  
 F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC  
 25 REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs.20814:AI242922  
 F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729  
 F-MAMMA100009//Human c-yes-1mRNA//1.0e-48:447:77//Hs.75680:M15990  
 F-MAMMA100009  
 F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750  
 30 F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945  
 F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739  
 F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461  
 F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:  
 AA001281  
 35 F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-  
 50:367:75//Hs.133089:AF064019  
 F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840  
 F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067  
 F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:  
 40 AB011174  
 F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//  
 Hs.90357:U40705  
 F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:  
 AB011792  
 45 F-MAMMA1000117  
 F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508  
 F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402  
 F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319  
 F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843  
 50 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:  
 AB014585  
 F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:  
 219:87//Hs.129724:AF031924  
 F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050  
 55 F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695  
 F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530  
 F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657  
 F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739  
 F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035  
 F-MAMMA1000227//ESTs//0.010:268:60//Hs.16412:AA506926  
 F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913  
 5 F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873  
 F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587  
 F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543  
 F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015  
 F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874  
 10 F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087  
 F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726  
 F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361  
 F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505  
 F-MAMMA1000284  
 15 F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087  
 F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641  
 F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243  
 F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529  
 F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519  
 20 F-MAMMA1000313  
 F-MAMMA1000331  
 F-MAMMA1000339  
 F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963  
 25 F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892  
 F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.158095:AB007953  
 F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503  
 F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087  
 30 F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569  
 F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344  
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:98//Hs.32170:AB015132  
 F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590  
 35 F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503  
 F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:117:84//Hs.83916:U53468  
 F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725  
 F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092  
 40 F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111  
 F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532  
 F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:AF061573  
 45 F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459  
 F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641  
 F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:AF034546  
 F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830  
 50 F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:AB011166  
 F-MAMMA1000446  
 F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:93//Hs.9043:W21827  
 55 F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, complete cds//0.58:311:63//Hs.66721:D49818  
 F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830  
 F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830  
 F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948  
 F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482  
 F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219  
 5 F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878  
 F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352  
 F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497  
 F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352  
 F-MAMMA1000565  
 10 F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//5.8e-51:404:80//Hs.125231:AF068006  
 F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045  
 F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780  
 F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete 15 cds//8.8e-45:390:78//Hs.159523:AF001622  
 F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744  
 F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886  
 F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519  
 F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494  
 20 F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478  
 F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605  
 F-MAMMA1000623  
 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751  
 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial 25 cds//0.092:365:59//Hs.75474:AF023674  
 F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353  
 F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4),3' end//9.0e-30:531:64//Hs.139107:K00629  
 F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490  
 30 F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743  
 F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:U13220  
 F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627  
 F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081  
 35 F-MAMMA1000713//Acetylcholinesterase {I4-E5 domain} [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72//Hs.157124:S71129  
 F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:6//Hs.27414:U79275  
 F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648  
 F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247  
 40 F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685:AA700024  
 F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513  
 F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs.158095:AB007953  
 45 F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075  
 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575:AF100141  
 F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580  
 50 F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468:AB011147  
 F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494  
 F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663  
 F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative products}//6.2e-47:341:82//Hs.53217:Z48051  
 55 F-MAMMA1000761//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//9.8e-19:131:76//Hs.118972:AA761369  
 F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288  
 F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114  
 F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137  
 F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575  
 F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849  
 5 F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130  
 F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089  
 F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e48:241:74//Hs.155464:AF088219  
 F-MAMMA1000841  
 10 F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//  
 Hs.82210:U47742  
 F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696  
 F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877  
 F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022  
 F-MAMMA1000855  
 15 F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906  
 F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135  
 F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342  
 F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172  
 F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812  
 20 F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777  
 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459  
 F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147  
 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-91:  
 484:94//Hs.138938:AA012894  
 25 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812  
 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465  
 F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:  
 X67055  
 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683  
 30 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506  
 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081  
 F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628  
 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239  
 35 F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.0e-25:312:66//Hs.  
 116007:S79267  
 F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968  
 F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid  
 dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785  
 F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734  
 40 F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303  
 F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714  
 F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474  
 F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//  
 Hs.129735:AF010144  
 45 F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814  
 F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096  
 F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802  
 F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062  
 F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007  
 50 F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724  
 F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711  
 F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:  
 Y15718  
 F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968  
 55 F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds//3.6e-32:753:  
 61//Hs.98384:AF062006  
 F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857  
 F-MAMMA1001038

F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178  
F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI419882  
F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.  
135623:AA134719  
5 F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503  
F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585  
F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116  
F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.  
135251:L09749  
10 F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503  
F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420  
F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896  
F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:  
AB018254  
15 F-MAMMA1001092//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:  
K00627  
F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//  
Hs.97905:AF016045  
F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915  
20 F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219  
F-MAMMA1001133  
F-MAMMA1001139  
F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534  
F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217  
25 F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741  
F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:  
AB011147  
F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299  
F-MAMMA1001181  
30 F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:  
313:81//Hs.97203:U83171  
F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083  
F-MAMMA1001198  
F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348  
35 F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974  
F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:  
275:75//Hs.105292:AA504776  
F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200  
F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087  
40 F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:  
AB014534  
F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587  
F-MAMMA1001244  
45 F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476  
F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121  
F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149  
F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:  
AB014561  
50 F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503  
F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747  
F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522  
F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832  
F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998  
55 F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426  
F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305  
F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for  
GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//  
1.9e-58:295:97//Hs.102336:Z83838

F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087  
F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147  
F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806  
F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197  
5 F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267  
F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:75//Hs.109358:AB018258  
F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:273:80//Hs.42674:U61981  
F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
PRECURSOR//4.6e-09:415:58//Hs.839:M86826  
10 F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:67//Hs.61333:D83402  
F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763  
F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.0:176:64//Hs.82001:U50928  
F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80//Hs.43681:AL022394  
F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//0.00042:125:75//Hs.  
15 46328:D87942  
F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:543:71//Hs.37181:D64108  
F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321  
F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590  
F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040  
20 F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053  
F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//2.0e-24:273:72//Hs.75939:  
D78335  
F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3.2e-25:397:68//Hs.116874:  
AA524909  
25 F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366  
F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0.99:258:61//Hs.154196:U87269  
F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795  
F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506  
F-MAMMA1001547  
30 F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5e-130:614:98//Hs.129937:  
AB007931  
F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//0.71:181:62//Hs.118866:  
AI017072  
F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M61764  
35 F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339  
F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132  
F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375  
F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23642:U79266  
F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152  
40 F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.158229:U28727  
F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc  
Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen Ki-  
67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger  
protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DDX1003 and  
45 DDX1055//1.4e-40:447:73//Hs.154353:AL022165  
F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:611:67//Hs.57679:U57796  
F-MAMMA1001635  
F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524  
F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.00069:140:  
50 68//Hs.59829:AB014602  
F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.015:135:71//Hs.27349:  
AB007917  
F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819:  
AI027548  
55 F-MAMMA1001671  
F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317  
F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889  
F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765

F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549  
 F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, complete cds//8.0e-45:323:83//Hs.  
 46468:U45984  
 F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548  
 5 F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926  
 F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.5e-111:725:84//Hs.  
 159154:U47634  
 F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098  
 F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768  
 10 F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245  
 F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-67:822:69//Hs.23094:M19503  
 F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (HOHO1) mRNA, complete cds//  
 1.0e-36:583:65//Hs.79351:U33632  
 F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822  
 15 F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109  
 F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcript, partial//6.6e-41:309:84//Hs.  
 102576:AJ010230  
 F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072  
 20 F-MAMMA1001768//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//  
 2.2e-05:504:60//Hs.96028:AF042832  
 F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:686:79//Hs.113283:AF018080  
 F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//0.00071:392:60//Hs.32981:  
 U38276  
 25 F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940  
 F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549  
 F-MAMMA1001788//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//6.7e-21:212:77//Hs.103948:  
 K00627  
 F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72//Hs.5158:AB007869  
 30 F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987  
 F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884  
 F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:N47096  
 F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582  
 F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589  
 35 F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds//0.082:153:66//  
 Hs.114948:AF059293  
 F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742  
 F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691  
 F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315, complete cds//2.0e-29:641:62//Hs.  
 56808:D88827  
 40 F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665  
 F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028  
 F-MAMMA1001854  
 F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218  
 F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060  
 45 F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.084:672:58//  
 Hs.152455:AF044209  
 F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687  
 F-MAMMA1001878  
 F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944  
 50 F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576  
 F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078  
 F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521  
 F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874  
 F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529  
 55 F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859  
 F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:81//Hs.91916:AF035317  
 F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878  
 F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sapiens]//7.9e-09:150:72//Hs.118222:

N91115  
F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633  
F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826  
F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915  
5 F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159  
F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.2e-54:455:70//Hs.  
158095:AB007953  
F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580  
F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225  
10 F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256  
F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305  
F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-36:382:75//Hs.23094:M19503  
F-MAMMA1002078  
15 F-MAMMA1002082  
F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012  
F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//0.54:388:57//Hs.99423:  
AJ010840  
F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120  
F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932  
20 F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs.155464:AF088219  
F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:AI272963  
F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:H52638  
F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338  
F-MAMMA1002145//EST//0.12:204:60//Hs.160983:AI392837  
25 F-MAMMA1002153  
F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335:97//Hs.88424:AA281385  
F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)//0.99:310:58//Hs.87149:M35999  
F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196  
F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X17206  
30 F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:U39400  
F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:121:98//Hs.146354:Z22548  
F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362  
F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120  
F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:  
35 100//Hs.118849:AA215645  
F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:AI024063  
F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//4.6e-69:  
344:90//Hs.76822:AI359536  
F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//0.99:454:56//Hs.  
40 122755:AF032986  
F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903  
F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:AI308841  
F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427:61//Hs.  
69949:M94172  
45 F-MAMMA1002269  
F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715  
F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440  
F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.8e-  
60:387:75//Hs.133089:AF064019  
50 F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349:64//Hs.  
92614:M62302  
F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460  
F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57//Hs.77234:AB001914  
F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935  
55 F-MAMMA1002308//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-41:  
293:83//Hs.105292:AA504776  
F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA, complete cds//0.0037:173:67//  
Hs.69423:AF055481

F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-41:473:65//Hs.92381:AB007956  
 F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291  
 F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908  
 5 F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536  
 F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515  
 F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPIP8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026  
 10 F-MAMMA1002332//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.2e-26:342:72//Hs.103948:K00627  
 F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:58//Hs.5333:AB018254  
 F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6940:Z48633  
 15 F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-14:146:81//Hs.163073:R02591  
 F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907  
 F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:AI247086  
 F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539  
 20 F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78//Hs.32511:AB007901  
 F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733  
 F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818  
 F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830  
 F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923  
 F-MAMMA1002362//EST//0.25:304:58//Hs.1.62427:AA576345  
 25 F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34677  
 F-MAMMA1002384//ESTs//1.1 e-05:220:65//Hs.141388:R52022  
 F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-118:578:97//Hs.25516:AI086362  
 F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624  
 30 F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632  
 F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737  
 F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745  
 F-MAMMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788  
 F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030  
 35 F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087  
 F-MAMMA1002446  
 F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809  
 F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6.3e-06:595:59//Hs.99932:L38707  
 F-MAMMA1002470  
 40 F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.75074:U12779  
 F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059  
 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:560:98//Hs.155223:AF055460  
 45 F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628  
 F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:63//Hs.133013:AA604920  
 F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392  
 50 F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214  
 F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788  
 F-MAMMA1002554  
 F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:62//Hs.62354:M83822  
 F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421  
 55 F-MAMMA1002571//EST//0.28:115:66//Hs.156768:AI351368  
 F-MAMMA1002573//ESTs//2.1e-4.8:265:94//Hs.155128:AI224516  
 F-MAMMA1002585  
 F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831

F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:AI334107  
 F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958  
 F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220  
 F-MAMMA1002612//ESTs, Moderately similar to hCDC10 protein [H.sapiens]//8.3e-18:353:65//Hs.60895:  
 AA428463  
 F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357  
 F-MAMMA1002618  
 F-MAMMA1002619  
 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90//Hs.47344:AF041449  
 F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:N52300  
 F-MAMMA1002625  
 F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//1.1e-35:355:76//Hs.  
 158241:AB007976  
 F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-05:439:61//Hs.91400:  
 AB006626  
 F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733  
 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385  
 F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190  
 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:AI393335  
 F-MAMMA1002662//EST//0.99:95:63//Hs.144074:AI005489  
 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64//Hs.8262:U36336  
 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-06:272:64//Hs.106070:U22398  
 F-MAMMA1002673  
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.2e-162:752:99//Hs.3363:  
 D86987  
 F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:N69915  
 F-MAMMA1002698//ESTs//2.5e-09:190:68//Hs.138292:AI220397  
 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81//Hs.22396:AF062085  
 F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:AI274697  
 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.1e-51:307:79//Hs.  
 46328:D87942  
 F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:N25041  
 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692  
 F-MAMMA1002727//EST//0.97:137:63//Hs.145153:AI150165  
 F-MAMMA1002728//ESTs, Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE [Saccha-  
 romyces cerevisiae]//2.6e-12:129:81//Hs.154181:AA193502  
 F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853  
 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312  
 F-MAMMA1002748  
 F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848  
 F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98//Hs.32168:AB007902  
 F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293  
 F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782  
 F-MAMMA1002769  
 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//  
 7.6e-84:417:97//Hs.77705:U07563  
 F-MAMMA1002780//EST//0.78:210:63//Hs.149413:AI273988  
 F-MAMMA1002782  
 F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:AI380710  
 F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919  
 F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:AI778514  
 F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-57:286:88//Hs.15731:  
 AB011135  
 F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:72//Hs.22271:D26067  
 F-MAMMA1002835  
 F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 [Locusta mi-  
 gratoria]//7.7e-38:179:78//Hs.141344:H29951  
 F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590

F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4e-137:635:99//Hs.7531:  
 AB018353  
 F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:329:58//Hs.107747:AI357868  
 F-MAMMA1002858  
 5 F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643  
 F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696:78//Hs.83987:U09284  
 F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423  
 F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:AI183632  
 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//3.8e-30:680:61//Hs.129732:  
 10 D45027  
 F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504:60//Hs.19944:U04270  
 F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657  
 F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666  
 F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265  
 15 F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.00053:382:57//Hs.61796:U85658  
 F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952  
 F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125  
 F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730  
 F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.9e-103:485:99//Hs.  
 20 102928:AI346344  
 F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.6e-194:910:98//Hs.31720:  
 AB014598  
 F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:AI423389  
 F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:AI313418  
 25 F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:60//Hs.54697:AB007884  
 F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400  
 F-MAMMA1002972  
 F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932  
 F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944  
 30 F-MAMMA1002987//EST//0.044:254:59//Hs.135014:AI095645  
 F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//3.9e-22:185:83//Hs.62192:J02931  
 F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.0e-16:343:61//Hs.  
 159897:AB007970  
 F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979  
 35 F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2e-51:620:69//Hs.75258:  
 AF054174  
 F-MAMMA1003013//Human HOX4C mRNA for a homeobox protein//0.73:347:58//Hs.74061:X59372  
 F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062  
 F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:AI374951  
 40 F-MAMMA1003026//EST//1.0:136:67//Hs.9123:T50137  
 F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549  
 F-MAMMA1003035  
 F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391  
 F-MAMMA1003040//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.5e-93:339:85//Hs.5247:AF029750  
 45 F-MAMMA1003044/Cyclin D2//1.0:234:61//Hs.75586:D13639  
 F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans//1.0:209:60//Hs.99491:  
 Y12336  
 F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742  
 F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518  
 50 F-MAMMA1003056  
 F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein MD6 [M.musculus]//1.3e-88:334:97//Hs.  
 96500:AI206781  
 F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:AI022618  
 F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5e-51:329:71//Hs.75154:  
 55 AB014531  
 F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA, complete cds//8.5e-44:288:  
 88//Hs.81008:AF043045  
 F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:213:60//Hs.42945:Y08136

F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200:64//Hs.32950:X82634  
 F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, complete cds//5.4e-27:421:66//Hs.5394:  
 AF105424  
 F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786  
 5 F-MAMMA1003140  
 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//7.2e-82:397:97//Hs.151344:Y15062  
 F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.00019:297:61//Hs.108945:  
 AB011087  
 F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:487:65//Hs.3847:U59632  
 10 F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//Hs.79706:U53204  
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:92//Hs.82510:D31886  
 F-NT2RM1000032  
 F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:81//Hs.78442:D83782  
 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5e-108:542:95//Hs.60103:  
 15 AB014590  
 F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//Hs.79706:U53204  
 F-NT2RM1000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:353:96//Hs.154980:AA948067  
 F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.029:281:59//  
 Hs.46465:U45285  
 20 F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210  
 F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:97//Hs.3439:AC004472  
 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.8e-116:550:97//Hs.65238:  
 AB014561  
 F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190:63//Hs.431:L13689  
 25 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00086:126:70//Hs.92693:  
 AF007155  
 F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054  
 F-NT2RM1000127  
 F-NT2RM1000131  
 30 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene en-  
 coding mitochondrial protein, complete cds//3.7e-92:448:97//Hs.49767:AF044959  
 F-NT2RM1000153//Homo sapiens mRNA for MTG8-related protein MTG16a, complete cds//1.0:546:58//Hs.  
 110099:AB010419  
 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00081:126:70//Hs.92693:  
 35 AF007155  
 F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:AI424382  
 F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.87:454:59//Hs.47061:AF045458  
 F-NT2RM1000242  
 F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.97:  
 40 135:66//Hs.27910:AF049105  
 F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190  
 F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248:69//Hs.1674:M90516  
 F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H.sapiens]//2.9e-98:530:93//Hs.104650:  
 AI037879  
 45 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:80//Hs.23106:D50920  
 F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047  
 F-NT2RM1000272  
 F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]//1.3e-21:308:  
 50 73//Hs.15071:AA781144  
 F-NT2RM1000300  
 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708:92//Hs.5719:D63880  
 F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e-35:182:99//Hs.9837:D79205  
 F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976  
 F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798  
 55 F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7e-75:387:95//Hs.108619:W28608  
 F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691  
 F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.sapiens]//7.4e-91:481:95//Hs.  
 163707:AA137181

F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X80507  
 F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353  
 F-NT2RM1000399  
 F-NT2RM1000421  
 5 F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.2e-85:418:97//  
 Hs.20815:AF084928  
 F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapiens]//1.6e-38:201:97//Hs.106262:AI052382  
 F-NT2RM1000539//EST//0.070:145:62//Hs.149711:AI284660  
 F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847  
 10 F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:AI359957  
 F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:58//Hs.79706:U53204  
 F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//0.98:226:61//Hs.17931:AB006625  
 F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]//6.2e-51:254:98//Hs.132096:AA314601  
 15 F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds//8.5e-55:276:97//Hs.19122:  
 AF038957  
 F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60//Hs.113936:AB005297  
 F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:AI188279  
 F-NT2RM1000672  
 20 F-NT2RM1000691//Homo sapiens mRNA for HRIHFB2060, partial cds//7.0e-121:582:98//Hs.146282:AB015348  
 F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101  
 F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706  
 F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//1.5e-66:435:85//Hs.5038:AJ004832  
 F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.6e-127:690:92//Hs.147946:  
 25 AB011139  
 F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2e-68:524:83//Hs.112360:AF027208  
 F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465  
 F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:321:63//Hs.150390:AB007885  
 F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.053:271:60//Hs.139745 :  
 30 U39067  
 F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frames//6.9e-20:128:94//Hs.23094:M19503  
 F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845  
 F-NT2RM1000800  
 F-NT2RM1000802  
 35 F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2e-64:490:84//Hs.112360:AF027208  
 F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:AI359957  
 F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//0.92:283:58//Hs.2314:X15422  
 F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:178:67//Hs.1376:U26726  
 F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequence//3.8e-06:384:59//Hs.90314:L05148  
 40 F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//3.0e-149:726:97//Hs.99423:  
 AJ010840  
 F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643  
 F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//5.3e-54:277:96//Hs.11125:AI015619  
 F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239  
 45 F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1  
 gene//4.0e-155:750:97//Hs.132898:AC004770  
 F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//8.8e-158:762:97//Hs.  
 26285:AF082516  
 F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds//6.3e-19:310:67//Hs.65238:  
 50 AB014561  
 F-NT2RM1000894  
 F-NT2RM1000898  
 F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:AI268701  
 F-NT2RM1000924//HOMEobox protein HOX-A5//0.00051:458:59//Hs.37034:M26679  
 55 F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cds//0.084:386:58//Hs.101474:AB018350  
 F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:299:59//Hs.83419:D87440  
 F-NT2RM1000978  
 F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.3e-161:760:98//



AI141736  
F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220  
F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs.74369:AF032108  
F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.89631:U48508  
5 F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128  
F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs.55609:W37993  
F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs.3363:  
D86987  
10 F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220  
F-NT2RM2000594  
F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs.102402:  
AF040963  
F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313  
15 F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548  
F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs.6150:AB011093  
F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258  
F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs.19542:  
AB018272  
20 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs.7278:AB014558  
F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702  
F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs.115763:  
AB014576  
F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:AI337371  
25 25 F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs.  
5321:AF006083  
F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:64//Hs.7938:D86984  
F-NT2RM2000718//Homo sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:594:98//Hs.136058:AB015342  
F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107:X59244  
30 F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC  
REGION [Saccharomyces cerevisiae]//4.2e-85:464:91//Hs.161551:W24286  
F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-82:640:81//Hs.5247:AF029750  
F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//Hs.105919:AB002338  
F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:AI346701  
35 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2.8e-185:847:99//Hs.137580:  
AB015046  
F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//6.2e-94:441:99//Hs.59075:  
AI023761  
F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//Hs.84753:D87433  
40 F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831  
F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//2.9e-48:282:93//Hs.  
17035:AI080471  
F-NT2RM2001065  
F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:  
45 62//Hs.75111:D87258  
F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//  
0.00079:274:59//Hs.102732:U88153  
F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190  
F-NT2RM2001141  
50 F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042  
F-NT2RM2001177  
F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [C.elegans]//2.4e-23:149:93//Hs.10618:AI288739  
F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959  
F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630  
55 F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349  
F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766  
F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U65928  
F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:

AF039694  
 F-NT2RM2001256  
 F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845  
 F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601  
 5 F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615  
 F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:  
 AI138605  
 F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567  
 F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706  
 10 F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905  
 F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61//Hs.82925:U70322  
 F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382  
 F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378  
 15 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:  
 AJ007509  
 F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303  
 F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903  
 F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969  
 20 F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459  
 F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262  
 F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582:  
 25 64//Hs.1042:M62800  
 F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077  
 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902  
 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729  
 30 F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431  
 F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis  
 familiaris]//1.3e-17:181:75//Hs.131840:AI016073  
 F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918  
 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:  
 35 AB014518  
 F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952  
 F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92//  
 Hs.22142:AA814725  
 F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis  
 familiaris]//1.3e-17:181:75//Hs.131840:AI016073  
 40 F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301  
 F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287  
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-  
 173:802:99//Hs.31323:AF044195  
 F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATSCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:  
 45 671:97//Hs.27721:U17907  
 F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:  
 AB011129  
 F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356  
 F-NT2RM2001675  
 F-NT2RM20016811//ESTs//0.16:197:63//Hs.20585:R10305  
 F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211  
 50 F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216  
 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937  
 F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415  
 F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817  
 F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//  
 55 0.95:270:61//Hs.15791:AF027826  
 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788  
 F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650  
 F-NT2RM2001718  
 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123

F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:  
AB007931

F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:  
AB011132

5 F-NT2RM2001743  
F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399  
F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

10 F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:AI222742  
F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669:71//Hs.2479:X78933  
F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698

15 F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:AI193595  
F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770

20 F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763  
F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:  
U29175

25 F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195

30 F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341  
F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068  
F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691

35 F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759  
F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:86//Hs.113283:AF018080

40 F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567  
F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421:66//Hs.8763:W30741  
F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723

45 F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198:  
AB014610  
F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and  
IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892

50 F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937:  
AB007931  
F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:  
U52840

55 F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U66688  
F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//2.2e-139:653:98//Hs.21811:  
AF091080  
F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392  
F-NT2RM2001982  
F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds//1.2e-21:123:98//Hs.6454:  
AF089816

60 F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.104135:AJ006778  
F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538  
F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:271:60//Hs.63888:AA203398

65 F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5e-37:509:65//Hs.6214:AB018274  
F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:429:58//Hs.79090:D89729  
F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822:73//Hs.1674:M90516

70 F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427  
F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154  
F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377

75 F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.89631:U48508  
F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.5e-165:776:98//Hs.99423:  
AJ010840  
F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435  
F-NT2RM2002128

EP 1 074 617 A2

F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274  
F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.4e-144:800:  
92//Hs.20815:AF084928  
F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7e-165:787:97//Hs.11147:  
AB007936  
F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//0.064:291:61//Hs.  
99936:X14487  
F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59//Hs.148027:X63563  
F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074  
F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464  
F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674  
F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI038511  
F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product is related to human RNA helicase A. [H.  
sapiens]//1.6e-30:369:70//Hs.114623:AI204280  
F-NT2RM4000086  
F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds//  
1.3e-24:345:69//Hs.13128:AF060865  
F-NT2RM4000139  
F-NT2RM4000155  
F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632  
F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete cds//9.8e-30:676:61//  
Hs.159228:AF041853  
F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044  
F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190  
F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744  
F-NT2RM4000199//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//0.13:322:  
61//Hs.145088:AI221147  
F-NT2RM4000200  
F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.0027:424:60//HS.91400:  
AB006626  
F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.4e-184:856:98//Hs.111138:  
AB018255  
F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013:358:60//Hs.75055:M93651  
F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.65:572:60//Hs.47061:AF045458  
F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582  
F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439  
F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccharomyces pombe]//1.1e-16:112:92//Hs.  
93841:AA442297  
F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.8e-48:229:83//Hs.  
46328:D87942  
F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds//2.5e-154:609:93//Hs.  
31305:M99438  
F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds//0.070:460:59//Hs.5372:  
AB000712  
F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707  
F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]//2.7e-83:432:95//Hs.  
12796:W27884  
F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:68//Hs.155291:D13630  
F-NT2RM4000354//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//0.0078:55:92//Hs.59075:  
M023761  
F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI418425  
F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3e-135:628:99//Hs.8152:AB014542  
F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745  
F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene  
for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:  
843:68//Hs.23796:AL022718  
F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029

F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//4.9e-17:114:94//Hs.137580:  
 AB015046  
 F-NT2RM4000421  
 F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432:74//Hs.154872:  
 5 AB011166  
 F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543:58//Hs.2175:M59820  
 F-NT2RM4000457  
 F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178:631/Hs.  
 10 66369:U95040  
 F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:AI280004  
 F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632  
 F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915  
 F-NT2RM4000514  
 F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409  
 15 F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:AI221305  
 F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756:96//  
 Hs.125870:AI364967  
 F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:H78987  
 F-NT2RM4000534  
 20 F-NT2RM4000585  
 F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593:62//Hs.7764:  
 AB007938  
 F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III  
 25 [Caenorhabditis elegans]//3.1e-104:532:96//Hs.6092:T75227  
 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305:68//Hs.40100:AB002390  
 F-NT2RM4000611//EST//0.76:268:58//Hs.150031:AI292068  
 F-NT2RM4000616  
 F-NT2RM4000674  
 F-NT2RM4000689  
 30 F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529  
 F-NT2RM4000700  
 F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744:77//Hs.  
 42400:AF022789  
 F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]  
 35 //2.6e-163:771:97//Hs.6823:W18181  
 F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:M84605  
 F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743:98//Hs.137168:  
 AB018303  
 F-NT2RM4000741  
 40 F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388:96//Hs.  
 112361:R99396  
 F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:H67815  
 F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731  
 F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173:810:98//Hs.18586:  
 45 AB007920  
 F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186  
 F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:98//Hs.25817:AC005306  
 F-NT2RM4000795//ESTs, Highly Similar to LIVER CARBOXYLESTERASE PRECURSOR [Homo sapiens]//6.7e-  
 50 19:160:80//Hs.124902:AI337820  
 F-NT2RM4000796//Human K+ channel subunit gene, complete cds//0.96:292:62//Hs.124212:M64676  
 F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301  
 F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
 55 cds//0.052:238:64//Hs.113265:AF032387  
 F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H16568  
 F-NT2RM4000833  
 F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374:61//Hs.7841:AB002322  
 F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934  
 F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 [Homo sapi-

ens]//4.4e-29:164:95//Hs.115095:AI392943  
 F-NT2RM4000887  
 F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete  
 cds//6.8e-22:407:64//Hs.21293:AB011004  
 5 F-NT2RM4000950  
 F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546  
 F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77//Hs.7289:AB007875  
 F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381:67//Hs.2481:X78926  
 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6e-171:803:98//Hs.19542:  
 10 AB018272  
 F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1e-126:584:99//Hs.15711:  
 AB014539  
 F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.8e-05:469:58//Hs.5333:  
 AB018254  
 15 F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus]//7.0e-56:340:92//Hs.87310:  
 AI247543  
 F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM" PRECURSOR//  
 0.79:142:69//Hs.77424:M63835  
 F-NT2RM4001084  
 20 F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62//Hs.108947:D30758  
 F-NT2RM4001116  
 F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:61//Hs.134989:L12701  
 F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730  
 F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:AI004145  
 25 F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351  
 F-NT2RM4001187  
 F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220  
 F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799:69//Hs.2479:X78933  
 F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.4e-153:707:99//Hs.  
 30 14934:AF004828  
 F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME  
 III [Caenorhabditis elegans]//0.19:291:62//Hs.31582:AA877205  
 F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds//7.0e-63:715:70//  
 Hs.104925:AF059611  
 35 F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-67:208:96//Hs.  
 26676:AA033997  
 F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.0019:435:59//Hs.6360:  
 AB007950  
 F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:59//Hs.26971:AC003003  
 40 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973  
 F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335  
 F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:66//Hs.87435:D89016  
 F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AI418988  
 45 F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTER-  
 GENIC REGION [Saccharomyces cerevisiae]//0.0096:284:58//Hs.120997:R56714  
 F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7  
 protein [C.elegans]//3.7e-52:252:100//Hs.15301:AA167818  
 F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI277656  
 50 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790:98//Hs.5151:  
 AF098799  
 F-NT2RM4001384  
 F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575  
 F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64//Hs.105052:AB000520  
 F-NT2RM4001412  
 55 F-NT2RM4001414//ESTs, Moderately similar to 18547\_1 [H.sapiens]//5.2e-18:133:87//Hs.28209:AI073817  
 F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:70//Hs.154326:D42087  
 F-NT2RM4001444  
 F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658

F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914  
 F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784  
 5 F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:AB014585  
 F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619  
 F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae]//1.3e-114:536:99//Hs.88820:  
 AA456247  
 10 F-NT2RM4001557  
 F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487  
 F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:  
 255:60//Hs.14207:U86453  
 F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859  
 F-NT2RM4001582  
 15 F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566  
 F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:  
 AB011094  
 F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077  
 20 F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:  
 AB018334  
 F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739  
 F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens]  
 //0.0042:153:68//Hs.114832:AI147946  
 25 F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339  
 F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320  
 F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323  
 F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638  
 F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384  
 F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957  
 30 F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905  
 F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903  
 F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318  
 F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306  
 35 F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//  
 2.0e-27:205:83//Hs.110601:AA206719  
 F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:  
 X97630  
 F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:  
 AB018270  
 40 F-NT2RM4001783//ESTs, Weakly similar to T12D8.i [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677  
 F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:  
 446:58//Hs.27910:AF049105  
 F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547  
 F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins) //1.4e-35:195:95//Hs.963:M37712  
 45 F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:  
 AI379442  
 F-NT2RM4001828//Zinc finger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687  
 F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824  
 F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204  
 50 F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814  
 F-NT2RM4001856  
 F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete  
 cds//8.0e-10:244:66//Hs.22138:U49250  
 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.3e-150:704:98//Hs.61628:  
 Y17711  
 55 F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984  
 F-NT2RM4001880  
 F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212

F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:AI312633  
 F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356:  
 AJ224875  
 F-NT2RM4001938  
 5 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:  
 AF098162  
 F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087  
 F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//1.8e-65:337:96//Hs.  
 10 130135:AA905493  
 F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862  
 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:  
 AB018341  
 F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082  
 F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936  
 15 F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271  
 F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601  
 F-NT2RM4002034  
 F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048  
 F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912  
 20 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:  
 AB014540  
 F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]  
 //7.0e-94:396:94//Hs.59346:AI126802  
 F-NT2RM4002063  
 25 F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:  
 AF071309  
 F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040  
 F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302  
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.  
 30 122967:AF059569  
 F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//9.2e-34:532:65//Hs.  
 146459:X66975  
 F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.  
 69360:U63743  
 35 F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542  
 F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877  
 F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158  
 F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens]//1.6e-135:646:97//Hs.104650:  
 AI037879  
 40 F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535  
 F-NT2RM4002174  
 F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998  
 F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:  
 U38276  
 45 F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454  
 F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182  
 F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]  
 //8.4e-125:588:98//Hs.23900:U82984  
 F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966  
 50 F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764  
 F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118  
 F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180  
 F-NT2RM4002281  
 F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979  
 55 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457  
 F-NT2RM4002301  
 F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331  
 F-NT2RM4002339

F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454  
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708:98//Hs.26163:  
 AB014549  
 5 F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303:63//Hs.23741:AB018263  
 F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293  
 F-NT2RM4002390  
 F-NT2RM4002398  
 F-NT2RM4002409  
 10 F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-55:282:96//Hs.  
 26676:AA033997  
 F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:AF052151  
 F-NT2RM4002452  
 F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:81//Hs.115263:D30783  
 F-NT2RM4002460//EST//1.0:142:65//Hs.145370:AI252780  
 15 F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777:98//Hs.  
 8765:AF083255  
 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:97//Hs.94781:  
 AB014591  
 F-NT2RM4002493  
 20 F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347  
 F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219  
 F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290:60//Hs.154968:  
 U02020  
 F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075  
 25 F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AI/AVP mRNA, complete cds//1.0:100:70//  
 Hs.159483:AF054176  
 F-NT2RM4002558//Homo sapiens amphiphysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004  
 F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:  
 D84273  
 30 F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans]//3.3e-88:484:93//Hs.105837:AA536054  
 F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase [H.sa-  
 piens]//0.059:121:70//Hs.155413:AA429394  
 F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151  
 35 F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:  
 499:59//Hs.79357:D78275  
 F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402  
 F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587  
 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:  
 AJ012449  
 40 F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907  
 F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647  
 F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834  
 F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792:  
 AF044924  
 45 F-NT2RP1000111  
 F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699  
 F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:AI084025  
 F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:  
 382:94//Hs.127842:W38901  
 50 F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90//  
 Hs.3760:AF011792  
 F-NT2RP1000170//EST//0.68:130:63//Hs.146994:AI184430  
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535  
 F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499  
 55 F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703  
 F-NT2RP1000243  
 F-NT2RP1000259  
 F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.

4214:AF067730  
 F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661  
 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551  
 5 F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231  
 F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204  
 F-NT2RP1000357  
 F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807  
 10 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:86//Hs.77864:AB014538  
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96//Hs.120360:AF064594  
 F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031  
 15 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:98//Hs.21862:AB011159  
 F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//7.3e-177:857:97//Hs.6823:W18181  
 F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.46:222:  
 20 60//Hs.89230:AF031815  
 F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603  
 F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862  
 F-NT2RP1000460  
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence//3.7e-134:  
 25 665:96//Hs.143187:AC002985  
 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs.  
 159154:U47634  
 F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102  
 F-NT2RP1000493  
 30 F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977  
 F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992  
 F-NT2RP1000547//H.sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098  
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.  
 104105:AF017418  
 35 F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213  
 F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385  
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1  
 gene//2.2e-49:506:73//Hs.132898:AC004770  
 F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.  
 40 152936:D63475  
 F-NT2RP1000630  
 F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:  
 U24576  
 F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553  
 45 F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:  
 AI141736  
 F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148  
 F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D30612  
 F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens]//6.2e-40:297:84//Hs.18122:AI338045  
 50 F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644  
 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete  
 cds//2.6e-123:604:96//Hs.21771:AF101434  
 F-NT2RP1000746  
 F-NT2RP1000767  
 55 F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023  
 F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401  
 F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for  
 GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//

2.7e-23:147:91//Hs.102336:Z83838  
F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424:  
96//Hs.18953:AF067223  
F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332903  
5 F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI267990  
F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI288838  
F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875  
F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023  
F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094  
10 F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218683  
F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:AI248847  
F-NT2RP1000916//ESTs, Weakly similar to coded for by *C. elegans* cDNA cm04e9 [C.elegans]//2.2e-27:159:94//  
Hs.122153:AA780270  
F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248  
15 F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400  
F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//2.7e-26:  
185:87//Hs.108332:U39317  
F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:AB002803  
F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847  
20 F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M17885  
F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858  
F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866  
F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:L13435  
F-NT2RP1001011  
25 F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163  
F-NT2RP1001014  
F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764  
F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901  
F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531  
30 F-NT2RP1001080//Homo sapiens forkhead protein (FKHLR1) mRNA, complete cds//0.57:215:64//Hs.14845:  
AF032886  
F-NT2RP1001113//ESTs, Weakly similar to coded for by *C. elegans* cDNA CEESB82F [C.elegans]//1.4e-65:293:  
95//Hs.32751:H38087  
F-NT2RP1001173  
35 F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258:  
AF054174  
F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524  
F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150  
F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.  
40 25195:U81523  
F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094  
F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:  
AJ002231  
F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724  
45 F-NT2RP1001294  
F-NT2RP1001302  
F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341  
F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815  
F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1  
50 gene//3.1e-87:437:97//Hs.132898:AC004770  
F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tauru  
rus]//6.8e-101:480:94//Hs.75017:AA166853  
F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859  
F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673  
55 F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081  
F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700  
F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700  
F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149

F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104  
 F-NT2RP1001466  
 F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742  
 F-NT2RP1001482  
 5 F-NT2RP1001494  
 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400  
 F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277  
 F-NT2RP1001569  
 F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds//2.5e-41:496:74//Hs.12956:U90913  
 10 F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420  
 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//4.7e-137:685:96//Hs.93677:  
 AF091081  
 F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C.elegans]//8.2e-47:300:89//Hs.6473:AA853955  
 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390  
 15 F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763  
 F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//  
 2.0e-26:214:82//Hs.140385:AA773359  
 F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867  
 F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290  
 20 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//  
 7.8e-97:467:97//Hs.6216:AF061749  
 F-NT2RP2000054//HOMEobox/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433  
 F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.  
 155991:X54134  
 25 F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene  
 for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:  
 767:61//Hs.23796:AL022718 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155),  
 complete sequence//6.5e-08:344:58//Hs.159402:AC005609  
 30 F-NT2RP2000076//H.sapiens mRNA for TFIIAI//0.00023:356:62//Hs.121686:D14887  
 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.  
 54877:AF050078  
 F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879  
 F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:  
 35 AB018338  
 F-NT2RP2000091  
 F-NT2RP2000097  
 F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963  
 F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390  
 40 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706:  
 AB018356  
 F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III  
 [C.elegans]//0.019:72:81//Hs.5268:W22670  
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:  
 45 607:96//Hs.159273:AF054177  
 F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195  
 F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.  
 152936:D63475  
 F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910  
 50 F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291  
 F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190  
 F-NT2RP2000173  
 F-NT2RP2000175  
 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//  
 55 Hs.100058:AB006713  
 F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:AI148761  
 F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050  
 F-NT2RP2000208

F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:243:61//Hs.143641:AB009462  
 F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990  
 F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342:59//Hs.8546:U97669  
 5 F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//Hs.47822:AB002378  
 F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719  
 F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.51:227:60//Hs.30223:X90846  
 F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691  
 F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011  
 10 F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599  
 F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910  
 F-NT2RP2000288  
 F-NT2RP2000289  
 F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744:70//Hs.  
 15 37138:U35376  
 F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:AI123467  
 F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//4.3e-13:140:  
 80//Hs.58218:U82381  
 F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:AI417006  
 20 F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:AI332905  
 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66//Hs.101642:  
 X60673  
 F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:126:69//Hs.153706:AF026547  
 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.2e-130:627:  
 25 97//Hs.76556:U83981  
 F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.56:464:57//Hs.12259:AB014530  
 F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047  
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67:375:93//Hs.808:L28010  
 F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapiens]//3.9e-75:413:92//Hs.36779:  
 30 AA626790  
 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//6.7e-128:609:  
 96//Hs.5819:AF102265  
 F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381  
 F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402:AI393918  
 35 F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e-22:158:87//Hs.154655:Z68747  
 F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293  
 F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702  
 F-NT2RP2000510  
 F-NT2RP2000516  
 40 F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B mRNA EDITING PROTEIN [Rattus norvegicus]  
 //3.2e-15:167:75//Hs.10984:AA806768  
 F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6e-38:196:98//Hs.14409:AB011144  
 F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//1.0:  
 242:57//Hs.114001:Z20656  
 45 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732:97//Hs.7314:AB014514  
 F-NT2RP2000644//ESTs//0.035:276:60//Hs.43660:N33174  
 F-NT2RP2000656  
 F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602  
 F-NT2RP2000668  
 50 F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:AI093453  
 F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN  
 CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233:78//Hs.114905:AA088442  
 F-NT2RP2000710  
 F-NT2RP2000715  
 55 F-NT2RP2000731  
 F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA573242  
 F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74:  
 445:89//Hs.21421:AA911739

F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101  
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:58//Hs.159275:AF030880  
 F-NT2RP2000814  
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182  
 5 F-NT2RP2000819  
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:70//Hs.20695:AB002292  
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//9.5e-29:167:94//Hs.  
 75794:U80811  
 F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:AI336850  
 10 F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I  
 [Schizosaccharomyces pombe]//6.4e-34:207:92//Hs.135235:AI081880  
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732:94//Hs.3615:  
 AB018284  
 15 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.50:189:65//  
 Hs.46146:AA418097  
 F-NT2RP2000931//MATRIN3//1.1e-130:610:98//Hs.78825:AB018266  
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326:97//Hs.15144:AC005014  
 F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408  
 20 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533:98//Hs.19822:  
 AB018298  
 F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494  
 F-NT2RP2000970  
 F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC  
 25 REGION [Saccharomyces cerevisiae]//7.3e-76:385:96//Hs.21875:AA243700  
 F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944  
 F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292  
 F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117  
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696:97//Hs.  
 30 67619:AB007957  
 F-NT2RP2001065  
 F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313  
 F-NT2RP2001081  
 F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:AI356560  
 F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219  
 35 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:63//Hs.80358:U52191  
 F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34:  
 201:91//Hs.118470:AI336362  
 F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582  
 F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:AI091361  
 40 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567:96//Hs.26247:  
 AB007949  
 F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011  
 F-NT2RP2001196  
 F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598  
 45 F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053  
 F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//Hs.69740:U09367  
 F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813  
 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353  
 F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277  
 50 F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:76//Hs.75848:U39412  
 F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287  
 F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387  
 F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs.76090:M80783  
 55 F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522  
 F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41883  
 F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418:91//Hs.107039:W27244  
 F-NT2RP2001378  
 F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:AI377558

F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//0.28:  
 225:62//Hs.159402:AC005609  
 F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767  
 F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088  
 5 F-NT2RP2001420  
 F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]//0.030:443:59//Hs.140506:AA308018  
 F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875  
 F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966  
 F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide//  
 10 9.8e-56:603:72//Hs.75544:Z82248  
 F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218  
 F-NT2RP2001449  
 F-NT2RP2001450  
 F-NT2RP2001467  
 15 F-NT2RP2001506  
 F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409:98//Hs.156161:AI333779  
 F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.4e-138:657:97//Hs.4277:  
 Y14494  
 F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134  
 20 F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//  
 5.2e-105:384:94//Hs.99742:AF035586  
 F-NT2RP2001560  
 F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs.  
 67619:AB007957  
 25 F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389  
 F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876  
 F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//Hs.82201:M55268  
 F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:  
 AB018340  
 30 F-NT2RP2001613  
 F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI082229  
 F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96//  
 Hs.58488:U97067  
 F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-  
 35 NA, complete cds//1.3e-145:687:97//Hs.159558:AF058718  
 F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328  
 F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58//Hs.96264:U72936  
 F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314  
 40 F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621 :  
 U52840  
 F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091  
 F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:  
 AI197870  
 F-NT2RP2001721  
 45 F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991  
 F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransf-  
 erase, geranyltranstransferase)//1.2e-19:151:86//Hs.77393:D14697  
 F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete\_cds//5.2e-34:191:96//Hs.47504:  
 AF091754  
 50 F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180  
 F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI052250  
 F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610  
 F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete\_cds//0.0013:174:62//Hs.9443:  
 AF027219  
 55 F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768  
 F-NT2RP2001883  
 F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR//3.0e-113:633:  
 90//Hs.142189:M74161

F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650  
 F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//0.37:263:62//Hs.106377:H29757  
 F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI393754  
 F-NT2RP2001936  
 5 F-NT2RP2001943  
 F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797  
 F-NT2RP2001947  
 F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489  
 F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892  
 10 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:AB011117  
 F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196  
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:AB018299  
 15 F-NT2RP2002032  
 F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI003543  
 F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336  
 F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509  
 F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284198  
 20 F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284  
 F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:66//Hs.44553:AF055634  
 F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241  
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183  
 25 F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014  
 F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI313156  
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533:97//Hs.155218:AJ007509  
 F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.  
 30 122755:AF032986  
 F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286  
 F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:M83363  
 F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112  
 F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314  
 35 F-NT2RP2002185//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//6.8e-61:354:91//Hs.109966:C06057  
 F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7e-37:194:97//Hs.91728:M58460  
 F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//  
 40 6.8e-15:228:67//Hs.111323:AF077954  
 F-NT2RP2002208  
 F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628  
 F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394318  
 F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264:U70439  
 45 F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.79:264:59//Hs.129748:AB011099  
 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//2.1e-51:315:89//Hs.150595:AF005418  
 F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//Hs.92137:M19720  
 F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//1.3e-31:206:88//Hs.4029:Z78373  
 50 F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079  
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//5.0e-95:467:96//Hs.  
 24812:AF069532  
 F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445  
 F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.3e-124:640:  
 55 95//Hs.31034:AB015594  
 F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60//Hs.75516:X54637  
 F-NT2RP2002373  
 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.1e-139:673:

97//Hs.109051:AF038958  
 F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U79289  
 F-NT2RP2002408//HOMEobox/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74095:L20433  
 F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098  
 5 F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326  
 F-NT2RP2002442//ESTs, Weakly similar to similar to molybdopterin biosynthesis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA904265  
 F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436  
 F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs.1560:D42045  
 10 F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:AI139929  
 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs.125856:AB005289  
 F-NT2RP2002498  
 F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs.102681:U95044  
 15 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs.23255:AB018334  
 F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563:M28212  
 F-NT2RP2002537  
 F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096  
 20 F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979  
 F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs.159277:AB018341  
 F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309  
 F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs.23094:M19503  
 25 F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs.334:U02082  
 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805  
 F-NT2RP2002621  
 30 F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs.155302:U57317  
 F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493  
 F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109857:AA088385  
 35 F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583  
 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs.6336:AB014572  
 F-NT2RP2002727  
 F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217  
 40 F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297  
 F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs.87435:D89016  
 F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs.146395:AB002329  
 F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709  
 F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705  
 45 F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs.79706:U53204  
 F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407  
 F-NT2RP2002800  
 F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763  
 F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:AI382142  
 50 F-NT2RP2002862  
 F-NT2RP2002880  
 F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0:237:62//Hs.106487:AB014573  
 F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606  
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.  
 55 116674:AF038392  
 F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:158:65//Hs.108447:AJ000517  
 F-NT2RP2002939  
 F-NT2RP2002954

F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//6.4e-21:  
 135:91//Hs.108332:U39317  
 F-NT2RP2002979  
 F-NT2RP2002980  
 5 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs.  
 122967:AF059569  
 F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:AI004740  
 F-NT2RP2002993  
 F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs.155464:AF088219  
 10 F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741  
 F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:  
 78//Hs.159176:U92019  
 F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190  
 F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs.153704:U11050  
 15 F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633  
 F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:AI291379  
 F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:  
 556:57//Hs.155321:J03161  
 F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544  
 20 F-NT2RP2003137  
 F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227:61//Hs.105958:AB014520  
 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581:93//Hs.9736:  
 D67025  
 F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:AI424170  
 25 F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944  
 F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:79//Hs.153014:AB002353  
 F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:N91123  
 F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:AI393223  
 F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594  
 30 F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794  
 F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947  
 F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP5K) mRNA, com-  
 plete cds//1.3e-62:543:77//Hs.108966:U48696  
 F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:  
 35 200:62//Hs.102732:U88153  
 F-NT2RP2003265  
 F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//5.8e-57:313:93//Hs.109966:  
 C06057  
 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714:96//Hs.154919:  
 40 AB014525  
 F-NT2RP2003280  
 F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243:65//Hs.21862:  
 AB011159  
 F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:AI269334  
 45 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 mediating protein, complete cds//2.0e-86:416:97//Hs.  
 7943:AB006572  
 F-NT2RP2003297//EST//0.99:240:60//Hs.133228:AI052312  
 F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752  
 F-NT2RP2003308  
 50 F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III  
 [Caenorhabditis elegans]//1.8e-102:532:95//Hs.6092:T75227  
 F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:AI346765  
 F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963  
 F-NT2RP2003367//Human HsLIM15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108  
 55 F-NT2RP2003391  
 F-NT2RP2003393  
 F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023  
 F-NT2RP2003401

F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]/3.7e-33:303:77//Hs.14038:R06800  
 F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893  
 F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273:61//Hs.159360:L22647  
 5 F-NT2RP2003456//EST//0.17:95:65//Hs.147190:AI193320  
 F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770  
 F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106  
 F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136  
 10 F-NT2RP2003506  
 F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.107164:M96803  
 F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:94//Hs.78482:Y16270  
 F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)/1.3e-24:151:95//Hs.1976:M12783  
 15 F-NT2RP2003522//Zinc finger protein 148 (pHZ-52)//1.1e-17:512:60//Hs.112180:AF039019  
 F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765  
 F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010  
 F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:AI356513  
 20 F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800  
 F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937:AB007931  
 F-NT2RP2003581//EST//1.0:59:76//Hs.158575:AI368947  
 F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//1.3e-63:224:95//Hs.34627:  
 25 AA126463  
 F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98//Hs.58488:U97067  
 F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166  
 F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252  
 30 F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006  
 F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:AI032875  
 F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247  
 F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561  
 35 F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44:269:91//Hs.139757:N95271  
 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097  
 F-NT2RP2003713  
 F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:  
 40 252:83//Hs.86371:AF054180  
 F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879  
 F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds//4.0e-55:  
 584:71//Hs.118797:U39318  
 F-NT2RP2003751  
 45 F-NT2RP2003760  
 F-NT2RP2003764  
 F-NT2RP2003769  
 F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677  
 F-NT2RP2003777  
 50 F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63:356:92//Hs.16131:AA568689  
 F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955  
 F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742  
 F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368  
 F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425  
 55 F-NT2RP2003859  
 F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780  
 F-NT2RP2003885  
 F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emericella nidulans]//2.2e-

113:632:92//Hs.50072:AI378221  
 F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]//1.0:146:67//Hs.  
 156920:AA489296  
 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs.  
 5 35086:AB014458  
 F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:  
 AB007916  
 F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347  
 F-NT2RP2003984  
 10 F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036  
 F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369  
 F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//7.0e-104:556:93//  
 Hs.111081:AI380378  
 F-NT2RP2004014  
 15 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780  
 F-NT2RP2004042  
 F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:  
 AF011573  
 F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942  
 20 F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199:  
 60//Hs.104315:AF054828  
 F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292  
 F-NT2RP2004142  
 25 F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872  
 F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666  
 F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966  
 F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501  
 F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.7e-16:276:67//Hs.36779:  
 AA626790  
 30 F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:  
 U57317  
 F-NT2RP2004196  
 F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756  
 35 F-NT2RP2004226//ESTs, Weakly Similar to teg292 protein [M.musculus]//1.8e-80:386:98//Hs.68791:AA527270  
 F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756  
 F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680  
 F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536  
 F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487  
 40 F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans]//8.2e-51:474:74//Hs.108990:  
 N25951  
 F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:80//Hs.12432:AC005263  
 F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:  
 157:67//Hs.37121:Z37544  
 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:  
 45 AF000416  
 F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735  
 F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510  
 F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632  
 50 F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202  
 F-NT2RP2004365  
 F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs.39163:  
 AF000986  
 F-NT2RP2004373  
 55 F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III  
 [Caenorhabditis elegans]//3.3e-97:477:98//Hs.30490:AA146916  
 F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588  
 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21//1.4e-174:875:95//Hs.152759:AC005164  
 F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans]//1.2e-92:519:91//Hs.13275:AI341468

F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367  
 F-NT2RP2004412  
 F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944  
 F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687  
 5 F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TASK) mRNA, complete cds//0.45:  
 208:61//Hs.24040:AF006823  
 F-NT2RP2004490  
 F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203  
 F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.3e-29:270:79//  
 10 Hs.73614:U83460  
 F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6e-139:687:96//Hs.129908:  
 AB011163  
 F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891  
 F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-06:291:61//Hs.132206:  
 15 AF039694  
 F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs.155464:AF088219  
 F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.98:136:64//Hs.28020:AB018309  
 F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.0:104:68//Hs.125729:N99898  
 F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.24756:U43895  
 20 F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-59:  
 273:93//Hs.12845:N28835  
 F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908  
 F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496:98//Hs.5198:AJ006291  
 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2e-155:728:98//Hs.29956:  
 25 AB007929  
 F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839  
 F-NT2RP2004681  
 F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327:94//Hs.154919:  
 AB014525  
 30 F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942  
 F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780  
 F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582:96//Hs.4236:  
 AB007947  
 F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242  
 35 F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183  
 F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]//  
 3.7e-110:548:96//Hs.85768:W16504  
 F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547:57//Hs.  
 107474:AF045451  
 40 F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121:64//Hs.2864:  
 L40157  
 F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//  
 4.9e-118:594:95//Hs.40820:AF058953  
 F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043  
 45 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:  
 AF054179  
 F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161  
 F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258  
 F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111  
 50 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144  
 F-NT2RP2004936  
 F-NT2RP2004959  
 F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763  
 F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478  
 55 F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735  
 F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927  
 F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.  
 41723:U37426

F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478  
 F-NT2RP2004999  
 F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//  
 Hs.124161:AF065164  
 5 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:  
 AB014515  
 F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200  
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141  
 F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600  
 10 F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433  
 F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067  
 F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035  
 F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612  
 F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:  
 15 AF055917  
 F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838  
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:98//Hs.22616:  
 AB014564  
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs.  
 20 100555:X98743  
 F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803  
 F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947  
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226:  
 AF045583  
 25 F-NT2RP2005147  
 F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI357582  
 F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:AI357868  
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:96//Hs.155218:  
 AJ007509  
 30 F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159  
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189  
 F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783  
 F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264:U70439  
 F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341  
 35 F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs.  
 81452:AF030555  
 F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI383932  
 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//  
 Hs.27007:AF060219  
 40 F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590  
 F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833  
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763:  
 AB014576  
 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.6e-23:166:90//Hs.  
 45 1569:U11701  
 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
 cds//0.016:353:62//Hs.113265:AF032387  
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138  
 F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958  
 50 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100:  
 489:96//Hs.107254:AC005943  
 F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122  
 F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs.  
 113252:U80761  
 55 F-NT2RP2005407  
 F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.28:338:57//Hs.6189:AB011133  
 F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068  
 F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164

F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tauru]/8.5e-48:295:90//Hs.75017:AA166853  
 F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243  
 F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//0.032:176:64//Hs.16:D10656  
 5 F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:AD78412  
 F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds//9.9e-48:432:77//Hs.15519:  
 AB018315  
 F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573  
 F-NT2RP2005491  
 10 F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:AI084164  
 F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-48:621:68//Hs.6833:AB002324  
 F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete cds//1.6e-63:503:78//Hs.7688:  
 M64930  
 F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.56:139:66//Hs.8546:U97669  
 15 F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//1.0:  
 291:59//Hs.89709:L35546  
 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//1.2e-82:  
 444:92//Hs.119023:AF092563  
 F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//2.2e-19:112:99//Hs.6232:  
 20 AB018307  
 F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1 [H.sapiens]//3.5e-50:366:83//Hs.  
 61833:AA036735  
 F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//9.4e-155:747:97//Hs.159597:  
 AJ012449  
 25 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.9e-131:618:98//Hs.62515:  
 AB007963  
 F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME  
 III [C.elegans]//2.5e-51:292:93//Hs.105684:H24407  
 F-NT2RP2005555//EST//0.046:308:57//Hs.145962:AI276822  
 30 F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:AI422839  
 F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436  
 F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:AI218627  
 F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071  
 F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:97//Hs.22396:AF062085  
 35 F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702  
 F-NT2RP2005635  
 F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905  
 F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:AI292145  
 F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:AI375440  
 40 F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.1433065:M86917  
 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-08:351:62//Hs.91400:  
 AB006626  
 F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239  
 F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//7.7e-96:462:98//  
 45 Hs.25664:AF089814  
 F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702  
 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79217:M77836  
 F-NT2RP2005694  
 50 F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds//0.15:496:  
 55//Hs.79326:L76703  
 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1e-126:599:97//Hs.61638:  
 AB018342  
 F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527  
 F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//Hs.69740:U09367  
 55 F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017  
 F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:AI334191  
 F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086  
 F-NT2RP2005741//Homo sapiens chondroadherin gene, 5'flanking region and//0.80:362:58//Hs.97220:U96769

F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688  
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//  
 Hs.159651:AF068868  
 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.  
 5 26285:AF082516  
 F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853  
 F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895  
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836  
 F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:  
 10 Z50115  
 F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556  
 F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.  
 34853:U28368  
 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820  
 15 F-NT2RP2005812  
 F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595  
 F-NT2RP2005835  
 F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//  
 20 Hs.59829:AB014602  
 F-NT2RP2005853  
 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:  
 98//Hs.50758:AF092564  
 F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567  
 F-NT2RP2005868  
 25 F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240:  
 L16782  
 F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943  
 F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360  
 F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399  
 30 F-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882:  
 AA292186  
 F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770  
 F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339  
 F-NT2RP2006023  
 35 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382  
 F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664  
 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093  
 F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469  
 F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416  
 40 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970  
 F-NT2RP2006100  
 F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135  
 F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349  
 F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240  
 45 F-NT2RP2006166  
 F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73//Hs.74368:X69910  
 F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-114:567:96//Hs.109299:  
 AB014554  
 F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:85//Hs.15519:  
 50 AB018315  
 F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503  
 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.153910:X96484  
 F-NT2RP2006237  
 F-NT2RP2006238  
 55 F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970  
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//0.019:111:71//Hs.157199:X97630  
 F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//2.4e-05:388:  
 60//Hs.75111:D87258

F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:97//Hs.3404:AF035262  
 F-NT2RP2006320//ESTs, Moderately similar to maternal transcript Maid [M.musculus]//1.9e-29:151:100//Hs.  
 36794:AI038407  
 F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371  
 5 F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:70//Hs.87202:D82344  
 F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892:  
 AF076974  
 F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174  
 F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501  
 10 F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341  
 F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.  
 95838:AF059734  
 F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934  
 F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509  
 15 F-NT2RP2006456  
 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein/1.1e-149:545:98//Hs.72160:AJ006266  
 F-NT2RP2006467  
 F-NT2RP2006472  
 F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048  
 20 F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134  
 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete  
 cds//2.1e-115:669:90//Hs.31218:AF038966  
 F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.  
 73864:U22029  
 25 F-NT2RP2006573  
 F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223  
 F-NT2RP300002//ESTs//3.6e-32:215:86//Hs.155446:AA188180  
 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-137:637:98//Hs.6764:  
 AJ011972  
 30 F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:  
 AF000560  
 F-NT2RP3000047  
 F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.  
 37138:U35376  
 35 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961  
 F-NT2RP3000068  
 F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769  
 F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670  
 F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:X14608  
 40 F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140  
 F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595  
 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:438:100//Hs.8173:AC005189  
 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:  
 AB011164  
 45 F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-20:133:94//Hs.23094:M19503  
 F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs.  
 127338:AB007961  
 F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779  
 50 F-NT2RP3000207  
 F-NT2RP3000220  
 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs.  
 122967:AF059569  
 F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740  
 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691:86//Hs.75863:D86972  
 55 F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733  
 F-NT2RP3000252  
 F-NT2RP3000255  
 F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568

F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214:67//Hs.  
80261:L43821

F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863

F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//  
5 0.0088:236:63//Hs.102732:U88153

F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:AI091242

F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.57:189:65//  
Hs.46146:AA418097

F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390  
10 F-NT2RP3000348

F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754

F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642:  
X60673

F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921  
15 F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymnaea stagnalis]//4.0e-116:  
596:95//Hs.21094:AI337016

F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639

F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873

F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307:  
20 AF071185

F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610:65//Hs.23094:M19503

F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948

F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487  
25 F-NT2RP3000441

F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:AI051562

F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.75562:U48705

F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068

F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:AI289822  
30 F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058

F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667

F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379  
35 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:63//Hs.79347:D86966

F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308

F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412  
40 F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404

F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723

F-NT2RP3000578

F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277

F-NT2RP3000584

F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904  
45 F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:57//Hs.77234:AB001914

F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811

F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:355:92//Hs.114622:AA693492  
50 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:59//Hs.79170:D86980

F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:AI421203

F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683

F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162

F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:AI017333

F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904  
55 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.155464:AF088219

F-NT2RP3000661

F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.  
13063:AF017789

F-NT2RP3000685

F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001  
55 F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884

F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854

F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:AI369426

EP 1 074 617 A2

F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765  
 F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245:91//Hs.  
 2427:D89937  
 F-NT2RP3000815  
 5 F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132  
 F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700  
 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapi-  
 ens]//1.1e-71:363:96//Hs.23803:AA126476  
 F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012  
 10 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593:68//Hs.157199:  
 X97630  
 F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520  
 F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:86//Hs.155464:AF088219  
 F-NT2RP3000852  
 15 F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699918  
 F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476  
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete  
 cds//6.4e-31:766:60//HS.15432:U53445  
 F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60//Hs.79706:U53204  
 20 F-NT2RP3000875  
 F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101  
 F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI348374  
 F-NT2RP3000917  
 25 F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340:60//Hs.109895:X68277  
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X84407  
 F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:AI204212  
 F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411  
 F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N92198  
 F-NT2RP3001007  
 30 F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//  
 2.9e-121:588:98//Hs.128781:AA160707  
 F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282:97//Hs.  
 30303:AI244662  
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534:74//  
 35 Hs.27007:AF060219  
 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474:60//Hs.21264:AB018325  
 F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.4e-16:428:60//Hs.155481:  
 AJ006470  
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:64//Hs.82292:D86969  
 40 F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:AI337050  
 F-NT2RP3001111  
 F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088  
 F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023  
 F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779  
 45 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:61//Hs.12107:AF042384  
 F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687:75//Hs.69740:U09367  
 F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:60//Hs.94790:  
 AB018318  
 F-NT2RP3001133//Homeo box A4//0.00011:484:59//Hs.77637:M74297  
 50 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:98//Hs.5378:AB018305  
 F-NT2RP3001147  
 F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605  
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891:98//Hs.72160:AJ006266  
 F-NT2RP3001176  
 55 F-NT2RP3001214//EST//0.88:218:60//Hs.161147:AI417859  
 F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W19981  
 F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512:95//Hs.103816:AA130866  
 F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010

F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756  
 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:L06237  
 F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132  
 F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:293:60//Hs.32934:U27109  
 5 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:64//Hs.107809:  
 AB018269  
 F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.2e-42:454:  
 72//Hs.41728:L75847  
 F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566  
 10 F-NT2RP3001274  
 F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811  
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:69//Hs.31463:D87457  
 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437:  
 U44060  
 15 F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glyco-  
 gen storage disease type III)//0.012:522:56//Hs.904:U84010  
 F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731  
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966  
 F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:  
 20 AB007920  
 F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.00019:473:  
 61//Hs.124161:AF065164  
 F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 [H.sapiens]//  
 1.1e-81:421:96//Hs.32508:H29831  
 25 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487  
 F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022  
 F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451  
 F-NT2RP3001384//Homo sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332  
 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595  
 30 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783  
 F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.0e-05:189:  
 66//Hs.41728:L75847  
 F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end//0.77:132:66//Hs.  
 111024:L77567  
 35 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658  
 F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047  
 F-NT2RP3001426  
 F-NT2RP3001427  
 F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:431:91//Hs.85844:X66397  
 40 F-NT2RP3001432//ESTs, Moderately similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!! [H.sapiens]//6.9e-  
 05:195:65//Hs.115868:AA568393  
 F-NT2RP3001447  
 F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.89631:U48508  
 F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212  
 45 F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323  
 F-NT2RP3001459  
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//4.2e-10:168:70//Hs.32317:  
 AF072836  
 F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877  
 50 F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231  
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//  
 2.8e-172:804:98//Hs.28285:AF064801  
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds//9.4e-139:743:  
 91//Hs.85283:U36500  
 55 F-NT2RP3001529//ESTs, Moderately similar to topoisomerase IC-terminal fragment [H.sapiens]//0.28:224:65//Hs.  
 105912:AI431328  
 F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074  
 F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.147918:U38291

F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302  
 F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)//0.049:185:65//Hs.1686:  
 M69013  
 F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.6e-51:345:82//Hs.144563:  
 AF057280  
 F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688  
 F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349  
 F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435  
 F-NT2RP3001629  
 F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:276:97//Hs.9899:AF099149  
 F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173  
 F-NT2RP3001646  
 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e-172:816:98//Hs.159597:  
 AJ012449  
 F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027  
 F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//9.0e-53:  
 375:85//Hs.41127:AA555184  
 F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071  
 F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III  
 [Caenorhabditis elegans]//4.0e-111:518:99//Hs.20364:AI420022  
 F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198  
 F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329  
 F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219  
 F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [D.mela-  
 nogaster]//1.4e-31:191:94//Hs.131279:AA486291  
 F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862  
 F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]  
 //7.6e-159:747:98//Hs.6823:W18181  
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:  
 565:97//Hs.159273:AF054177  
 F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III  
 [Caenorhabditis elegans]//3.5e-116:554:98//Hs.144332:AA046836  
 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:78//Hs.90998:D50918  
 F-NT2RP3001739  
 F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.116549:AL009172  
 F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete  
 cds//0.10:528:56//Hs.22138:U49250  
 F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2.4e-47:725:64//Hs.41688:  
 U27193  
 F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds//0.42:198:61//Hs.  
 57783:U78525  
 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1e-153:710:98//Hs.28169:  
 AB007928  
 F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.79024:L03532  
 F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361  
 F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L41162  
 F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379:58//Hs.32950:X82634  
 F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729  
 F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.8e-35:481:67//Hs.158225:  
 U68727  
 F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706  
 F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.elegans]//2.9e-94:452:98//Hs.54952:  
 AA872675  
 F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6139:AL022326  
 F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896  
 F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185  
 F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247  
 F-NT2RP3001931

F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022:268:61//Hs.106070:U22398  
 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.8e-167:815:96//Hs.15869:  
 AB014575  
 5 F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335  
 F-NT2RP3001969  
 F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180  
 F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs.155464:AF088219  
 F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.75087:X86779  
 F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946  
 10 F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821  
 F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67//Hs.147189:D88153  
 F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]//3.8e-48:353:81//Hs.127507:  
 AA993745  
 F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0e-25:212:83//Hs.71622:AA195155  
 15 F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens]//4.2e-82:  
 407:97//Hs.131888:AI091806  
 F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503  
 F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710  
 F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//  
 20 0.91:194:65//Hs.1298:J03779  
 F-NT2RP3002081  
 F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA partial cds//0.073:  
 297:61//Hs.102732:U88153  
 F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256  
 25 F-NT2RP3002108  
 F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018  
 F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260  
 F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with  
 some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative  
 30 CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009  
 F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644  
 F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985  
 F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]  
 //3.0e-61:340:93//Hs.11379:AA594140  
 35 F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046  
 F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME  
 III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915  
 F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA30643  
 F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic1)//0.98:  
 40 242:57//Hs.114001:Z20656  
 F-NT2RP3002248  
 F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261  
 F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.  
 110637:AC004080  
 45 F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139  
 F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386  
 F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910  
 F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871  
 F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383  
 50 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65:  
 588:75//Hs.154672:X16396  
 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//4.2e-166:770:98//Hs.6483:  
 Y16355  
 F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200  
 55 F-NT2RP3002399  
 F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274  
 F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:  
 AB014578

F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:AI291310  
 F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108  
 F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935  
 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.  
 5 57738:U35246  
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542:  
 AB018272  
 F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510:70//Hs.  
 10 96759:AA469984  
 F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706  
 F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054  
 F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919  
 F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508  
 F-NT2RP3002603  
 15 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:61//Hs.3845:AB014888  
 F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.121287:AF029900  
 F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.6e-13:441:63//Hs.155481:  
 AJ006470  
 F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.  
 20 151518:U38847  
 F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308  
 F-NT2RP3002663//ESTs, Highly similar to OXYSTEROOL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70//  
 Hs.41086:AI337400  
 F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI421991  
 25 F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:294:100//Hs.128750:AI367584  
 F-NT2RP3002687  
 F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI352200  
 F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI393657  
 F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279514  
 30 F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291  
 F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161:62//  
 Hs.129736:AF040753  
 F-NT2RP3002785  
 F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713  
 35 F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:423:93//Hs.41068:AA844350  
 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940:  
 AF004715  
 F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070  
 F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582  
 40 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895  
 F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040  
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314  
 F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765  
 F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//  
 45 Hs.3826:U69560  
 F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599:  
 AB011160  
 F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262  
 F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870  
 50 F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997  
 F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI287703  
 F-NT2RP3002985//Human TFIIB related factor hBRF (hBRF) mRNA, complete cds//0.071:550:58//Hs.32935:  
 U28838  
 F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308  
 55 F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083  
 F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446  
 F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749  
 F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609

F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928  
 F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079  
 F-NT2RP3003078  
 F-NT2RP3003101  
 5 F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//0.98:  
 88:68//Hs.99715:AA292700  
 F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740  
 F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1)  
 mRNA, complete cds//0.013:438:57//Hs.101299:AF017061  
 10 F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975  
 F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:  
 63//Hs.118397:AF053944  
 F-NT2RP3003150  
 F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.  
 15 37138:U35376  
 F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093  
 F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:X78933  
 F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211  
 F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854  
 20 F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308  
 F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325  
 F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525  
 F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:  
 D44497  
 25 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:  
 AF055460  
 F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200  
 F-NT2RP3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//  
 Hs.620:M69225  
 30 F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792:  
 AF044924  
 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983  
 F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953  
 F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947  
 35 F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503  
 F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947  
 F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058  
 F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200  
 F-NT2RP3003330  
 40 F-NT2RP3003344  
 F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339  
 F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833  
 F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542  
 F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791  
 45 F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:H16363  
 F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850  
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:  
 63//Hs.113272:U90653  
 F-NT2RP3003411//Human metallothionein-1e gene (HMT-1e)//0.99:116:62//Hs.74170:M10942  
 50 F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830  
 F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:M93425  
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-182:853:98//Hs.  
 14934:AF004828  
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:98//Hs.26450:  
 AB018268  
 F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98330  
 F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302  
 F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:626:58//Hs.150828:

AF038169  
 F-NT2RP3003552  
 F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:AI418322  
 F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365  
 5 F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311  
 F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247  
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56741  
 F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:564:61//Hs.104:  
 D14012  
 10 F-NT2RP3003625  
 F-NT2RP3003656  
 F-NT2RP3003659  
 F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586  
 F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184  
 15 F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds//0.013:190:  
 63//Hs.44585:U58334  
 F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246:62//Hs.118463:AF055000  
 F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848  
 F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61//Hs.48998:AB007865  
 20 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700:98//Hs.48513:  
 AB018300  
 F-NT2RP3003746  
 F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230  
 F-NT2RP3003799  
 25 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog//4.7e-41:432:73//Hs.1422:  
 M19722  
 F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:  
 242:57//Hs.114001:Z20656  
 F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//  
 30 5.1e-07:624:59//Hs.96028:AF042832  
 F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171:63//Hs.  
 102877:U41315  
 F-NT2RP3003825  
 F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:AI346481  
 35 F-NT2RP3003831  
 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300:  
 AF070611  
 F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:M73780  
 F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268  
 40 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738:  
 AB018343  
 F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243:90//Hs.124832:AA846576  
 F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE  
 PRECURSOR [D.melanogaster]//1.1e-107:499:99//Hs.105794:AA701659  
 45 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49:  
 404:77//Hs.9006:AF057358  
 F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396  
 F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006  
 50 F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433:58//Hs.  
 93909:AF042498  
 F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//2.8e-127:617:97//Hs.  
 142151:AA984061  
 F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs.  
 155302:U57317  
 55 F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234  
 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:67//Hs.26441:AB002317  
 F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875  
 F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520:90//Hs.

100007:X76091  
 F-NT2RP3004093  
 F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258  
 F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390  
 5 F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:AI096509  
 F-NT2RP3004145  
 F-NT2RP3004148  
 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:  
 10 AF032900  
 F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706  
 F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640  
 F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:  
 15 62//Hs.101047:M31523  
 F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835  
 F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361  
 F-NT2RP3004242  
 F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240  
 F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:AI149140  
 20 F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067  
 F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.  
 158471:AF088982  
 F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597:61//Hs.19261:AF007871  
 F-NT2RP3004332  
 25 F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285  
 F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426  
 F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999  
 F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME  
 III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141429:AA631915  
 30 F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//  
 4.3e-125:608:98//Hs.128781:AA160707  
 F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1//2.3e-141:804:90//Hs.123122:  
 X97249  
 F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:96//Hs.20132:AA203113  
 35 F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.153638:AF010403  
 F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.00023:357:59//Hs.99948:M97016  
 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583:99//Hs.27349:  
 AB007917  
 F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399:58//Hs.22616:AB014564  
 40 F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219  
 F-NT2RP3004472  
 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715:98//Hs.5003:AB007925  
 F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//  
 4.6e-118:547:99//Hs.124768:AA307735  
 45 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752:97//Hs.158311:AB012851  
 F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [M.musculus]//3.5e-89:425:99//Hs.126082:AI077718  
 F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256  
 F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370:59//Hs.158244:AB007948  
 F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.7647:M94046  
 50 F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110  
 F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571  
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679:98//Hs.75970:  
 AB014532  
 55 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793:98//Hs.74750:  
 AB011126  
 F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362:94//Hs.  
 125870:AI364967  
 F-NT2RP3004569

F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF50) mRNA, complete cds//3.3e-181:860:97//  
Hs.122752:AF026445

F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928:  
AB007923

5 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266

F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger protein, efp [H.sapiens]//6.4e-13:356:64//  
Hs.124138:AI266336

F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232

F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204

10 F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436

F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98//  
Hs.118991:AA675919

F-NT2RP4000023//ESTs//1-4e-33:182:96//Hs.122722:AA455668

F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495

15 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761

F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481:  
AJ006470

F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720:97//Hs.159597:  
AJ012449

20 F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743

F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538

F-NT2RP4000111

F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:  
AB007952

25 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069

F-NT2RP4000150

F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356

F-NT2RP4000159

F-NT2RP4000167

30 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946

F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:  
AB014600

F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006

F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731

35 F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.  
46468:U45984

F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481:  
AJ006470

F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:  
384:89//Hs.115498:AA436298

40 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:  
AF091092

F-NT2RP4000263

F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580

45 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481

F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.  
143648:AB000732

F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112

F-NT2RP4000355

50 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:  
AB018281

F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-  
137:649:97//Hs.31323:AF044195

F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECUR-  
SOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073

F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//  
0.098:291:59//Hs.994:M95678

55 F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965

F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368  
 F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688  
 F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:  
 AF027156  
 5 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:431:73//Hs.  
 46468:U45984  
 F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087  
 F-NT2RP4000449//EST//0.84:113:65//Hs.145274:AI249468  
 F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853  
 10 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:  
 532:57//Hs.78683:Z72499  
 F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535  
 F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742  
 F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.  
 15 159234:U89995  
 F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293  
 F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594  
 F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904  
 F-NT2RP4440518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:  
 20 AJ010840  
 F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372  
 F-NT2RP4000524  
 F-NT2RP4000528  
 F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154  
 25 F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.  
 25597:H93026  
 F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351  
 F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053  
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.  
 30 4214:AF067730  
 F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513  
 F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396  
 F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:  
 60//Hs.144626:AF100907  
 35 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676:  
 98//Hs.50748:AB004848  
 F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, com-  
 plete cds//6.9e-07:494:61//Hs.113286:U77783  
 F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.111817:T80622  
 40 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178  
 F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440  
 F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058  
 F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162  
 F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123  
 45 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:  
 AB007939  
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189  
 F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833  
 F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603  
 50 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.  
 75875:U49278  
 F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367  
 F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:AI206803  
 F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843  
 55 F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142  
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901  
 F-NT2RP4000918  
 F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503  
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//  
 Hs.24812:AF069532  
 F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371  
 5 F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542  
 F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888  
 F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058  
 F-NT2RP4000979  
 F-NT2RP4000984  
 10 F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913  
 F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068  
 F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204  
 F-NT2RP4001004  
 15 F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718  
 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.  
 113287:AF009204  
 F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494  
 F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:  
 L40157  
 20 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157  
 F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481:  
 AJ006470  
 F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497  
 F-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase, partial//1.4e-131:634:98//Hs.  
 25 106778:AJ010953  
 F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//0.025:166:66//Hs.  
 146459:X66975  
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164  
 F-NT2RP4001095  
 30 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054  
 F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis  
 familiaris]//2.2e-26:171:92//Hs.14038:R06800  
 F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142  
 F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:  
 35 100//Hs.126925:AA931237  
 F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.1433 82:AA476266  
 F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261  
 F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207  
 F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171  
 40 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734  
 F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324  
 F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264  
 F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324  
 F-NT2RP4001207  
 45 F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636  
 F-NT2RP4001213//KRAB zinc finger protein {alternative products}//1.1e-45:187:74//Hs.22556:U37251  
 F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262  
 F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.  
 122967:AF059569  
 50 F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778  
 F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463  
 F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59kD, acidic component)//0.015:246:62//  
 Hs.31121:U40571  
 F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578  
 55 F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736  
 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding  
 mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250  
 F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917

F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110  
 F-NT2RP4001339  
 F-NT2RP4001343  
 F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39:686:64//Hs.112125:M12625  
 5 F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//2.0e-31:784:62//Hs.15432:U53445  
 F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356  
 F-NT2RP4001372  
 10 F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194  
 F-NT2RP4001375  
 F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190  
 F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918  
 F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109  
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957  
 15 F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:X78933  
 F-NT2RP4001442  
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:  
 AB018326  
 20 F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.  
 26676:AA033997  
 F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523  
 F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]//0.25:216:60//Hs.  
 63220:AA522707  
 F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395  
 25 F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:61//Hs.5923:X82260  
 F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:AI377863  
 F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494  
 F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481:  
 U13220  
 30 F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U50534  
 F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174  
 F-NT2RP4001567  
 F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-CBR5 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:AA167836  
 35 F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410  
 F-NT2RP4001574  
 F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228  
 F-NT2RP4001592  
 F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903  
 40 F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952  
 F-NT2RP4001634  
 F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKH1-STH1 INTERGENIC  
 REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436  
 F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409  
 45 F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECUR-  
 SOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629  
 F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162:  
 67//Hs.30250:AF055376  
 F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080  
 50 F-NT2RP4001696  
 F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927  
 F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.  
 92614:M62302  
 F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198  
 55 F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878  
 F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656  
 F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:  
 AC004522

F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete  
 cds//0.028:580:58//Hs.2363:L36069  
 F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131  
 F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:  
 5 U11690  
 F-NT2RP4001828  
 F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888  
 F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749  
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336:  
 10 AB014572  
 F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.8e-12:  
 84:94//Hs.140232:AA705170  
 F-NT2RP4001889  
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:97//Hs.15144:AC005014  
 15 F-NT2RP4001896  
 F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848  
 F-NT2RP4001927  
 F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.8e-54:375:84//Hs.119294:  
 20 AI379442  
 F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894  
 F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063  
 F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868  
 25 F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene  
 for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:  
 788:65//Hs.23796:AL022718 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete  
 cds//0.0019:279:65//Hs.159439:AF092047  
 F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//0.58:463:55//Hs.  
 30 3826:U69560  
 F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139  
 F-NT2RP4002052  
 F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873  
 F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//  
 35 Hs.100030:AF002999  
 F-NT2RP4002075  
 F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.0e-38:243:90//Hs.139115:  
 AA325104  
 F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654  
 F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:M96684  
 40 F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284  
 F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204  
 F-NT2RP4002888  
 F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960  
 F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96//Hs.74456:U34995  
 45 F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071  
 F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067  
 F-NT2RP5003492  
 F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase, complete cds//6.1e-56:750:69//  
 50 Hs.132884:AB006179  
 F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-14:348:62//Hs.154050:  
 AC004131  
 F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.94:202:63//Hs.8152:AB014542  
 F-NT2RP5003522  
 F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943  
 55 F-NT2RP5003534  
 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0e-69:373:94//Hs.108258:  
 AB007934  
 F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729

F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina moschata]//4.4e-75:355:99//Hs.36727:  
AI051983  
 F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304  
 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:815:98//Hs.81449:AF058922  
 5 F-OVARC1000017//Homo sapiens mRNA for NTAK, complete cds//0.50:482:58//Hs.113264:AB005060  
 F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:238:89//Hs.69469:AF064603  
 F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549  
 F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapiens]//6.7e-60:305:97//Hs.31696:  
H50008  
 10 F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798  
 F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543  
 F-OVARC1000085  
 F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442  
 F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete . cds//0.00017:414:59//Hs.106387:AF029778  
 15 F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600  
 F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]//2.9e-73:406:92//Hs.109463:AI205174  
 F-OVARC1000109  
 F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-  
135:663:96//Hs.3688:AF069250  
 20 F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.4e-43:532:72//Hs.118401:  
AB011134  
 F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010  
 F-OVARC1000139  
 F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293  
 25 F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414  
 F-OVARC1000151  
 F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305  
 F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth  
and development factor)//0.10:504:59//Hs.154083:U70136  
 30 F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131  
 F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840  
 F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834  
 F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]  
//2.7e-31:264:79//Hs.151895:AA196379  
 35 F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984  
 F-OVARC1000288//TESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.00084:170:65//Hs.107747:AI357868  
 F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306  
 F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287  
 40 F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECUR-  
SOR [Felis catus]//0.51:193:66//Hs.6194:AI378579  
 F-OVARC1000321  
 F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60//  
Hs.122359:AF051946  
 F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444  
 45 F-OVARC1000347  
 F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1)  
mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450  
 F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64//Hs.156016:D50930  
 F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162  
 50 F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682  
 F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58//Hs.156016:D50930  
 F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7e-25:190:84//Hs.139513:AA259082  
 F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615  
 F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93 :281:60//Hs.76279:X53416  
 55 F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//Hs.83987:U09284  
 F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423  
 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.2e-140:566:99//Hs.12334:  
AB014583

F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:AI024524  
 F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.108112:AF070640  
 F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854  
 F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926  
 5 F-OVARC1000479  
 F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036  
 F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327  
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:539:99//Hs.111285:AF051850  
 F-OVARC1000526//ESTs//2.9e-08:368:611//Hs.42771:N26740  
 10 F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492  
 F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475  
 F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667  
 F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410  
 F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135:  
 15 66//Hs.85302:U76421  
 F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358  
 F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200  
 F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729  
 F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63//Hs.3080:U29725  
 20 F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722  
 F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881  
 F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097  
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-  
 25 plete cds//1.6e-78:424:93//Hs.86859:D43772  
 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536:94//Hs.111862:  
 AB011162  
 F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:AI277106  
 F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279  
 F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639  
 30 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549:99//Hs.  
 125315:AF027156  
 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306  
 F-OVARC 1000700  
 F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320  
 35 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//  
 1.2e-110:451:91//Hs.13476:AF038661  
 F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318:91//Hs.7049:  
 AI141736  
 F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411  
 40 F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196  
 F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194:99//  
 Hs.157059:W28130  
 F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793  
 F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835  
 45 F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584  
 F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032  
 F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390  
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432:100//Hs.155995:  
 AB014543  
 50 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//Hs.18910:AF045584  
 F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6.1e-31:183:93//Hs.108620:AA418155  
 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133:69//Hs.  
 159234:U89995  
 F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143  
 55 F-OVARC1000885//EST//0.91:152:63//Hs.160765 :AI313323  
 F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777  
 F-OVARC 1000890  
 F-OVARC1000891

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F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818  
F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:AI376601  
F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419:97//Hs.9028:AF039691  
F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456  
5 F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623:72//Hs.114440:  
M11119  
F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078  
F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157:97//Hs.  
136243:AA307843  
10 F-OVARC 1000948  
F-OVARC1000959//EST//0.65:293:55//Hs.134725:AI088986  
F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952  
F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288  
F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:AI283069  
15 F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661  
F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs.  
155302:U57317  
F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458:  
AF088219  
20 F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114  
F-OVARC1001004  
F-OVARC1001010  
F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234:99//Hs.110327:AA205866  
F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.0076:  
25 624:57//Hs.75063:AL023584  
F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578:89//Hs.111974:AI050735  
F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733:97//Hs.9899:AF099149  
F-OVARC 1001040//ESTs//2.2e-38:204:96//Hs.128927:AI168074  
F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385  
30 F-OVARC1001051  
F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381:81//Hs.  
154968:U02020  
F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:AI312873  
F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183:84//Hs.46680:AA809451  
35 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620:98//Hs.  
3426:AF082657  
F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013  
F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937  
40 F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X98248  
F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,  
LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.3e-75:289:95//Hs.21753:AJ005897  
F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//Hs.12912:AF015913  
F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.1e-151:710:98//Hs.26584:  
AF051782  
45 F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102  
F-OVARC1001118  
F-OVARC1001129  
F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008  
F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725  
50 F-OVARC1001162  
F-OVARC1001167  
F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:AI078279  
F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287  
F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159  
55 F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 PRECURSOR [Homo sapi-  
ens]//1.8e-11:192:69//Hs.130020:AA887581  
F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//Hs.91103:AC005551  
F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//1.5e-13:199:71//Hs.109966:

C06057  
 F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324:90//Hs.114673:W72675  
 F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889  
 5 F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X51688  
 F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745676  
 F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424825  
 F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.75243:D42040  
 F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:AI377837  
 10 F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821  
 F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224  
 F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8e-144:644:96//Hs.155995:  
 AB014543  
 F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:355:60//Hs.108812:AA044835  
 15 F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172  
 F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.20:188:64//Hs.  
 152455:AF044209  
 F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264  
 F-OVARC1001330  
 20 F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like  
 1)//0.021:232:62//Hs.79410:U62531  
 F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:363:99//Hs.105837:AA536054  
 F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA897493  
 F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:N67251  
 25 F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198:61//Hs.105940:  
 AF004715  
 F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:AI264633  
 F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:AI025777  
 30 F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533:74//Hs.109299:  
 AB014554  
 F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365:73//Hs.  
 129735:AF010144  
 F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//4.1e-149:683:99//  
 Hs.151428:AJ224819  
 35 F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.097:235:  
 65//Hs.25674:AF072242  
 F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28225  
 F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651  
 F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586:69//Hs.74597:U52426  
 40 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651  
 F-OVARC1001436  
 F-OVARC1001442  
 F-OVARC1001453  
 45 F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGEN-  
 IC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.110950:AI041823  
 F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568  
 F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343  
 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA; complete cds//2.6e-86:479:92//Hs.6534:  
 AF016507  
 50 F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-97:538:92//Hs.75813:L33243  
 F-OVARC1001525  
 F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786  
 F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595  
 F-OVARC1001555  
 55 F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA//6.8e-57:275:98//Hs.155160:  
 AF031166  
 F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.0035:  
 271:60//Hs.108465:AI144299

F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:216:99//Hs.120002:AI038398  
 F-OVARC1001611  
 F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500  
 F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144  
 5 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582:  
 AB006867  
 F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229  
 F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858  
 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807  
 10 F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863  
 F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825  
 F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588  
 F-OVARC1001762  
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//  
 15 1.4e-150:706:98//Hs.155377:U97670  
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:  
 AB014575  
 F-OVARC1001768//ESTs//0.035:179:64//Hs.87279:AI218697  
 F-OVARC1001791  
 20 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830  
 F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI005102  
 F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:  
 AB018287  
 25 F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.  
 69949:M94172  
 F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825  
 F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453  
 F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567  
 30 F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537  
 F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973  
 F-OVARC1001861  
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:  
 AF070611  
 35 F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel sub-unit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709  
 F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127  
 F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.  
 158095:AB007953  
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//  
 40 2.6e-57:300:96//Hs.6216:AF061749  
 F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834  
 F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261  
 F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263  
 F-OVARC1001928  
 45 F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204  
 F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III  
 [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794  
 F-OVARC1001949//KRAB zinc finger protein {alternative products}//1.8e-17:294:67//Hs.22556:U37251  
 F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228  
 50 F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639  
 F-OVARC1001989//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.2e-23:  
 213:78//Hs.105292:AA504776  
 F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417  
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258:  
 55 AB007934  
 F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865  
 F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063  
 F-OVARC1002107

F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498:96//Hs.75258:  
 AF054174  
 F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913  
 F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:62//Hs.112725:AF056022  
 5 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795  
 F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097  
 F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:AI357868  
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929:  
 X79568  
 10 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517  
 F-PLACE1000044//ESTs//0.79:332:59//Hs.120221:AA731230  
 F-PLACE1000055//ESTs//1.8e-10:89:87//Hs.158913:AI378928  
 F-PLACE1000077//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs.  
 42400:AF022789  
 15 F-PLACE1000014  
 F-PLACE1000031  
 F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088  
 F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494  
 F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755  
 20 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499  
 F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-47:266:  
 93//Hs.30026:AI356771  
 F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-  
 15:203:70//Hs.157422:R85366  
 25 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30:324:60//Hs.76460:U49082  
 F-PLACE1000094  
 F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//  
 Hs.111081:AI380378  
 F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:  
 30 AA632135  
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.  
 151017:AF058291  
 F-PLACE1000185  
 F-PLACE1000213  
 35 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255  
 F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226  
 F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022  
 F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202  
 F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294  
 40 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047  
 F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675  
 F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:  
 M37197  
 F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:  
 45 262:58//Hs.102732:U88153  
 F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024  
 F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516  
 F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:  
 93//Hs.19501:AA742260  
 50 F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174  
 F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:  
 U33053  
 F-PLACE1000424  
 F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590  
 55 F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)  
 //2.7e-52:421:80//Hs.69747:M35531  
 F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638  
 F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

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F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60//Hs.153014:AB002353  
F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573  
F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.  
75578:M85289  
5 F-PLACE1000562  
F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538  
F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//Hs.21838:AF038179  
F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542  
F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597:  
10 AJ012449  
F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751  
F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542  
F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986  
F-PLACE1000636  
15 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.0e-154:747:  
96//Hs.5819:AF102265  
F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and  
LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.29595:AJ005896  
F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//1.0e-57:675:  
20 69//Hs.128763:AF009353  
F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949  
F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447  
F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288  
F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:331:57//Hs.37110:U10694  
25 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858  
F-PLACE1000769  
F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921:  
AB014548  
F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215  
30 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079  
F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189  
F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180  
F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:U80736  
F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000  
35 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428  
F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455  
F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201  
F-PLACE1000948  
40 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs.  
80261:L43821  
F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk28h2.5 [C.elegans]//9.3e-45:309:88//  
Hs.13531:R61789  
F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.8597:L11672  
F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:96//Hs.158497:  
45 AB018267  
F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913  
F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:61//Hs.1974:M92432  
F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6940:Z48633  
F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876  
50 F-PLACE1001024  
F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741  
F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:U53204  
F-PLACE1001062  
55 F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859  
F-PLACE1001088  
F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485  
F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817  
F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:

71//Hs.150406:AF022158  
 F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704  
 F-PLACE1001168  
 F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135  
 5 F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741  
 F-PLACE1001238  
 F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494  
 F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929  
 F-PLACE1001272//COATOMER BETA'SUBUNIT//0.012:50:96//Hs.75724:X70476  
 10 F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283  
 F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:  
 58//Hs.124161:AF065164  
 F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs.  
 16533:D87930  
 15 F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:370:60//Hs.42672:AF016052  
 F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385  
 F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591  
 F-PLACE1001351  
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8e-26:155:95//Hs.61638:AB018342  
 20 F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44:393:79//Hs.152005:  
 AF009615  
 F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748  
 F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09:  
 117:84//Hs.21301:AF093419  
 25 F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE  
 EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646  
 F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete  
 CDS//0.0038:496:57//Hs.97681:AJ223333  
 F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.  
 30 154069:U06452  
 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404:  
 AF091087  
 F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232  
 F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987  
 35 F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510  
 F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455  
 F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716  
 F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529  
 F-PLACE1001503  
 40 F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914  
 F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753  
 F-PLACE1001545  
 F-PLACE1001551  
 F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835  
 45 F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233  
 F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987  
 F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230  
 F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005  
 50 F-PLACE1001611//Human facio-genital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690  
 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:  
 AB018341  
 F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198  
 F-PLACE1001640  
 F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927  
 55 F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-  
 148:726:96//Hs.3688:AF069250  
 F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN  
 [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI125696

F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.101555:U93869  
 F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776  
 F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686  
 5 F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094  
 F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.1480:M60052  
 F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159  
 F-PLACE1001745  
 F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361  
 10 F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//2.8e-160:773:97//Hs.4812:AF061243  
 F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-35:269:83//Hs.5247:AF029750  
 F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283  
 15 F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, complete cds//3.4e-52:548:72//Hs.150981:U47050  
 F-PLACE1001781  
 F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115  
 F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138  
 20 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//3.6e-110:546:96//Hs.40820:AF058953  
 F-PLACE1001821  
 F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494  
 F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214  
 F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906  
 25 F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257  
 F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220  
 F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-153:685:95//Hs.17839:AF099936  
 F-PLACE1001928//H.sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837  
 30 F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58//Hs.106387:AF029778  
 F-PLACE1001989  
 F-PLACE1002004  
 F-PLACE1002046  
 F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108  
 35 F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555  
 F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707  
 F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178  
 F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//  
 Hs.5171:AF069765  
 40 F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637  
 F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831  
 F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:  
 75//Hs.144290:T61747  
 F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631  
 45 F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390  
 F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891  
 F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627  
 F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674  
 F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.90798:U79289  
 50 F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989  
 F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI024442  
 F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935  
 F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-75:434:83//Hs.23094:M19503  
 F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675  
 55 F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279  
 F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291  
 F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710  
 F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067

F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458:66//Hs.  
40993:AF000148

F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI368947

F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:  
66//Hs.150406:AF022158

5 F-PLACE1002465

F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:AJ007581

F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523

F-PLACE1002493

10 F-PLACE1002499

F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.  
111967:U76010

F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482

15 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:  
AB018256

F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566:96//Hs.99348:  
AC004774

F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369

F-PLACE1002571//Homo sapiens mRNA for TP55, complete cds//0.99:274:59//Hs.138202:AF027866

20 F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627

F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI393725

F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:  
D44497

F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187

25 F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI198915

F-PLACE1002625

F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04412

F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706

30 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:  
804:97//Hs.124903:AF068180

F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903

F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:  
U92971

35 F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080

F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728

F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827

F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:  
AF082516

F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:AI368926

40 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994

F-PLACE1002815

F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691

F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:AI089163

45 F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:AI334167

F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405

F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024

F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627

F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:AI040029

50 F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056

F-PLACE1002962

F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:AI041815

F-PLACE1002991

F-PLACE1002993

F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans]//1.3e-12:104:86//Hs.124808:T86959

55 F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:  
AB007979

F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632:97//Hs.129872:  
AB011088

F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7e-14:555:58//Hs.154740:  
 AB014567  
 F-PLACE1003045  
 F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491  
 5 F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//Hs.102137:U31875  
 F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419  
 F-PLACE1003136  
 F-PLACE1003145  
 F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590  
 10 F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997  
 F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797  
 F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA, complete cds//0.98:  
 221:60//Hs.139756:U59209  
 F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532  
 15 F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:AI208770  
 F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208  
 F-PLACE1003249//Insulin-like growth factor 1 (somatomedia C)//0.99:175:62//Hs.85112:X57025  
 F-PLACE1003256  
 F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802  
 20 F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106  
 F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.  
 37138:U35376  
 F-PLACE1003334  
 F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308  
 25 F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568  
 F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//  
 2.6e-144:773:92//Hs.6564:U92715  
 F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:  
 78//Hs.163820:H7.1277  
 30 F.-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575  
 F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858  
 F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009  
 F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069  
 F-PLACE1003383  
 35 F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:  
 94//Hs.125175:AI142546  
 F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178  
 F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.40:206:62//Hs.30223:X90846  
 F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912  
 40 F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874  
 F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635  
 F-PLACE1003516//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.4e-85:357:86//Hs.103948:K00627  
 F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145  
 F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:Z48633  
 45 F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248  
 F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543:97//Hs.120416:AA057428  
 F-PLACE1003553  
 F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780  
 F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367  
 50 F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932  
 F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194  
 F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//1.4e-50:287:  
 93//Hs.154799:AA130620  
 F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965  
 55 F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961  
 F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97//Hs.56851:D83200  
 F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:64//Hs.22116:  
 AF064104

F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896  
 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:87//Hs.23094:M19503  
 F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105  
 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762  
 5 F-PLACE1003669//ESTs, Weakly similar to 3'- gene product [H.sapiens]//0.021:445:58//Hs.158275:AI365413  
 F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299  
 F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:669:95//Hs.98658:  
 AF053305  
 F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101  
 10 F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor protein//8.5e-09:393:60//Hs.103527:  
 AJ000553  
 F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928:  
 AI346344  
 F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648  
 15 F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983  
 F-PLACE1003768//Human kpni repeat mRNA (cdna clone pcd-kpni-4), 3' end//2.7e-40:608:68//Hs.139107:K00629  
 F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944  
 F-PLACE1003783  
 20 F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:57//Hs.62318:AB018308  
 F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169  
 F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786  
 F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165  
 F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124  
 F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359  
 25 F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257  
 F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770  
 F-PLACE1003886  
 F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:D42108  
 F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050  
 30 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944  
 F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142  
 F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR  
 [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069  
 F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585  
 35 F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537  
 F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536  
 F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522:  
 71//Hs.3136:U42412  
 F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812  
 40 F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940  
 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516  
 F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene spi1//0.85:164:64//Hs.  
 153045:X52056  
 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-41:422:74//Hs.3620:  
 45 X04526  
 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:AI333779  
 F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552  
 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:D83785  
 F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666  
 50 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201  
 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//  
 1.3e-145:695:98//Hs.24640:AF069493  
 F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722  
 F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273  
 55 F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689  
 F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-98:479:97//Hs.  
 31718:N29128  
 F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736

F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139:AB007914  
 F-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds//2.0e-157:756:  
 97//Hs.127007:AF084830  
 5 F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884  
 F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576  
 F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677  
 F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588  
 F-PLACE1004336  
 10 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:  
 688:97//Hs.16232:AF100153  
 F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552  
 F-PLACE1004384//Human HsLIM15 mRNA for HsLiml5, complete cds//2.0e-49:466:76//Hs.37181:D64108  
 F-PLACE1004388  
 15 F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871  
 F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579  
 F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190  
 F-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene  
 20 encoding mitochondrial protein, complete cds//9.9e-131:536:99//Hs.155410:U49283  
 F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867  
 F-PLACE1004460  
 F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363  
 F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085  
 F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416  
 25 F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163  
 F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680  
 F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699:97//  
 Hs.122752:AF026445  
 F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150  
 30 F-PLACE1004518  
 F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314  
 F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:  
 AA058854  
 F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371  
 35 F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299  
 F-PLACE1004645  
 F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991  
 F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590  
 F-PLACE1004664  
 40 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//  
 1.5e-66:357:95//Hs.77705:U07563  
 F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.  
 80019:AF035606  
 F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589  
 45 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561  
 F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131  
 F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845  
 F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542  
 F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891  
 50 F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148  
 F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680  
 F-PLACE1004743  
 F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-  
 2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90//Hs.6863:W52470  
 55 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-172:828:97//Hs.104715:AF084367  
 F-PLACE1004777//Human myosin IXb mRNA, complete cds//1.0e-29:556:63//Hs.159629:U42391  
 F-PLACE1004793  
 F-PLACE1004804

F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340  
 F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//2.4e-78:415:95//Hs.80965:AA493284  
 F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:69//Hs.22111:AB002362  
 5 F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047  
 F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943  
 F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97669  
 F-PLACE1004838  
 F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X80910  
 10 F-PLACE1004868  
 F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772  
 F-PLACE1004900  
 F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382  
 F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929  
 15 F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs.118910:U82130  
 F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839:AF099936  
 F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592  
 20 F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851  
 F-PLACE1004969  
 F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:235:60//Hs.27610:U34605  
 F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:  
 25 AB011147  
 F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520  
 F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831  
 F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459  
 F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159  
 30 F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943  
 F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594  
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:  
 AB011148  
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757:56//Hs.  
 35 122967:AF059569  
 F-PLACE1005077//EST//0.79:283:591//Hs.89276:AA283899  
 F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740  
 F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:  
 AB011147  
 40 F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401  
 F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//  
 8.9e-18:538:62//Hs.104640:AF000561  
 F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366  
 F-PLACE1005111//ESTs//0.66:191.63//Hs.106446:N93227  
 45 F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661  
 F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360:63//Hs.142177:  
 H11741  
 F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:72//Hs.154326:D42087  
 F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:60//Hs.128316:  
 50 AB014541  
 F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.elegans]//4.4e-126:583:99//Hs.25347:  
 AI138605  
 F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417  
 F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009  
 55 F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192:60//  
 Hs.47334:W72370  
 F-PLACE1005243  
 F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941

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F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252  
F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:98//Hs.118087:  
AB011182  
F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947  
5 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66//Hs.101642:  
X60673  
F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//0.83:239:62//Hs.80684:X62534  
F-PLACE1005313  
10 F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.elegans]//6.0e-81:459:91//Hs.146177:  
R51650  
F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794  
F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.96:510:56//Hs.159183:AB018297  
F-PLACE1005373  
15 F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348  
F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751  
F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951  
F-PLACE1005467//HOMEobox/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433  
F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925  
20 F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5e-126:744:87//Hs.23094:M19503  
F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323  
F-PLACE1005481//EST//0.27:153:-64//Hs.120066:AA707973  
F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029  
F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105  
25 F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747  
F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572  
F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335  
F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385  
F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144  
30 F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR  
[Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:W81261  
F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278  
F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436  
F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594  
F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851  
35 F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057  
F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234  
F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867  
F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991  
40 F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:  
AF083255  
F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618  
F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:  
AB007917  
F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457  
45 F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437  
F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944  
F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//  
Hs.75111:D87258  
F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302  
50 F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN  
[Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI125696  
F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493  
F-PLACE1005802  
F-PLACE1005803  
55 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315:  
AF027156  
F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:  
AF065482

F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.1e-42:  
 327:81//Hs.138404:R70986  
 F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58//Hs.75770:L41870  
 F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497  
 5 F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905  
 F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242  
 F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487  
 F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552  
 F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300  
 10 F-PLACE1005898  
 F-PLACE1005921  
 F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504  
 F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274  
 F-PLACE1005932//TYROSINE-PROTEIN KINASE EPH PRECURSOR//0.97:342:57//Hs.89839:  
 15 M18391  
 F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142  
 F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:X69978  
 F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357  
 F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468  
 20 F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:66//Hs.107747:AI357868  
 F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:  
 U13948  
 F-PLACE1005968  
 F-PLACE1005990  
 25 F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:77//Hs.42674:U61981  
 F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256  
 F-PLACE1006011  
 F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743  
 F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:64//Hs.158319:  
 30 AB018332  
 F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:X99906  
 F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395  
 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679:99//Hs.4976:  
 AF039023  
 35 F-PLACE1006129  
 F-PLACE1006139  
 F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:79//Hs.153014:AB002353  
 F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.sapiens]//2.9e-12:119:84//Hs.23153:  
 R92857  
 40 F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868  
 F-PLACE10061641//ESTs//0.099:223:60//Hs.8108:AA902721  
 F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:92//Hs.152894:AC005239  
 F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:AI074005  
 F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464:AF091433  
 45 F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608  
 F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369:88//Hs.  
 135623:AA134719  
 F-PLACE1006205  
 F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]  
 50 //0.0089:166:63//Hs.127179:AI279486  
 F-PLACE1006225  
 F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668  
 F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185  
 F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802  
 55 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3e-168:791:98//Hs.31921:  
 AB014548  
 F-PLACE1006262  
 F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.7277:AJ001625

F-PLACE1006318  
F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503  
F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:AI361492  
F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249  
5 F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481  
F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.153529:AF070581  
F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403:61//Hs.105940:  
AF004715  
F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693  
10 F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:97//Hs.22396:AF062085  
F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:74//Hs.21560:AB002296  
F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.  
15 131846:AF069735  
F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:  
AB011129  
F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//  
1.0:248:60//Hs.88219:AF060866  
F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381  
F-PLACE1006470  
20 F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//  
5.0e-46:520:71//Hs.131953:AF059194  
F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511  
F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493  
F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:  
25 56//Hs.75063:AL023584  
F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542  
F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358  
F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:AI356219  
F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784  
30 F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529  
F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:  
AB018280  
F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//  
2.2e-168:781:99//Hs.155377:U97670  
35 F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088  
F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858  
F-PLACE1006629//Homo sapiens (clone s22i71) mRNA fragment//0.097:229:63//Hs.26956:L40396  
F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:AI131473  
40 F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12:113:83//Hs.3385:N25917  
F-PLACE1006678  
F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153638:AF010403  
F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382:63//Hs.43627:  
U35612  
F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354  
45 F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152  
F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M97252  
F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:AI075783  
F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:AI051228  
F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84:95//Hs.  
50 123642:M83941  
F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:AI422017  
F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892  
F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403:56//Hs.15832:AB014518  
F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103:619:87//Hs.23094:M19503  
55 F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876  
F-PLACE1006860//EST//0.0062:206:65//Hs.158793:AI376773  
F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273  
F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268:58//Hs.5333:AB018254

F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601  
 F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI089187  
 F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443  
 F-PLACE1006917  
 5 F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913  
 F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211  
 F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565  
 F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127:L12723  
 F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]//3.2e-07:67:98//Hs.  
 10 21806:AA630312  
 F-PLACE1006962//H.sapiens ir1B mRNA//2.3e-16:202:71//Hs.135202:X63417  
 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:  
 191:67//Hs.8813:AF032922  
 F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753  
 15 F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//  
 3.1e-05:594:58//Hs.32951:AF034102  
 F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971  
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775:84//Hs.23094:M19503  
 F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.129811:AJ223957  
 20 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.75813:L33243  
 F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987  
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glyco-  
 gen storage disease type III)//0.18:268:63//Hs.904:U84010  
 F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385  
 25 F-PLACE1007112  
 F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:AI160121  
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601  
 F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965  
 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669  
 30 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204  
 F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//2.0e-58:405:87//  
 Hs.80598:D50495  
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141  
 F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467  
 35 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909  
 F-PLACE1007274  
 F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)//0.94:167:64//Hs.606:  
 L06133  
 F-PLACE1007282  
 40 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436  
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412  
 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA, complete cds//0.88:298:58//  
 Hs.144877:AF029403  
 F-PLACE1007342  
 45 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.7e-121:  
 567:98//Hs.76596:AF096870  
 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:X98173  
 F-PLACE1007375  
 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642  
 50 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287  
 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//  
 Hs.14387:AF093771  
 F-PLACE1007416  
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436  
 55 F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359  
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93//Hs.6445:L40391  
 F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714  
 F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103

F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975  
 F-PLACE1007488  
 F-PLACE1007507//ESTs//1.2e-99:274:98//Hs.123462:AA903385  
 F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503  
 5 F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296  
 F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979  
 F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468:57//Hs.113283:AF018080  
 F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:AI076755  
 10 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733:71//Hs.65238:  
 AB014561  
 F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863  
 F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257  
 F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI089163  
 15 F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778:56//Hs.33010:AB014533  
 F-PLACE1007621  
 F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867  
 F-PLACE1007645  
 F-PLACE1007649  
 20 F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266  
 F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI027055  
 F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:AI348503  
 F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63//Hs.1103:X02812  
 F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.75789:D87953  
 25 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709:97//Hs.4812:  
 AF061243  
 F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233:89//Hs.108797:  
 AA476815  
 F-PLACE1007729//ESTs, Moderately similar to RETRO VIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:  
 30 64//Hs.104129:AA923278  
 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121:  
 AB014585  
 F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424  
 F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030  
 35 F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:AI089469  
 F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656  
 F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504  
 F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107  
 F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841  
 40 F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261635  
 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396:77//Hs.23094:M19503  
 F-PLACE1007852  
 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020:  
 45 AB018309  
 F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:AI038387  
 F-PLACE1007877  
 F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943  
 F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs.  
 50 92381:AB007956  
 F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002  
 F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538  
 F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.  
 55 5671:AF084530  
 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:  
 730:98//Hs.78106:AF079529  
 F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:264:92//Hs.42222:  
 W28567  
 F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:AI097043  
 F-PLACE1008000//Homo sapiens veli 1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:AF087693

F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031  
 F-PLACE1008044  
 F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382  
 F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:  
 5 U44060  
 F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494:  
 U60975  
 F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.  
 10 100431:AF044197  
 F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769  
 F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874  
 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI218683  
 F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.1e-  
 15 20:124:95//Hs.146238:AI263135  
 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427  
 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524  
 F-PLACE1008201  
 F-PLACE1008209  
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856  
 20 25 F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385  
 F-PLACE1008273  
 F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113  
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.  
 159897:AB007970  
 25 F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.  
 4076:AF081287  
 F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071  
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:  
 AB011129  
 30 F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362  
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579  
 F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:  
 AF059569  
 F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911  
 35 40 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171  
 F-PLACE1008398  
 F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:  
 62//Hs.25674:AF072242  
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326  
 F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943  
 45 F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding  
 for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel  
 gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653  
 F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499  
 F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, epidermoid carcinoma cell line A431,  
 50 mRNA, 3 genes, 1718 nt]//0.019:530:58//Hs.72248:S72487  
 F-PLACE1008437  
 F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335  
 F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901  
 F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63//Hs.27590:AB002381  
 F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:  
 U10886  
 F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.0:304:  
 55 60//Hs.24040:AF006823  
 F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI274697  
 F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081  
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-45:507:71//Hs.8003:AC004997  
 F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.0:95:71//Hs.117546:U31767

F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:AI283069  
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175:812:98//Hs.23255:  
 AB018334  
 F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350:66//Hs.151087:  
 AA649326  
 F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794  
 F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560  
 F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458  
 F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211  
 F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394  
 F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535  
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.  
 147967:AF044333  
 F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728  
 F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit pre-  
 cursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.90443:  
 AF038406  
 F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741  
 F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080  
 F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285:69//Hs.35460:H65503  
 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503:97//Hs.6458:  
 AF060543  
 F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:68//Hs.111380:AA258772  
 F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542  
 F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:  
 376:98//Hs.7179:AF011905  
 F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883  
 F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium fal-  
 ciparum (isolate k1 / thailand)]//0.73:354:59//Hs.26322:AA156858  
 F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:AI052728  
 F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:AI221563  
 F-PLACE1008877//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503  
 F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323  
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318:  
 AB018308  
 F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W84771  
 F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026  
 F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937  
 F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:  
 U75308  
 F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950  
 F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112  
 F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762  
 F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689  
 F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689:  
 S70585  
 F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:AI239698  
 F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:AI090525  
 F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800  
 F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091  
 F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:AI337031  
 F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011  
 F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:AI040890  
 F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788  
 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//  
 1.1e-139:671:97//Hs.99742:AF035586  
 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:59//Hs.35804:D25215  
 F-PLACE1009150//Human HsLIM15 mRNA for HsLim15, complete cds//1.7e-50:440:78//Hs.37181:D64108

F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-46:440:69//Hs.  
158095:AB007953

F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:245:61//Hs.92614:  
M62302

5 F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250

F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770

F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:AI282821

F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100

10 F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//3.6e-117:588:95//Hs.54943:  
Z78396

F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689

F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131

F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.146403:M29540

F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575

15 F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//  
1.9e-21:121:98//Hs.124768:AA307735

F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338

F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411:  
59//Hs.23731:U83192

20 F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594:86//Hs.23094:M19503

F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767

F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473

F-PLACE1009368

F-PLACE1009375

25 F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81//Hs.43681:AL022394

F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M27878

F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101174:AF047863

F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210:86//Hs.3404:AF035262

F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:68//Hs.155291:D13630

30 F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:58//Hs.82128:AJ012159

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.76987:AF012872

F-PLACE1009459//H.sapiens garp gene mRNA, complete CDS//1.0:241:60//Hs.151641:Z24680

F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//  
0.00039:347:60//Hs.994:M95678

35 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//4.1e-91:464:96//Hs.155049:  
AC004531

F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:AI308839

F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:63//Hs.16165:AB002405

F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:U70728

40 F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417

F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:AI416956

F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866

F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291

F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806

45 F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:66//Hs.13889:AI341394

F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080

F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:AI074011

F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:AI094085

F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773

50 F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087

F-PLACE1009639

F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:  
AB011159

F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494

55 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534

F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN  
HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926

F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650

F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789  
F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024  
F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989  
F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-  
5 quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene  
Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER; TYK3) pseudogenes, and part of a novel gene  
similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-  
130:600:95//Hs.16411:AL030996  
F-PLACE1009845  
10 F-PLACE1009861  
F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021  
F-PLACE1009886  
F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889  
F-PLACE1009908  
15 F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717  
F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379  
F-PLACE1009925  
F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153  
F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446  
20 F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345  
F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114  
F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540  
F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:  
AB014529  
25 F-PLACE1010023  
F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878  
F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.  
142151:AA984061  
F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596  
30 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:  
AF065482  
F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424  
F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925  
35 F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus  
musculus]//1.8e-38:212:95//Hs.98067:AA236822  
F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:100:89//Hs.11469:  
U69567  
F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:  
AF020761  
40 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.  
122967:AF059569  
F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682  
F-PLACE1010134//H.sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889  
F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740  
45 F-PLACE1010152  
F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792  
F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582  
F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225:  
H69637  
50 F-PLACE1010231  
F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:  
AB007917  
F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590  
F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540  
55 F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813  
F-PLACE1010310//HOMEobox/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433  
F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248  
F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659  
 F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117  
 F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855  
 F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648  
 5 F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986  
 F-PLACE1010401  
 F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61//Hs.125257:U70824  
 F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313:  
 AF039081  
 10 F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500  
 F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100  
 F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175:  
 64//Hs.159273:AF054177  
 F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472  
 15 F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979  
 F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148  
 F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06  
 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661  
 20 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete  
 cds//9.9e-148:707:97//Hs.19851:AF045186  
 F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394  
 F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858  
 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778  
 25 F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//0.012:258:62//Hs.144375:AA484200  
 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461  
 F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225  
 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102  
 F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076  
 F-PLACE1010662  
 30 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.  
 37138:U35376  
 F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027  
 F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:  
 96//Hs.50758:AF092564  
 35 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:  
 AJ131244  
 F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391  
 F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus lae-  
 vis]//5.1e-80:407:96//Hs.80965:AA493284  
 40 F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]  
 //6.0e-45:251:94//Hs.11379:AA594140  
 F-PLACE1010786  
 F-PLACE1010800  
 F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157  
 45 F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085  
 F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1 [H.sapiens]//2.9e-28:245:79//Hs.  
 132736:AA583494  
 F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048  
 50 F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//5.8e-67:336:97//Hs.  
 130135:AA905493  
 F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244  
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:  
 AB011182  
 F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671  
 55 F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:65//Hs.1050:M85169  
 F-PLACE1010900  
 F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981  
 F-PLACE1010917

F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537  
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:98//Hs.74750:  
 AB011126  
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437:98//Hs.66392:  
 AF064244  
 F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985  
 F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154  
 F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444:59//Hs.585:X04506  
 F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632  
 F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721  
 F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931  
 F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032  
 F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179:67//Hs.1177:  
 U10886  
 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-  
 11:207:68//Hs.994:M95678  
 F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-35:310:78//Hs.2407:Z49194  
 F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228:61//  
 Hs.153640:U56998  
 F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320  
 F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663  
 F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037  
 F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317  
 F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370857  
 F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949  
 F-PLACE1011160  
 F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443  
 F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114  
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds//6.9e-  
 124:576:99//Hs.159140:AF038664  
 F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7e-101:469:99//Hs.8241:AA283057  
 F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEESL70F [C.elegans]//2.6e-62:221:  
 88//Hs.101821:W27452  
 F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751  
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4e-147:675:99//Hs.23168:  
 AB011101  
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:98//Hs.15144:AC005014  
 F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803  
 F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191:65//Hs.140950:  
 AF070637  
 F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915  
 F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160  
 F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310  
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:  
 99//Hs.5819:AF102265  
 F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs.  
 159897:AB007970  
 F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535  
 F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Raw3 [R.norvegicus]//6.7e-68:325:99//  
 Hs.107245:AA627053  
 F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868  
 F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552  
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801:  
 AB011102  
 F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557:72//Hs.23094:M19503  
 F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:AI025204  
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703:99//Hs.111138:  
 AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:  
AF065482

F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264

F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997

5 F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319

F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476

F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333

F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:  
268:86//Hs.86371:AF054180

10 F-PLACE1011586//Homo sapiens hLRpl05 mRNA for LDL receptor related protein 105, complete cds//0.98:153:  
65//Hs.143641:AB009462

F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778

F-PLACE1011641

15 F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631

F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661

F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086

F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745

F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234

20 F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366

F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350

F-PLACE1011725

F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853

F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891

25 F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240

F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693

F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660

F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664

F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775

30 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152

F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913

F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:AI357868

F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817

F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:  
35 AF059617

F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763

F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514

F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591

F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514

40 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756:  
AB018256

F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs.  
92381:AB007956

F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503

45 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330

F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627

F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831

F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627

F-PLACE2000017

50 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds//  
5.7e-85:844:72//Hs.7928:AF082557

F-PLACE2000030

F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512

F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.94653:AB011179

55 F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59//Hs.79706:U53204

F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128

F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966

F-PLACE2000061

F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:662:86//Hs.23759:M98457  
 F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:  
 AF027219  
 F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333  
 5 F-PLACE2000100  
 F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219  
 F-PLACE2000111//H.sapiens mRNA for l-acylglycerol-3-phosphate O-acyltransferase//0.76:215:65//Hs.6587:  
 U56417  
 F-PLACE2000115  
 10 F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:79//Hs.153014:AB002353  
 F-PLACE2000132  
 F-PLACE2000136//ESTS, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:  
 AA718911  
 F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U54645  
 15 F-PLACE2000164  
 F-PLACE2000170  
 F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179  
 F-PLACE2000176  
 F-PLACE2000187  
 20 F-PLACE2000216  
 F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933  
 F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:63//Hs.21560:AB002296  
 F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338  
 F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:  
 25 AB007958  
 F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522  
 F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560  
 F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869  
 F-PLACE2000317  
 30 F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:  
 M89796  
 F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088  
 F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299  
 F-PLACE2000347//ESTs, Moderately similar to F18547\_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817  
 35 F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645  
 F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045  
 F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861  
 F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032  
 F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638  
 40 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.  
 158095:AB007953  
 F-PLACE2000398  
 F-PLACE2000399  
 F-PLACE2000404  
 45 F-PLACE2000411  
 F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080  
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966  
 F-PLACE2000427  
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719  
 50 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257  
 F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2)//1.9e-  
 20:418:64//Hs.130181:X85019  
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080  
 F-PLACE2000455//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.0e-  
 55 05:100:73//Hs.104239:AA488082  
 F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241  
 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381  
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080

F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262 ,  
 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384  
 F-PLACE3000020//Prostaglandin 12 (prostacyclin) receptor (IP)//0.00081:500:61//Hs.393:D38128  
 F-PLACE3000029  
 5 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248  
 F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842  
 F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//1.0:186:62//Hs.  
 10 122752:AF026445  
 F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295  
 F-PLACE3000121  
 F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081  
 F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603  
 F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243  
 15 F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016  
 F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871  
 F-PLACE3000148  
 F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:  
 AB014572  
 F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023  
 20 F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:  
 U79666  
 F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:  
 AB011147  
 F-PLACE3000160  
 25 F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219  
 F-PLACE3000194  
 F-PLACE3000197  
 F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546  
 F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975  
 30 F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//  
 Hs.77522:X62744  
 F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216  
 F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377  
 35 F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-  
 56:200:85//Hs.133089:AF064019  
 F-PLACE3000226  
 F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568  
 F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-  
 Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene  
 40 and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and ge-  
 nomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046  
 F-PLACE3000244  
 F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858  
 F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650  
 45 F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944  
 F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770  
 F-PLACE3000310  
 F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586  
 F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219  
 50 F-PLACE3000331  
 F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:  
 AB014545  
 F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741  
 F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis ele-  
 gans]//2.9e-59:474:77//Hs.125850:AA885355  
 F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194  
 55 F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:  
 234:63//Hs.7498:U41514

F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441  
 F-PLACE3000363  
 F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928  
 F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641  
 5 F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432  
 F-PLACE3000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73919:X81637  
 F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785  
 F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270  
 F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715  
 10 F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541  
 F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:  
 116:78//Hs.77579:AF013263  
 F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:  
 H61502  
 15 F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:  
 AB018344  
 F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161  
 F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:  
 183:93//Hs.108326:AB006202  
 20 F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874  
 F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888  
 F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190  
 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:  
 AB018352  
 25 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:  
 AC004131  
 F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533  
 F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.  
 40993:AF000148  
 30 F-PLACE4000063  
 F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713  
 F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819  
 F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058  
 35 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:  
 AB007931  
 F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751  
 F-PLACE4000129  
 F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627  
 F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856  
 40 F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367  
 F-PLACE4000192  
 F-PLACE4000211  
 F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594  
 F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329  
 45 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317  
 F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding  
 mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250  
 F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609  
 F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886  
 50 F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200  
 F-PLACE4000261  
 F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:  
 100//Hs.118849:AA215645  
 F-PLACE4000270  
 55 F-PLACE4000300  
 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966  
 F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365  
 F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292  
 F-PLACE4000367  
 F-PLACE4000369  
 F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256  
 5 F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823  
 F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046  
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026:  
 AB014540  
 F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:AI275982  
 10 F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263:92//Hs.2397:Z70200  
 F-PLACE4000445  
 F-PLACE4000450  
 F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874  
 F-PLACE4000487//Sialophorin (gpL115, leukosialin, CD43)//3.0e-14:189:71//Hs.80738:X52075  
 15 F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951  
 F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289  
 F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731  
 F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECUR-  
 20 SOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022  
 F-PLACE4000548  
 F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.0035:510:59//Hs.39163:  
 AF000986  
 F-PLACE4000581  
 F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine leukemia virus (isolate 57)]//3.4e-  
 25 13:275:68//Hs.113980:AI034080  
 F-PLACE4000593//ESTS, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239:79//Hs.109084:AI004675  
 F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074  
 F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.5e-47:562:69//Hs.129685:  
 AB002446  
 30 F-PLACE4000650  
 F-PLACE4000654  
 F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132  
 F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05299  
 F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila  
 35 melanogaster]//2.5e-36:197:96//Hs.118634:U66688  
 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-148:706:98//Hs.109299:  
 AB014554  
 F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:M23254  
 F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877  
 40 F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313  
 F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-35:299:81//Hs.2407:Z49194  
 F-THYRO1000034  
 F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099  
 F-THYRO1000040//ESTs//0.30:331:59//Hs.87176:AI148326  
 45 F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63//Hs.101996:AB002345  
 F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//Hs.6654:AB014557  
 F-THYRO1000085  
 F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065  
 F-THYRO1000107  
 50 F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8e-106:690:86//Hs.23094:M19503  
 F-THYRO1000121  
 F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//Hs.103502:U70732  
 F-THYRO1000129//Homo sapiens TED protein (TED).mRNA, complete cds//2.8e-155:732:98//Hs.87619:  
 AF087142  
 55 F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203  
 F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416  
 F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs.155464:AF088219  
 F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-05:261:61//Hs.

152936:D63475  
F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:87//Hs.101238:Y11312  
F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270  
F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883  
5 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:99//Hs.43445:  
AJ005698  
F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:84//Hs.79672:  
AB014552  
F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848  
10 F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:U79297  
F-THYRO1000241//EST//0.48:102:69//Hs.160764:AI313322  
F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M27878  
F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs.60103:AB014590  
F-THYRO1000270  
15 F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500  
F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068  
F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C.elegans]//7.6e-92:431:99//Hs.  
122719:AA777803  
F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.80731:M63175  
20 F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs.12002:  
AB018333  
F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//6.9e-34:177:84//Hs.7833:  
U29091  
F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919  
25 F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs.118401:  
AB011134  
F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855  
F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.elegans]//5.8e-39:245:91//Hs.119095:  
T79413  
30 F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572  
F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238  
F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773  
F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs.155024:U00115  
F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X52520  
35 F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-22:248:76//Hs.162011:AA513663  
F-THYRO1000488  
F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200  
F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298  
F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120  
40 F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877  
F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61//  
Hs.100058:AB006713  
F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949  
F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs.  
45 151411:AF075587  
F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322  
F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331  
F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2685:Z50053  
F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081  
50 F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941  
F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125  
F-THYRO1000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs.  
116007:S79267  
F-THYRO1000662  
55 F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157  
F-THYRO1000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//5.7e-49:281:77//Hs.  
116007:S79267  
F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46:368:57//Hs.26557:AA480380

F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452  
 F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324  
 F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59//Hs.79706:U53204  
 F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085  
 5 F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74//Hs.7977:AB007871  
 F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:  
 AF061573  
 F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481  
 F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:  
 10 452:58//Hs.11538:AF006084  
 F-THYRO1000787  
 F-THYRO1000793  
 F-THYRO1000796  
 F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.4e-36:561:68//Hs.129685:  
 15 AB002446  
 F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087  
 F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339  
 F-THYRO1000843  
 F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788  
 20 F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170  
 F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-33:  
 190:75//Hs.133526:N21103  
 F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531  
 F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.  
 25 92381:AB007956  
 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.0e-179:  
 839:98//Hs.78106:AF079529  
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836  
 F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs.112432:AC005263  
 30 F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:D86963  
 F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear  
 gene encoding mitochondrial protein, complete cds//2.7e-15:123:90//Hs.106469:AF042169  
 F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907  
 F-THYRO1000983  
 35 F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646  
 F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307  
 F-THYRO1001003  
 F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369  
 F-THYRO1001033//H.sapiens mRNA for cyclin II//0.0061:287:60//Hs.3232:Z46788  
 40 F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.51048:X68830  
 F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:72//Hs.153014:AB002353  
 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end//2.1e-74:741:74//Hs.159249:Z99130  
 F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:62//Hs.124024:AF053700  
 F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416  
 45 F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425  
 F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074  
 F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788  
 F-THYRO1001173  
 F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385  
 50 F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163  
 F-THYRO1001204  
 F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219  
 F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461  
 F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:AJ002309  
 55 F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:  
 AF027156  
 F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836  
 F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182

F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872  
 F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68//Hs.153563:AF011333  
 F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545  
 F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207  
 5 F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939  
 F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79//Hs.12385:AB007877  
 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4e-157:740:97//Hs.138488:  
 AB014607  
 F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993  
 10 F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946  
 F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694  
 F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62//Hs.477:U05659  
 F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788  
 F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//4.6e-33:153:81//  
 15 Hs.102877:U41315  
 F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099  
 F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71//Hs.44782:Z82215  
 F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.51048:X68830  
 F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943  
 20 F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904  
 F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663  
 F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211  
 F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046  
 F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335  
 25 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//Hs.25306:AF070572  
 F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27655  
 F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs.75551:L12535  
 F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849  
 F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071  
 30 F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046  
 F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2e-13:108:86//Hs.141045:AA191659  
 F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:540:55//Hs.95958:  
 M91463  
 F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568  
 35 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//8.0e-166:780:98//  
 Hs.118633:AJ225089  
 F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF010238  
 F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.122908:AF070552  
 F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691  
 40 F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//2.5e-51:296:92//  
 Hs.3826:U69560  
 F-THYRO100173 8//EST//6.9e-30:180:94//Hs.58641:W81229  
 F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813  
 F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590  
 45 F-THYRO1001772//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-21:  
 182:81//Hs.118053:N75725  
 F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324  
 F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//Hs.11711:AB002295  
 F-THYRO1001828  
 50 F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823  
 F-THYRO1001895//Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288:65//Hs.  
 51061:M24283  
 F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198  
 F-VESEN1000122  
 55 F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885  
 F-Y79AA1000033  
 F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:230:66//Hs.431:L13689  
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:

U78521  
 F-Y79AA100065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680  
 F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053  
 F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//  
 5 0.0022:684:58//Hs.83190:U29344  
 F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860  
 F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.  
 9242:AF081192  
 F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079  
 10 F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623  
 F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134  
 F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365  
 F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919  
 F-Y79AA1000328  
 15 F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:  
 AF071309  
 F-Y79AA1000346  
 F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853  
 F-Y79AA1000355  
 20 F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908  
 F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897  
 F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219  
 F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018  
 25 F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:  
 AF082516  
 F-Y79AA1000480  
 F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871  
 F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521  
 30 F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356  
 F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:  
 AF068706  
 F-Y79AA1000574//Human mRNA for GC box bindig protein, complete cds//0.95:258:62//Hs.150557:D31716  
 F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:  
 AF091080  
 35 F-Y79AA10006277//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:  
 AF060503  
 F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513  
 F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:  
 40 98//Hs.83023:AF093670  
 F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969  
 F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377  
 F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067  
 F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468  
 45 F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:  
 AF098799  
 F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231  
 F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085  
 F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:  
 AF059569  
 50 F-Y79AA1000805  
 F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568  
 F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//  
 0.0048:630:57//Hs.83190:U29344  
 F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956  
 55 F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368:99//Hs.86660:AA398644  
 F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288:  
 D16815  
 F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699

F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//6.9e-69:  
 310:94//Hs.76822:AI359536  
 F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270  
 F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M23892  
 5 F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204  
 F-Y79AA1001023  
 F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329  
 F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590  
 F-Y79AA1001061//ESTs//3.3e-41:303:84//Hs.55855:AA621381  
 10 F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511  
 F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047  
 F-Y79AA1001078  
 F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.  
 55967:AF022654  
 15 F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381  
 F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293  
 F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248  
 F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646  
 F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965  
 20 F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054  
 F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436  
 F-Y79AA1001233//ESTRADOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879  
 F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and  
 IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892  
 25 F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240  
 F-Y79AA1001299//Human In1 mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847  
 F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395  
 F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555  
 F-Y79AA1001384  
 30 F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599  
 F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424:96//Hs.154221:H23167  
 F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489  
 F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683  
 F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465  
 35 F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Homo sapiens]//0.95:  
 256:63//Hs.29974:AI360447  
 F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744  
 F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659  
 F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851  
 40 F-Y79AA1001581//Cyclin-dependept kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398  
 F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783  
 F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109  
 F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426  
 F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:  
 45 AB014583  
 F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421:94//Hs.107039:W27244  
 F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385  
 F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:  
 X04526  
 50 F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302  
 F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877  
 F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:  
 609:58//Hs.77297:L76191  
 F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:AI018620  
 55 F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//Hs.113082:AB007903  
 F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079  
 F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//2.9e-62:313:  
 98//Hs.15709:W81213

F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533  
 F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142:90//Hs.103349:AI141124  
 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:67//Hs.104115:X52332  
 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62//Hs.106387:AF029778  
 5 F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173  
 F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs.  
 78501:L13720  
 F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382  
 F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611  
 10 F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943  
 F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348:88//Hs.18122:AI338045  
 F-Y79AA1002093  
 F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865  
 F-Y79AA1002115  
 15 F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395  
 F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165:90//Hs.6473:AA853955  
 F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393:62//Hs.77864:AB014538  
 F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515  
 F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldovenax]//2.3e-113:568:  
 20 96//Hs.111637:AA305890  
 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338:73//Hs.26662:U55984  
 F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477  
 F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508  
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:63//Hs.1560:D42045  
 25 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821:98//Hs.100729:  
 AB014592  
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903  
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731:  
 AB014555  
 30 F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489  
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622:97//Hs.30898:  
 AB014534  
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999  
 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete  
 35 cds//0.028:587:58//Hs.2363:L36069  
 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377  
 F-Y79AA1002399  
 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569  
 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142  
 40 F-Y79AA1002431  
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318  
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973  
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765  
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302  
 45

Homology Search Result Data 5.

- [0310] The result of the homology search of the Human Unigene using the clone sequence of 3'-end.  
 [0311] Data include

50 the name of clone,  
 title of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

- 55 [0312] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.  
 [0313] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA100005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME III [Caenorhabditis elegans]//5.6e-93:501:93//Hs.13015:AA628434  
R-HEMBA1000030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233  
R-HEMBA1000042//Archain//1:4e-45:282:89//Hs.33642:X81198  
5 R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:72//Hs.154326:D42087  
R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243340  
R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329  
R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788  
R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]//4.4e-90:502:90//Hs.  
10 55918:AA151667  
R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514:94//Hs.27197:  
AB018340  
R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435:77//Hs.153026:  
AB014540  
15 R-nnnnnnnnnnnnnnnnn//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//7.7e-92:428:  
100//Hs.126925:AA931237  
R-HEMBA1000158  
R-nnnnnnnnnnnnnnnnn//ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58:91//Hs.5570:AI377863  
R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545  
20 R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366  
R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927  
R-HEMBA1000201//Human Ini1 mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847  
R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311  
R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532  
25 R-nnnnnnnnnnnnnnnnn//EST//2.2e-100:498:96//Hs.161570:W80404  
R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70//Hs.127649:AB007874  
R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276:75//Hs.5737:  
AB007944  
R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019  
30 R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808  
R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424  
R-nnnnnnnnnnnnnnnnn//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.9e-14:208:73//Hs.93332:  
AA811920  
R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485  
35 R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962  
R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409  
R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122:67//Hs.129748:AB011099  
R-nnnnnnnnnnnnnnnnn//ESTs//7.4e-76:386:97//Hs.22276:AA191323  
40 R-nnnnnnnnnnnnnnnnn//Human Ca<sup>2+</sup>-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160:98//  
Hs.151301:U36448  
R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e-103:489:99//Hs.108881:AI018024  
R-nnnnnnnnnnnnnnnnn//ESTs//9.3e-99:472:98//Hs.163512:AA903238  
R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560  
45 R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//  
Hs.73614:U83460  
R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243  
R-HEMBA1000357//Human kpnI repeat mrna (cdna clone pcd-kpnI-4), 3' end//9.4e-89:432:87//Hs.139107:  
K00629  
R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857  
50 R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938  
R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960  
R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//  
Hs.73614:U83460  
R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878  
55 R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:AI340248  
R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]//1.1e-44:447:75//Hs.42849:N31920  
R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//6.1e-92:373:99//Hs.48675:  
AI005282

R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700  
R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140  
R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:AJ001189  
R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143  
5 R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014  
R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349  
R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316  
R-HEMBA1000460  
R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370  
10 R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155464:AF088219  
R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster  
ring canel protein. [H.sapiens]//1.1e-31:181:94//Hs.61454:AA312449  
R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528  
R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087  
15 R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571  
R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318  
R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531  
R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885  
R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414  
20 R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280  
R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:  
U15782  
R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.  
99722:AI422277  
25 R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809  
R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317  
R-nnnnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699  
R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881  
R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:  
30 W74481  
R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196  
R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128  
R-nnnnnnnnnnnnn  
R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788  
35 R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944  
R-HEMBA1000591//Homo sapiens mRNA for EIB-55kDa-associated protein//3.9e-113:591:94//Hs.155218:  
AJ007509  
R-HEMBA1000592//TYROSINE-PROTEIN KINASE  
ITK/TSK//0.024:309:61//Hs.89519:L10717  
40 R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041  
R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.  
158334:U86136  
R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424  
R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438  
45 R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:  
AA643235  
R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:  
AB014590  
R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390  
50 R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929  
R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136  
R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922  
R-HEMBA1000682//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:  
55 AI141736  
R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:  
AF057280  
R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213  
R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-COA hydratases/isomerases [C.elegans]//7.2e-113:  
5 572:95//Hs.28644:AI018612  
R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449:75//Hs.74478:  
U33931  
R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777  
R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110  
R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs.155464:AF088219  
R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131  
10 R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309:75//Hs.  
10458:AF088219  
R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612  
R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen,  
15 antigen detected by monoclonal and antibody IA4)//1.3e-48:284:90//Hs.103458:X53795  
R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:87//Hs.154326:D42087  
R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939  
R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027  
R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-  
20 44:228:98//Hs.18192:AF048977  
R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410:77//Hs.154103:AF061258  
R-HEMBA1000851  
R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284:80//Hs.159608:  
U46689  
R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:AI265794  
25 R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202  
R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608  
R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951  
R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219  
R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:AI203154  
30 R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672  
R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508  
R-HEMBA1000919  
R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597  
R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619  
35 R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:  
AB018291  
R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074  
R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:81//Hs.5247:AF029750  
R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362:84//Hs.  
40 159187:AB007977  
R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:AI363498  
R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.44766:AJ007590  
R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:AI018170  
R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878  
45 R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.147434:AI214464  
R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902  
R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:AI281881  
R-HEMBA1001007  
R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764  
50 R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:  
100//Hs.128738:AA970836  
R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587:95//Hs.158287:  
AB007937  
R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:95//Hs.58393:X05360  
55 R-HEMBA1001020//ESTs//0.52:86:72//Hs.69683:AA115292  
R-HEMBA1001022//ESTs//3.4e-18:102:100//Hs.63243:AI123912  
R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336  
R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:AI345543

R-nnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616  
 R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:79//Hs.132942:  
 AB014521  
 R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886  
 5 R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813  
 R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X14420  
 R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417:64//Hs.  
 127338:AB007961  
 R-HEMBA1001080  
 10 R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788  
 R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674  
 R-HEMBA1001094  
 R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245  
 R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs.155464:AF088219  
 15 R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974  
 R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320  
 R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:M15530  
 R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341  
 R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265  
 20 R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs.155464:AF088219  
 R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-  
 39:309:82//Hs.96337:AA225358  
 R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238:60//Hs.127338:  
 AB007961  
 25 R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896  
 R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305:  
 62//Hs.100238:U69194  
 R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080  
 R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316  
 30 R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932  
 R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728  
 R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435  
 R-nnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181  
 R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674  
 35 R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534  
 R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324  
 R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219  
 R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162  
 R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214  
 40 R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019  
 R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977  
 R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950  
 R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC  
 REGION [S.cerevisiae]//1.3e-77:458:92//Hs.9398:N41838  
 45 R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259  
 R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080  
 R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816  
 R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837  
 R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334  
 50 R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550  
 R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458  
 R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482  
 R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439  
 R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204  
 55 R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081  
 R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714  
 R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364  
 R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199  
R-HEMBA1001415  
R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82//Hs.42674:U61981  
R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704  
5 R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263  
R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982  
R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546  
R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077  
R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304:88//Hs.23094:M19503  
10 R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220  
R-HEMBA1001463  
R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66//Hs.36232:D80008  
R-HEMBA1001478  
R-HEMBA1001497  
15 R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426  
R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528:84//Hs.23094:M19503  
R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269  
R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA-702493  
R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723  
20 R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270  
R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348  
R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs.155464:AF088219  
R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324  
R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880  
25 R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030  
R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652  
R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329  
R-HEMBA1001589  
R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431:88//Hs.26625:W25874  
30 R-HEMBA1001608//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.3e-73:533:82//Hs.103948:K00627  
R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]//4.5e-93:537:90//Hs.20218:AA628530  
R-nnnnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362:60//Hs.132206:AF039694  
35 R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158  
R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623  
R-nnnnnnnnnnnnn//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442:95//Hs.63888:AA203398  
R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554  
R-HEMBA1001658  
40 R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:AF029343  
R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943  
R-HEMBA1001675  
45 R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962  
R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424  
R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916  
R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:  
50 AB014598  
R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960  
R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095  
R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus nor-  
vegicus]//1.8e-46:236:98//Hs.132948:AA194452  
55 R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs.155464:AF088219  
R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN  
SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105  
R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712

R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353  
R-HEMBA1001744  
R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623  
R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162  
5 R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145  
R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306  
R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721  
R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053  
R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243  
10 R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823  
R-nnnnnnnnnnnn/Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180:AF039019  
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//9.0e-114:548:98//Hs.  
118164:AB007969  
R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334  
15 R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179  
R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07290  
R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707  
R-nnnnnnnnnnnn//ESTs//2.2e-101:480:99//Hs.159940:AA971578  
R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210  
20 R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250  
R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513  
R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446  
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.1e-109:553:96//Hs.78946:  
AB014517  
25 R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853  
R-HEMBA1001866//Myelin oligodendrocyte glycoprotein {alternative products}//1.9e-37:357:76//Hs.53217:  
Z48051  
R-nnnnnnnnnnnn//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//2.3e-32:193:94//Hs.  
9489:R84329  
30 R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969  
R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128  
R-HEMBA1001910  
R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.5e-73:  
347:100//Hs.30991:AA994438  
35 R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//5.1e-57:320:91//Hs.  
91251:U66685  
R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706  
R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125  
R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107:  
40 534:96//Hs.154934:AF000145  
R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-  
99:482:98//Hs.96849:AA879470  
R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390  
R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668  
45 R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452  
R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866  
R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421  
R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048  
R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825  
50 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/  
Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains  
a putative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178  
R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932  
R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717  
55 R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353  
R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6e-91:448:97//Hs.5687:AJ005801  
R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930  
R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837

R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550  
R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538  
R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312  
R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-51:254:85//Hs.15731:  
5 AB011135  
R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764  
R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996  
R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354  
R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124:AF019369  
10 R-HEMBA1002113//Prostaglandin 12 (prostacyclin) synthase //1.4e-76:280:90//Hs.61333:D83402  
R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence//1.4e-87:362:94//Hs.103443:  
AF065854  
R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:AI357868  
15 R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X83957  
R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734  
R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199  
R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642  
R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337  
20 R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:  
AF023674  
R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915  
R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043  
R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081  
R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457  
25 R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete  
cds//6.0e-42:419:73//Hs.159523:AF001622  
R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:  
AB007958  
R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357  
30 R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503  
R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342  
R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315  
R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151  
R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:  
35 AB014606  
R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//  
Hs.25664:AF089814  
R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202  
R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426  
40 R-HEMBA1002257  
R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGEN-  
IC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675  
R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314  
R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595  
45 R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818  
R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679  
R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:  
AB018314  
R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822  
50 R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094  
R-nnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:  
661:93//Hs.119023:AF092563  
R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435  
R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237  
55 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954  
R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-87:429:96//Hs.13209:AI417849  
R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238AA476267  
R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:D38522

R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069  
R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085  
R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395  
R-nnnnnnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:488:95//Hs.108115:AA582193  
5 R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80//Hs.43681:AL022394  
R-HEMBA-1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs.155464:AF088219  
R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:AI188995  
R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133  
R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449  
10 R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990  
R-nnnnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:  
AJ011972  
R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715  
R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564:93//Hs.129928:  
15 AB007923  
R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700  
R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804  
R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:AI281881  
R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012  
20 R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs.32567:AF073519  
R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs.155464:AF088219  
R-nnnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587:97//Hs.151411:  
AF075587  
R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904  
25 R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838  
R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055  
R-HEMBA1002621  
R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380:97//Hs.91338:  
AB018351  
30 R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881  
R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA39815  
R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041  
R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970  
35 R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, com-  
plete cds//1.5e-53:406:81//Hs.108966:U48696  
R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:  
AB018307  
R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945  
R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-  
40 104:560:92//Hs.161748:T64896  
R-nnnnnnnnnnnn//EST//0.15:136:69//Hs.129570:AA995396  
R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282  
R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477  
R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302:86//Hs.15519:  
45 AB018315  
R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884  
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:  
AB014521  
R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168  
50 R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163  
R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526  
R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:AI375792  
R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090  
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545:95//Hs.74750:  
55 AB011126  
R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127  
R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491  
R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58//Hs.48824:D87717

R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75//Hs.153563:AF011333  
R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709  
R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320  
R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116:559:97//Hs.28307:  
5 AF071185  
R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//Hs.79706:U53204  
R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013  
R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25:137:98//Hs.  
10 5337:AA243757  
R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514  
R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830  
R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827  
R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670  
R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//  
15 Hs.33787:AF037261  
R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011  
R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820  
R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087  
R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481  
20 R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165  
R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679  
R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732  
R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:AI190892  
R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085  
25 R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369  
R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI000405  
R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579  
R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219  
R-nnnnnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064  
30 R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113:560:  
96//Hs.125749:AI377682  
R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:290:85//Hs. 113283:AF018080  
R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480  
R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577  
35 R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827  
R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366  
R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN  
CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:79//Hs.114905:AA088442  
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-  
40 119:578:97//Hs.44097:AF054182  
R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627  
R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238  
R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903  
R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:99//Hs.14146:W92235  
45 R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402  
R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249  
R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219  
R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223  
R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//  
50 Hs.104800:AA709155  
R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624  
R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058  
R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.  
118717:U86751  
55 R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:AI370845  
R-HEMBA1003136//ESTs, Weakly similar to MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharo-  
myces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615  
R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219



R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734  
 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522  
 R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058  
 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.  
 5 58598:AA625440  
 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099  
 R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892  
 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065  
 R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212  
 10 R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087  
 R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042  
 R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374  
 R-HEMBA1003615  
 R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167  
 15 R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387  
 R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888  
 R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021  
 R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//9.3e-24:  
 189:84//Hs.142208:AA209438  
 20 R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830  
 R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010  
 R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783  
 R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.  
 67619:AB007957  
 25 R-HEMBA1003662//Human TBX2 (TXB2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049  
 R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635  
 R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs.  
 9489:R84329  
 R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083  
 30 R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.  
 22934:AA581379  
 R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916  
 R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:  
 M29873  
 35 R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064  
 R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.  
 1139:X77777  
 R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080  
 R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.2e-  
 40 33:377:74//Hs.24040:AF006823  
 R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847  
 R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839  
 R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592  
 R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:AI147040  
 45 R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247  
 R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089  
 R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT  
 [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214  
 R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327  
 50 R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600  
 R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236  
 R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:AI357868  
 R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295  
 R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344  
 55 R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163  
 R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:AF088219  
 R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium  
 tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333

R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161  
R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033  
R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547  
R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911  
5 R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//Hs.61408:AF070621  
R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930  
R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF068179  
R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788  
10 R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187  
R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659  
R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276:81//Hs.72660:AB011157  
R-HEMBA1003939  
15 R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669  
R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545  
R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591  
R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562  
R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253  
R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525  
20 R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882  
R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-91:  
448:97//Hs.117834:AA766771  
R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756  
R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:81//Hs.150275:D87682  
25 R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105  
R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899  
R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011  
R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774  
R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461  
30 R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191  
R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253  
R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens]//1.5e-22:365:70//Hs.99692:AA811804  
R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469  
R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M11717  
35 R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754  
R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080  
R-HEMBA1004074//EST//1.0:152:61//Hs.149093:AI243988  
R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652  
R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251  
40 R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:D50918  
R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562  
R-HEMBA1004133  
R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736  
R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320  
45 R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs.155464:AF088219  
R-HEMBA1004150//GRANCALCIN//0.99:357:59//Hs.79381:M81637  
R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087  
R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96//Hs.59988:AF067855  
R-HEMBA1004199  
50 R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701  
R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552:94//Hs.  
10092:AI189282  
R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:  
AB014518  
55 R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748  
R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617  
R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.0e-  
16:117:91//Hs.92033:AA255832

R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353  
R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389  
R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258  
R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221:86//Hs.7089:W37284  
R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962  
R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//1.4e-89:465:95//Hs.113660:D20018  
R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931  
10 R-nnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:AF091081  
R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-92:559:89//Hs.28298:AA203228  
R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101766:AF022795  
15 R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884:U13061  
R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.6e-93:496:94//Hs.14337:AA534961  
20 R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426  
R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679  
R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199:X16281  
R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904  
25 R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714  
R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561  
R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231  
R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336  
R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240  
30 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:D89667  
R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353  
R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494  
35 R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869  
R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057  
R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264  
R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084  
R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219  
R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717  
40 R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933  
R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:AI123518  
R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503  
45 R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829  
R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033  
R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172  
R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306  
R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034  
50 R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941  
R-HEMBA1004507  
R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTER-GENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271  
R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:  
55 281:89//Hs.58414:AA196947  
R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972  
R-HEMBA1004554  
R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924

R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913  
 R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243  
 R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769  
 R-nnnnnnnnnnnnn//ESTs//6.0e-22:190:82//Hs.42530:N41661  
 5 R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767  
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327:85//Hs.  
 159897:AB007970  
 R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:AI375915  
 R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785  
 10 R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152  
 R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III  
 [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12263:AA282393  
 R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:AI278454  
 15 R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442  
 R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348  
 R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI057560  
 R-HEMBA1004672//EST//6.7-e-76:315:97//Hs.20821:R19368  
 R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI093252  
 R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562  
 20 R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA599042  
 R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:AI281881  
 R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs.155464:AF088219  
 R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:AI309235  
 R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequencer//2.1e-44:467:73//Hs.91916:AF035317  
 25 R-HEMBA1004733//EST//0.99:84:65//Hs.161372:AI423151  
 R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275  
 R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//9.5e-39:296:  
 82//Hs.51187:U82828  
 R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651  
 30 R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:AI279428  
 R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081  
 R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L06498  
 R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679  
 R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI049504  
 35 R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380  
 R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//  
 1.4e-47:379:81//Hs.141273:H66705  
 R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092  
 R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633  
 40 R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476  
 R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167  
 R-nnnnnnnnnnnnn  
 R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732  
 R-HEMBA1004806  
 45 R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N47676  
 R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI053784  
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:  
 M74002  
 R-HEMBA1004847  
 50 R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120  
 R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267  
 R-HEMBA1004864  
 R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362  
 R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409  
 55 R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676  
 R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:AI357470  
 R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011  
 R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:89//Hs.40100:AB002390

R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388  
 R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053  
 R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:  
 80//Hs.1361:M55053  
 5 R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:AI422883  
 R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215  
 R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434  
 R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007  
 R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074  
 10 R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040  
 R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035  
 R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065  
 R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404  
 R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.  
 15 129734:AJ001683  
 R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329  
 R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894  
 R-HEMBA1004995  
 R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520  
 20 R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212  
 R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:  
 AB014548  
 R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//  
 25 8.4e-95:491:94//Hs.16085:AI261382  
 R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:85//Hs.22271:D26067  
 R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443:78//Hs.139019:N99348  
 R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542:87//  
 Hs.16258:AI376436  
 R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145  
 30 R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451  
 R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.79385:U90905  
 R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789  
 R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U17077  
 R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958  
 35 R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545:96//Hs.11170:  
 AF080561  
 R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739  
 R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952  
 R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85//Hs.19949:X98173  
 40 R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394:75//Hs.  
 67619:AB007957  
 R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362:77//Hs.132206:  
 AF039694  
 R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397  
 45 R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914  
 R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766  
 R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239  
 R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191:  
 61//Hs.26931:AF061836  
 50 R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284  
 R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687  
 R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W84331  
 R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834  
 R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393896  
 55 R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1e-49:277:93//Hs.72660:AB011157  
 R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA668862  
 R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391  
 R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611

R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750  
R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs.155464:AF088219  
R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519  
R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046  
5 R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169  
R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472  
R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606  
R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI341467  
R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.  
10 129735:AF010144  
R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350  
R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653  
R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305  
15 R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.54486:X54150  
R-HEMBA1005394//ESTs, Weakly similar to coded for by *C. elegans* cDNA yk30b3.5 [*C.elegans*]//4.0e-88:489:  
92//Hs.43864:AA131568  
R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278  
R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725  
R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059  
20 R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757  
R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:  
453:99//Hs.4854:AF041248  
R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960  
R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//Hs.6445:L40391  
25 R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961  
R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494  
R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353  
R-HEMBA1005472//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//8.4e-73:464:87//Hs.103948:  
K00627  
30 R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445  
R-HEMBA1005497  
R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788  
R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//  
Hs.62608:S58544  
35 R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870  
R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [*C.elegans*]//2.6e-82:387:99//Hs.67466:  
AI219740  
R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322  
R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045  
40 R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981  
R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788  
R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [*Saccharomyces cerevisiae*]//8.6e-115:578:95//Hs.  
17035:AI080471  
R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350  
45 R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926  
R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627  
R-HEMBA1005558//ESTs, Weakly similar to unknown [*S.cerevisiae*]//5.3e-77:439:91//Hs.22897:R43193  
R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [*H.sapiens*]//3.4e-31:  
182:76//Hs.133526:N21103  
50 R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709  
R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497  
R-HEMBA1005577  
R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64//Hs.57929:AB011538  
R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392  
55 R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539  
R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990  
R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905  
R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820

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R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA573125  
R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390  
R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422  
R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//2.8e-95:539:92//Hs.  
5 19400:AA662845  
R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5e-38:317:78//Hs.1721:X58377  
R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:65//Hs.15245:AF041081  
R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA731522  
R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234:80//Hs.  
10 10458:AF088219  
R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973  
R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI279477  
R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:322:88//Hs.82193:M13450  
R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343:81//Hs.154103:AF061258  
15 R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235:64//Hs.159437:  
U44060  
R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//  
1.7e-47:376:84//Hs.26988:U66406  
R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055  
20 R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI159943  
R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)//1.2e-45:398:79//Hs.155481:  
AJ006470  
R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815  
R-nnnnnnnnnnnnn//EST//0.098:125:68//Hs.136945:AA765672  
25 R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096  
R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:  
U21936  
R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974  
R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.  
30 10458:AF088219  
R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:AI038601  
R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960  
R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI039201  
R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI080618  
35 R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911  
R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917  
R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970  
R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:AI022252  
R-HEMBA1005894  
40 R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:AI215686  
R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI076363  
R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632  
R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446:75//Hs.59403:  
AB011098  
45 R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867  
R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:AI199418  
R-HEMBA1005963  
R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.  
26285:AF082516  
50 R-HEMBA1005991//Human antisecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199  
R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:AI080618  
R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:AI379875  
R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436  
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268  
55 R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951  
R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508  
R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490  
R-nnnnnnnnnnnn

R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612  
 R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517  
 R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313  
 R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//  
 5 Hs.73614:U83460  
 R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297  
 R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293  
 R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931  
 R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635  
 10 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:  
 AB007958  
 R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542  
 R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212  
 R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930  
 15 R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627  
 R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906  
 R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125  
 R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557  
 R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//  
 20 Hs.23617:AA928683  
 R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522  
 R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:  
 AF083384  
 R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881  
 25 R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]//1.2e-97:529:93//Hs.  
 10552:AA524401  
 R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//2.7e-88:484:  
 92//Hs.104129:AA923278  
 R-nnnnnnnnnnnn//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770  
 30 R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.  
 cerevisiae]//1.6e-66:377:91//Hs.108674:W25821  
 R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735  
 R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019  
 R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037  
 35 R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:  
 U33931  
 R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculus]//5.6e-76:417:94//Hs.111754:  
 AI204587  
 R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219  
 40 R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184  
 R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204  
 R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:AI417075  
 R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382  
 45 R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008  
 R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787  
 R-HEMBA1006377//EST//0.0097:145:621//Hs.133027:AI049830  
 R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:  
 AB011166  
 50 R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651  
 R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:5 82:84//Hs.23094:M19503  
 R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923  
 R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778  
 R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878  
 55 R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004  
 R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964  
 R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380  
 R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033